5'-most EST	uC-osflcyp141f09a1
Seq. No.	388032
Contig ID	8342_1.R1084
5'-most EST	uC-osrocyp007b02a1
Method	BLASTX
NCBI GI	g4115377
BLAST score	182
E value	1.0e-13
Match length	67
% identity	61
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.	388033
Contig ID	8345_1.R1084
5'-most EST	LIB3431-059-P1-K1-F6
Method	BLASTN
NCBI GI	g3819233
BLAST score	73
E value	2.0e-32
Match length	213
% identity	86
NCBI Description	Hordeum vulgare partial mRNA; clone cMWG0770
Seq. No.	388034
Contig ID	8351_1.R1084
5'-most EST	LIB3431-059-P1-K1-G7
Method	BLASTX
NCBI GI	g3450889
BLAST score	454
E value	6.0e-45
Match length	208
% identity	58
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.	388035
Contig ID	8363_1.R1084
5'-most EST	LIB3431-059-P1-K1-H9
Method	BLASTX
NCBI GI	g3894197
BLAST score	412
E value	5.0e-40
Match length	167
% identity	47
NCBI Description	(AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.	388036
Contig ID	8371_1.R1084
5'-most EST	g569042
Method	BLASTX
NCBI GI	g5262202
BLAST score	353
E value	2.0e-42
Match length	273
% identity	39
NCBI Description	(AL080252) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	388037
Contig ID	8379_1.R1084
5'-most EST	g2431528
Seq. No.	388038
Contig ID	8380_1.R1084
5'-most EST	g2275928
Seq. No.	388039
Contig ID	8394_1.R1084
5'-most EST	LIB3431-060-P1-K1-D11
Seq. No.	388040
Contig ID	8403_1.R1084
5'-most EST	uC-osf1M202053d09b1
Method	BLASTX
NCBI GI	g5640111
BLAST score	360
E value	6.0e-34
Match length	177
% identity	47
NCBI Description	(AJ243875) RAD23 protein [Lycopersicon esculentum]
Seq. No.	388041
Contig ID	8404_1.R1084
5'-most EST	LIB3434-016-P1-K1-E10
Seq. No.	388042
Contig ID	8406_1.R1084
5'-most EST	LIB3431-060-P1-K1-E3
Method	BLASTX
NCBI GI	g4127456
BLAST score	192
E value	2.0e-14
Match length	48
% identity	46
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]
Seq. No.	388043
Contig ID	8451_1.R1084
5'-most EST	LIB3431-061-P1-K1-A6
Method	BLASTX
NCBI GI	g606751
BLAST score	194
E value	2.0e-14
Match length	121
% identity	39
NCBI Description	(L34934) RNA binding protein [Drosophila melanogaster]
Seq. No.	388044
Contig ID	8460_1.R1084
5'-most EST	LIB3431-061-P1-K1-B6
Method	BLASTX
NCBI GI	g3786016
BLAST score	571
E value	3.0e-85
Match length	332

% identity	56
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]
Seq. No.	388045
Contig ID	8463_1.R1084
5'-most EST	uC-osrocyp015g03b1
Seq. No.	388046
Contig ID	8464_1.R1084
5'-most EST	LIB3431-061-P1-K1-C1
Seq. No.	388047
Contig ID	8473_1.R1084
5'-most EST	uC-osflM202014b05b1
Method	BLASTX
NCBI GI	g4850382
BLAST score	147
E value	9.0e-09
Match length	69
% identity	43
NCBI Description	(AC007357) Similar to gb_D38124 EREBP-3 from Nicotiana tabacum and contains PF_00847 AP2 domain. [Arabidopsis thaliana]
Seq. No.	388048
Contig ID	8481_1.R1084
5'-most EST	LIB3431-061-P1-K1-D5
Method	BLASTX
NCBI GI	g4115913
BLAST score	236
E value	2.0e-19
Match length	78
% identity	54
NCBI Description	(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_ (AL049524) putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana]
Seq. No.	388049
Contig ID	8486_1.R1084
5'-most EST	g1632063
Method	BLASTX
NCBI GI	g4803924
BLAST score	956
E value	1.0e-103
Match length	253
% identity	74
NCBI Description	(AC006264) putative ER lumen protein retaining receptor [Arabidopsis thaliana]
Seq. No.	388050
Contig ID	8486_2.R1084
5'-most EST	uC-osroM202003b06a2
Seq. No.	388051

Contig ID	8487_1.R1084
5'-most EST	uC-osflcyp144h09b1
Method	BLASTX
NCBI GI	g2492519
BLAST score	1290
E value	1.0e-149
Match length	277
% identity	97
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No.	388052
Contig ID	8488_1.R1084
5'-most EST	g4715200

Seq. No.	388053
Contig ID	8489_1.R1084
5'-most EST	LIB3431-061-P1-K1-E12
Method	BLASTX
NCBI GI	g3135751
BLAST score	398
E value	1.0e-38
Match length	79
% identity	95
NCBI Description	(AJ006095) 26S protease regulatory subunit 6 [Cicer arietinum]

Seq. No.	388054
Contig ID	8492_2.R1084
5'-most EST	g2427952
Method	BLASTX
NCBI GI	g1076316
BLAST score	218
E value	5.0e-21
Match length	167
% identity	41
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	388055
Contig ID	8497_1.R1084
5'-most EST	LIB3432-022-P1-K1-E7
Method	BLASTX
NCBI GI	g3775987
BLAST score	844
E value	2.0e-90
Match length	231
% identity	69
NCBI Description	(AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.	388056
Contig ID	8500_2.R1084
5'-most EST	LIB3432-040-P1-K1-A4
Method	BLASTX
NCBI GI	g2653558

BLAST score	841
E value	3.0e-90
Match length	226
% identity	75
NCBI Description	(D50679) ferredoxin-sulfite reductase precursor [Zea mays]

Seq. No.	388057
Contig ID	8505_1.R1084
5'-most EST	LIB3431-061-P1-K1-F9
Method	BLASTN
NCBI GI	g6015437
BLAST score	40
E value	1.0e-12
Match length	51
% identity	67
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388058
Contig ID	8513_1.R1084
5'-most EST	LIB3431-061-P1-K1-G5

Seq. No.	388059
Contig ID	8515_1.R1084
5'-most EST	uC-osflm202099a01b1
Method	BLASTX
NCBI GI	g5931694
BLAST score	870
E value	1.0e-93
Match length	275
% identity	52
NCBI Description	(Y18470) Exportin1 (XPO1) protein [Arabidopsis thaliana]

Seq. No.	388060
Contig ID	8519_1.R1084
5'-most EST	g286845
Method	BLASTN
NCBI GI	g949979
BLAST score	56
E value	2.0e-22
Match length	185
% identity	83
NCBI Description	Z.mays Glossy2 locus DNA

Seq. No.	388061
Contig ID	8521_1.R1084
5'-most EST	g426261
Method	BLASTX
NCBI GI	g2435511
BLAST score	474
E value	3.0e-77
Match length	195
% identity	72
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	388062
Contig ID	8524_1.R1084

5'-most EST	LIB3432-016-P1-K1-D11
Method	BLASTX
NCBI GI	g1483213
BLAST score	601
E value	2.0e-65
Match length	236
% identity	54
NCBI Description	(X96480) PAC [Arabidopsis thaliana] >gi_5729705_gb_AAD48512.1_AC007927_2 (AC007927) pale cress protein [Arabidopsis thaliana]

Seq. No.	388063
Contig ID	8529_1.R1084
5'-most EST	LIB3431-062-P1-K1-A11

Seq. No.	388064
Contig ID	8545_1.R1084
5'-most EST	g3768130
Method	BLASTX
NCBI GI	g4982498
BLAST score	337
E value	2.0e-64
Match length	267
% identity	43
NCBI Description	(AC000107) F17F8.4 [Arabidopsis thaliana]

Seq. No.	388065
Contig ID	8546_1.R1084
5'-most EST	g3763386
Method	BLASTX
NCBI GI	g5091520
BLAST score	432
E value	2.0e-42
Match length	89
% identity	100
NCBI Description	(AB023482) ESTs AU058081(E30812),AU058365(E50679), AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome 37kD subunit.(X96974) [Oryza sativa]

Seq. No.	388066
Contig ID	8546_2.R1084
5'-most EST	LIB3431-062-P1-K1-C12
Method	BLASTX
NCBI GI	g5091520
BLAST score	499
E value	4.0e-59
Match length	165
% identity	73
NCBI Description	(AB023482) ESTs AU058081(E30812),AU058365(E50679), AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome 37kD subunit.(X96974) [Oryza sativa]

Seq. No.	388067
Contig ID	8547_1.R1084
5'-most EST	LIB3431-062-P1-K1-C2

Seq. No.	388068
Contig ID	8571_1.R1084
5'-most EST	LIB3431-062-P1-K1-E6
Method	BLASTX
NCBI GI	g4512705
BLAST score	604
E value	1.0e-62
Match length	167
% identity	74
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	388069
Contig ID	8614_1.R1084
5'-most EST	uC-osflcyp092a12b1
Method	BLASTX
NCBI GI	g3786010
BLAST score	151
E value	2.0e-09
Match length	202
% identity	30
NCBI Description	(AC005499) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	388070
Contig ID	8616_1.R1084
5'-most EST	uC-osflm202110a03b1
Method	BLASTX
NCBI GI	g4220533
BLAST score	405
E value	2.0e-39
Match length	158
% identity	55
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	388071
Contig ID	8619_1.R1084
5'-most EST	LIB3434-047-P1-K1-G4

Seq. No.	388072
Contig ID	8622_1.R1084
5'-most EST	LIB3431-063-P1-K1-B7

Seq. No.	388073
Contig ID	8639_1.R1084
5'-most EST	g2309724

Seq. No.	388074
Contig ID	8643_1.R1084
5'-most EST	g5607349

Seq. No.	388075
Contig ID	8645_1.R1084
5'-most EST	LIB3431-063-P1-K1-E10

Seq. No.	388076
Contig ID	8648_1.R1084
5'-most EST	LIB3431-063-P1-K1-E2

Seq. No.	388077
Contig ID	8669_1.R1084
5'-most EST	uC-osflcyp033f11b1

Seq. No.	388078
Contig ID	8671_1.R1084
5'-most EST	uC-osrocyp017g10b1
Method	BLASTX
NCBI GI	g2688828
BLAST score	203
E value	6.0e-19
Match length	165
% identity	41
NCBI Description	(U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No.	388079
Contig ID	8676_1.R1084
5'-most EST	g2309884
Method	BLASTX
NCBI GI	g4204265
BLAST score	781
E value	7.0e-83
Match length	257
% identity	62
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	388080
Contig ID	8681_1.R1084
5'-most EST	g4879567
Method	BLASTX
NCBI GI	g5903036
BLAST score	363
E value	1.0e-36
Match length	181
% identity	47
NCBI Description	(AC008016) F6D8.5 [Arabidopsis thaliana]

Seq. No.	388081
Contig ID	8681_2.R1084
5'-most EST	uC-osroM202019g04b1
Method	BLASTX
NCBI GI	g5903036
BLAST score	428
E value	5.0e-42
Match length	118
% identity	69
NCBI Description	(AC008016) F6D8.5 [Arabidopsis thaliana]

Seq. No.	388082
Contig ID	8698_1.R1084
5'-most EST	g2427302
Method	BLASTX

NCBI GI	g3660469
BLAST score	1815
E value	0.0e+00
Match length	410
% identity	86
NCBI Description	(AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No.	388083
Contig ID	8707_1.R1084
5'-most EST	LIB3431-031-P1-K1-E2

Seq. No.	388084
Contig ID	8713_1.R1084
5'-most EST	LIB3433-042-P1-K1-F8
Method	BLASTX
NCBI GI	g2944178
BLAST score	991
E value	1.0e-107
Match length	290
% identity	68
NCBI Description	(AF007778) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	388085
Contig ID	8719_1.R1084
5'-most EST	LIB3432-013-P1-K1-C3
Method	BLASTX
NCBI GI	g3643605
BLAST score	154
E value	6.0e-10
Match length	59
% identity	51
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388086
Contig ID	8724_1.R1084
5'-most EST	LIB3431-031-P1-K1-H1

Seq. No.	388087
Contig ID	8732_2.R1084
5'-most EST	LIB3431-022-P1-K1-D11
Method	BLASTX
NCBI GI	g3935175
BLAST score	326
E value	4.0e-30
Match length	84
% identity	76
NCBI Description	(AC004557) F17L21.18 [Arabidopsis thaliana]

Seq. No.	388088
Contig ID	8788_1.R1084
5'-most EST	g702099

Seq. No.	388089
Contig ID	8799_1.R1084

5'-most EST	uC-osflcyp012e10b1
Method	BLASTX
NCBI GI	g114009
BLAST score	157
E value	5.0e-10
Match length	61
% identity	48
NCBI Description	APAG PROTEIN >gi_72927_pir__BVECAG apaG protein - Escherichia coli >gi_40918_emb_CAA28418_ (X04711) URF (apaG) (AA 1-375) [Escherichia coli] >gi_216475_dbj_BAA01326_ (D10483) apaG protein [Escherichia coli] >gi_1786235 (AE000115) orf, hypothetical protein [Escherichia coli]

Seq. No.	388090
Contig ID	8814_1.R1084
5'-most EST	uC-osflcyp106a07b1

Seq. No.	388091
Contig ID	8854_1.R1084
5'-most EST	g3106485
Method	BLASTX
NCBI GI	g1773295
BLAST score	177
E value	1.0e-19
Match length	115
% identity	51
NCBI Description	(U76707) regulatory protein NPR1 [Arabidopsis thaliana] >gi_1916912 (U87794) transcription factor inhibitor I kappa B homolog [Arabidopsis thaliana]

Seq. No.	388092
Contig ID	8856_1.R1084
5'-most EST	uC-osflcyp116f07a1

Seq. No.	388093
Contig ID	8871_1.R1084
5'-most EST	g5003189
Method	BLASTX
NCBI GI	g6094303
BLAST score	930
E value	1.0e-112
Match length	304
% identity	66
NCBI Description	SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE) (SECYS-MT) >gi_4006848_emb_CAA10368_ (AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	388094
Contig ID	8871_2.R1084
5'-most EST	uC-osflcyp081c11b1
Method	BLASTX
NCBI GI	g6094303
BLAST score	251
E value	3.0e-48
Match length	165
% identity	64

NCBI Description	SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE) (SECYS-MT) >gi_4006848_emb_CAA10368_ (AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	388095
Contig ID	8871_3.R1084
5'-most EST	g427023
Method	BLASTX
NCBI GI	g6094303
BLAST score	141
E value	1.0e-08
Match length	50
% identity	60
NCBI Description	SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE) (SECYS-MT) >gi_4006848_emb_CAA10368_ (AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	388096
Contig ID	8873_1.R1084
5'-most EST	uC-osflm202107c05b1
Method	BLASTX
NCBI GI	g3319357
BLAST score	698
E value	1.0e-133
Match length	480
% identity	58
NCBI Description	(AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]

Seq. No.	388097
Contig ID	8876_1.R1084
5'-most EST	uC-osflM202097f10b1

Seq. No.	388098
Contig ID	8881_1.R1084
5'-most EST	uC-osflcyp141b09b1

Seq. No.	388099
Contig ID	8882_1.R1084
5'-most EST	LIB3474-009-P1-K1-D5
Method	BLASTN
NCBI GI	g4096078
BLAST score	44
E value	3.0e-15
Match length	68
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	388100
Contig ID	8887_1.R1084
5'-most EST	LIB3434-009-P1-K1-F5
Method	BLASTX
NCBI GI	g1709128
BLAST score	707
E value	1.0e-110
Match length	227

% identity	85
NCBI Description	GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-2 >gi_481019_pir__S37643 protein kinase MSK-2 (EC 2.7.1.-) - alfalfa >gi_313146_emb_CAA48473_ (X68410) protein kinase [Medicago sativa]
Seq. No.	388101
Contig ID	8887_2.R1084
5'-most EST	g2317349
Method	BLASTX
NCBI GI	g1709129
BLAST score	608
E value	2.0e-98
Match length	213
% identity	85
NCBI Description	GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3 >gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) - alfalfa >gi_313148_emb_CAA48472_ (X68409) protein kinase [Medicago sativa]
Seq. No.	388102
Contig ID	8895_1.R1084
5'-most EST	LIB3431-035-P1-K1-A5
Method	BLASTX
NCBI GI	g3786009
BLAST score	542
E value	2.0e-58
Match length	192
% identity	66
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.	388103
Contig ID	8896_1.R1084
5'-most EST	uC-osflcyp121h12b1
Seq. No.	388104
Contig ID	8935_1.R1084
5'-most EST	LIB3432-006-P1-K1-D6
Seq. No.	388105
Contig ID	8941_1.R1084
5'-most EST	g699702
Method	BLASTX
NCBI GI	g3355476
BLAST score	314
E value	5.0e-44
Match length	133
% identity	65
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.	388106
Contig ID	8948_1.R1084
5'-most EST	uC-osrocyp007c10b1
Method	BLASTX
NCBI GI	g4049341
BLAST score	557
E value	1.0e-112

Match length	336
% identity	66
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	388107
Contig ID	8948_2.R1084
5'-most EST	LIB3474-012-P1-K1-H5

Seq. No.	388108
Contig ID	8961_1.R1084
5'-most EST	LIB3434-035-P1-K1-D11
Method	BLASTX
NCBI GI	g100099
BLAST score	672
E value	1.0e-70
Match length	176
% identity	75
NCBI Description	DNA-binding protein VBP1 - fava bean >gi_1372966 (M81827) CREB-like protein [Vicia faba]

Seq. No.	388109
Contig ID	8971_1.R1084
5'-most EST	LIB3431-035-P1-K1-H7

Seq. No.	388110
Contig ID	8979_1.R1084
5'-most EST	LIB3431-036-P1-K1-A3

Seq. No.	388111
Contig ID	8996_1.R1084
5'-most EST	g5667482

Seq. No.	388112
Contig ID	8998_1.R1084
5'-most EST	LIB3431-037-P1-K1-E10
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	36
% identity	59
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388113
Contig ID	9001_1.R1084
5'-most EST	LIB3431-036-P1-K1-C2
Method	BLASTX
NCBI GI	g3914467
BLAST score	778
E value	5.0e-83
Match length	198
% identity	79
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum]

Seq. No. 388114

Contig ID	9002_1.R1084
5'-most EST	LIB3434-064-P1-K1-A4
Method	BLASTX
NCBI GI	g1762309
BLAST score	268
E value	2.0e-23
Match length	62
% identity	90
NCBI Description	(U53345) AP-1 Golgi-related complex component; clathrin coated vesicles; clathrin assembly protein [Camptotheca acuminata]

Seq. No.	388115
Contig ID	9004_1.R1084
5'-most EST	LIB3431-036-P1-K1-C5
Method	BLASTX
NCBI GI	g119784
BLAST score	443
E value	3.0e-48
Match length	115
% identity	87
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_100555_pir__A39356 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chloroplast - barley >gi_167065 (M60410) beta-ketoacyl-ACP synthase I [Hordeum vulgare]

Seq. No.	388116
Contig ID	9006_1.R1084
5'-most EST	LIB3474-001-P1-K1-F12
Method	BLASTX
NCBI GI	g4097547
BLAST score	260
E value	3.0e-22
Match length	124
% identity	31
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	388117
Contig ID	9025_1.R1084
5'-most EST	LIB3433-047-P1-K1-C7
Method	BLASTX
NCBI GI	g2944180
BLAST score	458
E value	2.0e-45
Match length	116
% identity	75
NCBI Description	(AF007779) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	388118
Contig ID	9041_1.R1084
5'-most EST	LIB3434-054-P1-K1-D12
Method	BLASTX
NCBI GI	g2130052
BLAST score	1028

E value	1.0e-112
Match length	211
% identity	91
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296809_emb_CAA64545_ (X95257) xylose isomerase [Hordeum vulgare]

Seq. No.	388119
Contig ID	9064_1.R1084
5'-most EST	uC-osflcyp151a08b1
Method	BLASTX
NCBI GI	g3738332
BLAST score	155
E value	7.0e-10
Match length	215
% identity	26
NCBI Description	(AC005170) putative eukaryotic initiation factor [Arabidopsis thaliana]

Seq. No.	388120
Contig ID	9088_1.R1084
5'-most EST	g701906
Method	BLASTX
NCBI GI	g5882720
BLAST score	347
E value	1.0e-32
Match length	119
% identity	60
NCBI Description	(AC008263) Similar to gb_D86180 phosphoribosylanthranilate transferase from Pisum sativum and contains 2 PF_00168 C2 (phospholipid binding) domains. ESTs gb_H76726, gb_T45544 and gb_N96377 come from this gene. [Arab

Seq. No.	388121
Contig ID	9093_1.R1084
5'-most EST	LIB3431-037-P1-K1-D2

Seq. No.	388122
Contig ID	9108_1.R1084
5'-most EST	LIB3432-028-P1-K1-H8
Method	BLASTX
NCBI GI	g402753
BLAST score	1639
E value	0.0e+00
Match length	360
% identity	86
NCBI Description	(X71439) translation elongation factor EF-G [Glycine max]

Seq. No.	388123
Contig ID	9121_1.R1084
5'-most EST	LIB3431-037-P1-K1-G10
Method	BLASTX
NCBI GI	g2347100
BLAST score	1203
E value	1.0e-132
Match length	272
% identity	85

NCBI Description	(U76846) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4567196_gb_AAD23612.1_AC007168_3 (AC007168) putative ubiquitin-specific protease [Arabidopsis thaliana]
Seq. No.	388124
Contig ID	9146_1.R1084
5'-most EST	uC-osflM202068f02b1
Method	BLASTX
NCBI GI	g2129826
BLAST score	964
E value	0.0e+00
Match length	497
% identity	81
NCBI Description	dynamin-like protein phragmoplastin 5 - soybean >gi_1218004 (U36430) SDL5A [Glycine max]
Seq. No.	388125
Contig ID	9148_1.R1084
5'-most EST	LIB3431-042-P1-K1-A8
Method	BLASTX
NCBI GI	g6056199
BLAST score	304
E value	2.0e-27
Match length	116
% identity	48
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]
Seq. No.	388126
Contig ID	9158_1.R1084
5'-most EST	LIB3431-042-P1-K1-B7
Seq. No.	388127
Contig ID	9170_1.R1084
5'-most EST	g2309961
Method	BLASTX
NCBI GI	g322867
BLAST score	736
E value	5.0e-78
Match length	250
% identity	61
NCBI Description	translation initiation factor eIF-4F isozyme form subunit p82 - wheat
Seq. No.	388128
Contig ID	9200_1.R1084
5'-most EST	LIB3434-032-P1-K1-C12
Method	BLASTX
NCBI GI	g3426051
BLAST score	338
E value	9.0e-41
Match length	181
% identity	53
NCBI Description	(AC005168) hypothetical protein [Arabidopsis thaliana]
Seq. No.	388129
Contig ID	9201_1.R1084
5'-most EST	uC-osflM202083b09b1

Method	BLASTX
NCBI GI	g3915096
BLAST score	602
E value	9.0e-69
Match length	161
% identity	82
NCBI Description	TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73) >gi_1574976 (U47293) trans-cinnamate 4-hydroxylase [Populus tremuloides]

Seq. No.	388130
Contig ID	9204_1.R1084
5'-most EST	LIB3431-042-P1-K1-H1
Method	BLASTX
NCBI GI	g128191
BLAST score	556
E value	4.0e-57
Match length	141
% identity	77
NCBI Description	NITRATE REDUCTASE [NAD(P)H] >gi_66210_pir__RDBHNP nitrate reductase (NAD(P)H) (EC 1.6.6.2) - barley >gi_19065_emb_CAA42739_ (X60173) nitrate reductase (NAD(P)H) [Hordeum vulgare]

Seq. No.	388131
Contig ID	9214_1.R1084
5'-most EST	g5455378

Seq. No.	388132
Contig ID	9214_2.R1084
5'-most EST	LIB3431-042-P1-K1-H8

Seq. No.	388133
Contig ID	9236_1.R1084
5'-most EST	g5005185
Method	BLASTX
NCBI GI	g126201
BLAST score	464
E value	2.0e-46
Match length	118
% identity	76
NCBI Description	3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_81676_pir__S20510 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor - rape >gi_17827_emb_CAA42596_ (X59970) 3-isopropylmalate dehydrogenase [Brassica napus]

Seq. No.	388134
Contig ID	9248_1.R1084
5'-most EST	g1632405

Seq. No.	388135
Contig ID	9252_1.R1084
5'-most EST	g701418

Seq. No.	388136

Contig ID	9259_1.R1084
5'-most EST	LIB3431-019-P1-K1-E10
Method	BLASTX
NCBI GI	g5103831
BLAST score	276
E value	7.0e-24
Match length	93
% identity	59
NCBI Description	(AC007591) ESTs gb_H37032, gb_R6425, gb_Z34651, gb_N37268, gb_AA713172 and gb_Z34241 come from this gene. [Arabidopsis thaliana]

Seq. No.	388137
Contig ID	9262_1.R1084
5'-most EST	uC-osrocyp028b06b1
Method	BLASTX
NCBI GI	g4539332
BLAST score	296
E value	2.0e-26
Match length	90
% identity	68
NCBI Description	(AL035539) glycosyltransferase like protein (fragment) [Arabidopsis thaliana]

Seq. No.	388138
Contig ID	9263_1.R1084
5'-most EST	LIB3431-019-P1-K1-E5
Method	BLASTN
NCBI GI	g6015437
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388139
Contig ID	9270_1.R1084
5'-most EST	uC-osrocyp012d02b1
Method	BLASTX
NCBI GI	g3150410
BLAST score	231
E value	9.0e-19
Match length	175
% identity	31
NCBI Description	(AC004165) unknown protein [Arabidopsis thaliana]

Seq. No.	388140
Contig ID	9281_1.R1084
5'-most EST	LIB3431-019-P1-K1-G3
Method	BLASTX
NCBI GI	g5834807
BLAST score	149
E value	2.0e-09
Match length	48
% identity	62
NCBI Description	(AL117212) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	388141
Contig ID	9290_1.R1084
5'-most EST	LIB3475-012-P1-K1-A12

Seq. No.	388142
Contig ID	9293_1.R1084
5'-most EST	LIB3432-029-P1-K1-G4
Method	BLASTX
NCBI GI	g2795806
BLAST score	536
E value	1.0e-70
Match length	170
% identity	80
NCBI Description	(AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	388143
Contig ID	9298_1.R1084
5'-most EST	LIB3477-001-P1-K1-E2

Seq. No.	388144
Contig ID	9299_1.R1084
5'-most EST	LIB3431-020-P1-K1-A3
Method	BLASTX
NCBI GI	g6056194
BLAST score	220
E value	9.0e-18
Match length	119
% identity	38
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	388145
Contig ID	9317_1.R1084
5'-most EST	LIB3431-020-P1-K1-C10

Seq. No.	388146
Contig ID	9322_1.R1084
5'-most EST	g572272
Method	BLASTX
NCBI GI	g3006145
BLAST score	970
E value	1.0e-105
Match length	389
% identity	38
NCBI Description	(AL022299) ABC transporter [Schizosaccharomyces pombe]

Seq. No.	388147
Contig ID	9322_2.R1084
5'-most EST	g3763351
Method	BLASTX
NCBI GI	g1169871
BLAST score	177
E value	2.0e-20
Match length	98
% identity	34
NCBI Description	GCN20 PROTEIN >gi_1363661_pir__S56146 GCN20 protein - yeast (Saccharomyces cerevisiae) >gi_643479 (U19971) Gcn20p [Saccharomyces cerevisiae] >gi_836764_dbj_BAA09248.1_

(D50617) YFR009W [Saccharomyces cerevisiae]

Seq. No.	388148
Contig ID	9342_1.R1084
5'-most EST	LIB3431-020-P1-K1-E3
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	9.0e-10
Match length	35
% identity	42
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388149
Contig ID	9349_1.R1084
5'-most EST	LIB3431-020-P1-K1-F10

Seq. No.	388150
Contig ID	9364_1.R1084
5'-most EST	uC-osrocyp027g09b1

Seq. No.	388151
Contig ID	9364_2.R1084
5'-most EST	uC-osflcyp064h05b1

Seq. No.	388152
Contig ID	9372_1.R1084
5'-most EST	LIB3479-003-Q6-K1-A1
Method	BLASTX
NCBI GI	g4583546
BLAST score	255
E value	1.0e-21
Match length	121
% identity	40
NCBI Description	(AJ010819) GrpE protein [Arabidopsis thaliana]

Seq. No.	388153
Contig ID	9373_1.R1084
5'-most EST	uC-osroM202014f11b1
Method	BLASTX
NCBI GI	g2459421
BLAST score	352
E value	9.0e-33
Match length	177
% identity	42
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	388154
Contig ID	9408_1.R1084
5'-most EST	g2801046
Method	BLASTX
NCBI GI	g4585873
BLAST score	867
E value	1.0e-122
Match length	302
% identity	72

NCBI Description	(AC005850) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	388155
Contig ID	9414_1.R1084
5'-most EST	LIB3431-021-P1-K1-D11
Method	BLASTX
NCBI GI	g4980489
BLAST score	174
E value	4.0e-12
Match length	100
% identity	38
NCBI Description	(AE001689) muconate cycloisomerase [Thermotoga maritima]

Seq. No.	388156
Contig ID	9455_1.R1084
5'-most EST	uC-osflcyp064c12b1
Method	BLASTX
NCBI GI	g5881940
BLAST score	153
E value	8.0e-20
Match length	143
% identity	45
NCBI Description	(AL117387) putative secreted protein [Streptomyces coelicolor A3(2)]

Seq. No.	388157
Contig ID	9464_1.R1084
5'-most EST	uC-osflcyp159h04a1
Method	BLASTX
NCBI GI	g1352468
BLAST score	340
E value	6.0e-32
Match length	76
% identity	83
NCBI Description	BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) >gi_1122439 (U16123) invertase [Zea mays]

Seq. No.	388158
Contig ID	9483_1.R1084
5'-most EST	g286800
Method	BLASTX
NCBI GI	g4982498
BLAST score	333
E value	6.0e-31
Match length	83
% identity	76
NCBI Description	(AC000107) F17F8.4 [Arabidopsis thaliana]

Seq. No.	388159
Contig ID	9490_1.R1084
5'-most EST	LIB3432-058-P1-K1-H12

Seq. No.	388160
Contig ID	9510_1.R1084
5'-most EST	g2310372
Method	BLASTX

NCBI GI	g2293288
BLAST score	141
E value	1.0e-12
Match length	157
% identity	35
NCBI Description	(AF008220) YtcB [Bacillus subtilis] >gi_2635571_emb_CAB15065_ (Z99119) similar to NDP-sugar epimerase [Bacillus subtilis]

Seq. No.	388161
Contig ID	9529_1.R1084
5'-most EST	LIB3431-022-P1-K1-F5
Method	BLASTX
NCBI GI	g6016736
BLAST score	240
E value	4.0e-20
Match length	90
% identity	57
NCBI Description	(AC009325) unknown protein [Arabidopsis thaliana]

Seq. No.	388162
Contig ID	9531_1.R1084
5'-most EST	LIB3432-035-P2-K1-A12
Method	BLASTX
NCBI GI	g5295954
BLAST score	384
E value	7.0e-37
Match length	81
% identity	93
NCBI Description	(AB026295) hypothetical protein [Oryza sativa]

Seq. No.	388163
Contig ID	9537_1.R1084
5'-most EST	LIB3431-022-P1-K1-G5
Method	BLASTX
NCBI GI	g629775
BLAST score	740
E value	1.0e-78
Match length	149
% identity	92
NCBI Description	beta-ketoacyl-ACP synthase - barley (fragment)

Seq. No.	388164
Contig ID	9550_1.R1084
5'-most EST	LIB3475-006-P1-K1-B8

Seq. No.	388165
Contig ID	9553_1.R1084
5'-most EST	g568626
Method	BLASTX
NCBI GI	g1657621
BLAST score	188
E value	3.0e-23
Match length	109
% identity	31
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

>gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]

Seq. No.	388166
Contig ID	9555_1.R1084
5'-most EST	uC-osflcyp175a03b1
Method	BLASTX
NCBI GI	g2829902
BLAST score	627
E value	4.0e-65
Match length	259
% identity	44
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	388167
Contig ID	9562_1.R1084
5'-most EST	LIB3475-002-P1-K2-B7
Method	BLASTX
NCBI GI	g6006848
BLAST score	1122
E value	1.0e-179
Match length	398
% identity	73
NCBI Description	(AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	388168
Contig ID	9564_2.R1084
5'-most EST	g287267
Method	BLASTX
NCBI GI	g3913425
BLAST score	1036
E value	1.0e-113
Match length	217
% identity	88
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	388169
Contig ID	9573_1.R1084
5'-most EST	uC-osflcyp108g05b1
Method	BLASTX
NCBI GI	g2660676
BLAST score	583
E value	2.0e-67
Match length	161
% identity	72
NCBI Description	(AC002342) Dreg-2 like protein [Arabidopsis thaliana]

Seq. No.	388170
Contig ID	9582_1.R1084
5'-most EST	LIB3431-023-P1-K1-C6
Method	BLASTX
NCBI GI	g3643608
BLAST score	376

E value	1.0e-35
Match length	249
% identity	49
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana] >gi_4874312_gb_AAD31374.1_AC006053_16 (AC006053) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388171
Contig ID	9592_1.R1084
5'-most EST	g2797800

Seq. No.	388172
Contig ID	9599_1.R1084
5'-most EST	g4715349
Method	BLASTX
NCBI GI	g124367
BLAST score	325
E value	1.0e-43
Match length	228
% identity	33
NCBI Description	ACETOLACTATE SYNTHASE I PRECURSOR (ACETOHYDROXY-ACID SYNTHASE I) (ALS I) >gi_68238_pir__YCNT1 acetolactate synthase (EC 4.1.3.18) class I precursor - common tobacco >gi_19777_emb_CAA30484_ (X07644) ALS SuRA gene (AA 1-667) [Nicotiana tabacum] >gi_226220_prf__1501386A acetolactate synthase [Nicotiana tabacum]

Seq. No.	388173
Contig ID	9604_1.R1084
5'-most EST	LIB3477-005-P1-K1-F11
Method	BLASTX
NCBI GI	g5922612
BLAST score	351
E value	6.0e-33
Match length	194
% identity	58
NCBI Description	(AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa]

Seq. No.	388174
Contig ID	9605_1.R1084
5'-most EST	uC-osflcyp168d09b1
Method	BLASTX
NCBI GI	g3202030
BLAST score	735
E value	9.0e-78
Match length	165
% identity	84
NCBI Description	(AF069318) geranylgeranyl hydrogenase [Mesembryanthemum crystallinum]

Seq. No.	388175
Contig ID	9614_1.R1084
5'-most EST	uC-osroM202041d03b1

Seq. No.	388176
Contig ID	9622_1.R1084
5'-most EST	LIB3431-023-P1-K1-G4

Seq. No.	388177
Contig ID	9635_2.R1084
5'-most EST	uC-osflcyp021g12b1
Method	BLASTX
NCBI GI	g5123939
BLAST score	595
E value	1.0e-61
Match length	176
% identity	64
NCBI Description	(AL079349) putative protein [Arabidopsis thaliana]

Seq. No.	388178
Contig ID	9648_1.R1084
5'-most EST	uC-osflcyp017f08b1

Seq. No.	388179
Contig ID	9665_1.R1084
5'-most EST	LIB3431-024-P1-K1-C5

Seq. No.	388180
Contig ID	9684_1.R1084
5'-most EST	uC-osflcyp071b12b1
Method	BLASTX
NCBI GI	g2827516
BLAST score	406
E value	2.0e-39
Match length	163
% identity	49
NCBI Description	(AL021633) DNA topoisomerase like-protein [Arabidopsis thaliana]

Seq. No.	388181
Contig ID	9696_1.R1084
5'-most EST	g572258
Method	BLASTX
NCBI GI	g4582436
BLAST score	917
E value	7.0e-99
Match length	459
% identity	61
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	388182
Contig ID	9700_1.R1084
5'-most EST	g1631698
Method	BLASTX
NCBI GI	g2564253
BLAST score	496
E value	2.0e-50
Match length	149
% identity	71
NCBI Description	(Z99996) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Hordeum vulgare]

Seq. No.	388183
Contig ID	9702_1.R1084
5'-most EST	LIB3431-024-P1-K1-G1
Method	BLASTX
NCBI GI	g2190543
BLAST score	176
E value	1.0e-12
Match length	118
% identity	37
NCBI Description	(AC001229) EST gb_N37484 comes from this gene. [Arabidopsis thaliana]

Seq. No.	388184
Contig ID	9713_1.R1084
5'-most EST	g3763786
Method	BLASTX
NCBI GI	g4508069
BLAST score	776
E value	1.0e-82
Match length	250
% identity	64
NCBI Description	(AC005882) 12246 [Arabidopsis thaliana]

Seq. No.	388185
Contig ID	9730_1.R1084
5'-most EST	g568494
Method	BLASTX
NCBI GI	g4115538
BLAST score	477
E value	1.0e-47
Match length	196
% identity	51
NCBI Description	(AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No.	388186
Contig ID	9738_1.R1084
5'-most EST	g426281
Method	BLASTX
NCBI GI	g2245136
BLAST score	449
E value	7.0e-78
Match length	234
% identity	65
NCBI Description	(Z97344) trehalose-6-phosphate synthase like protein [Arabidopsis thaliana]

Seq. No.	388187
Contig ID	9745_1.R1084
5'-most EST	LIB3431-025-P1-K1-D11

Seq. No.	388188
Contig ID	9799_1.R1084
5'-most EST	g4714456

Seq. No.	388189

Contig ID	9810_1.R1084
5'-most EST	uC-osflcyp124h01b1
Method	BLASTX
NCBI GI	g4490332
BLAST score	451
E value	1.0e-44
Match length	153
% identity	57
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	388190
Contig ID	9813_1.R1084
5'-most EST	uC-osroM202013g06b1
Method	BLASTX
NCBI GI	g3176690
BLAST score	686
E value	1.0e-124
Match length	368
% identity	63
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	388191
Contig ID	9821_1.R1084
5'-most EST	LIB3432-012-P1-K1-A1
Method	BLASTX
NCBI GI	g2673913
BLAST score	247
E value	6.0e-21
Match length	66
% identity	65
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388192
Contig ID	9831_1.R1084
5'-most EST	g6012842

Seq. No.	388193
Contig ID	9836_1.R1084
5'-most EST	LIB3431-026-P1-K1-F3

Seq. No.	388194
Contig ID	9838_1.R1084
5'-most EST	g2428914

Seq. No.	388195
Contig ID	9856_1.R1084
5'-most EST	LIB3431-026-P1-K1-H10

Seq. No.	388196
Contig ID	9863_1.R1084
5'-most EST	uC-osflcyp168d10b1
Method	BLASTX
NCBI GI	g3176725
BLAST score	200
E value	3.0e-15

Match length	98
% identity	41
NCBI Description	(AC002392) unknown protein [Arabidopsis thaliana]

Seq. No.	388197
Contig ID	9890_1.R1084
5'-most EST	LIB3431-027-P1-K1-C11
Method	BLASTX
NCBI GI	g3482977
BLAST score	319
E value	4.0e-29
Match length	244
% identity	35
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	388198
Contig ID	9896_1.R1084
5'-most EST	LIB3475-002-P1-K2-D11
Method	BLASTX
NCBI GI	g5922612
BLAST score	365
E value	2.0e-34
Match length	241
% identity	41
NCBI Description	(AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa]

Seq. No.	388199
Contig ID	9910_1.R1084
5'-most EST	uC-osflM202081a10b1
Method	BLASTX
NCBI GI	g4678948
BLAST score	378
E value	5.0e-36
Match length	164
% identity	50
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	388200
Contig ID	9914_1.R1084
5'-most EST	LIB3433-060-P1-K1-H3

Seq. No.	388201
Contig ID	9943_1.R1084
5'-most EST	LIB3432-022-P1-K1-C7

Seq. No.	388202
Contig ID	9944_1.R1084
5'-most EST	LIB3431-027-P1-K1-H1
Method	BLASTX
NCBI GI	g1169544
BLAST score	615
E value	9.0e-64
Match length	200
% identity	60

NCBI Description	ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) ERD1 protein [Arabidopsis thaliana]

Seq. No.	388203
Contig ID	9963_1.R1084
5'-most EST	uC-osflcyp174c05a1

Seq. No.	388204
Contig ID	9966_1.R1084
5'-most EST	LIB3431-028-P1-K1-B10
Method	BLASTX
NCBI GI	g5921189
BLAST score	413
E value	3.0e-40
Match length	191
% identity	45
NCBI Description	CYTOCHROME P450 71C4 >gi_550542_emb_CAA57425_ (X81831) cytochrome P450 [Zea mays] >gi_1850903_emb_CAA72196_ (Y11368) cytochrome p450 [Zea mays]

Seq. No.	388205
Contig ID	9971_1.R1084
5'-most EST	g2443047
Method	BLASTX
NCBI GI	g4894967
BLAST score	198
E value	4.0e-15
Match length	111
% identity	45
NCBI Description	(AF140759) FK506-binding protein FKBP51 [Saimiri boliviensis]

Seq. No.	388206
Contig ID	9972_1.R1084
5'-most EST	LIB3431-028-P1-K1-B6

Seq. No.	388207
Contig ID	9974_1.R1084
5'-most EST	LIB3431-028-P1-K1-B9

Seq. No.	388208
Contig ID	9976_1.R1084
5'-most EST	uC-osflcyp123d08b1

Seq. No.	388209
Contig ID	9985_1.R1084
5'-most EST	g701179
Method	BLASTX
NCBI GI	g2191161
BLAST score	229
E value	1.0e-18
Match length	120
% identity	49
NCBI Description	(AF007270) contains similarity to B. subtilus flagellar biosynthesis protein FLHA (SW:P35620) [Arabidopsis thaliana]

Seq. No.	388210
Contig ID	9991_1.R1084
5'-most EST	g5003680

Seq. No.	388211
Contig ID	10034_1.R1084
5'-most EST	uC-osrocyp033f04b1
Method	BLASTX
NCBI GI	g2499606
BLAST score	531
E value	1.0e-110
Match length	242
% identity	78
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2) (ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2 [Arabidopsis thaliana]

Seq. No.	388212
Contig ID	10054_1.R1084
5'-most EST	LIB3431-029-P1-K1-B5
Method	BLASTX
NCBI GI	g2493318
BLAST score	282
E value	6.0e-25
Match length	106
% identity	49
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	388213
Contig ID	10057_1.R1084
5'-most EST	g2799568

Seq. No.	388214
Contig ID	10061_1.R1084
5'-most EST	LIB3432-058-P1-K1-B7
Method	BLASTX
NCBI GI	g2708741
BLAST score	828
E value	1.0e-92
Match length	247
% identity	68
NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388215
Contig ID	10072_1.R1084
5'-most EST	LIB3431-029-P1-K1-E3
Method	BLASTX
NCBI GI	g5262204
BLAST score	286
E value	2.0e-25
Match length	75
% identity	77
NCBI Description	(AL080252) putative protein [Arabidopsis thaliana]

Seq. No.	388216
Contig ID	10079_1.R1084
5'-most EST	LIB3431-029-P1-K1-F12
Method	BLASTX
NCBI GI	g3063447
BLAST score	502
E value	1.0e-50
Match length	208
% identity	8
NCBI Description	(AC003981) F22O13.9 [Arabidopsis thaliana]

Seq. No.	388217
Contig ID	10090_1.R1084
5'-most EST	g2309889
Method	BLASTX
NCBI GI	g4406764
BLAST score	534
E value	4.0e-54
Match length	198
% identity	53
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No.	388218
Contig ID	10114_1.R1084
5'-most EST	LIB3431-001-P1-K1-D9
Method	BLASTX
NCBI GI	g320618
BLAST score	245
E value	7.0e-21
Match length	83
% identity	60
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	388219
Contig ID	10123_1.R1084
5'-most EST	LIB3431-001-P1-K1-C11

Seq. No.	388220
Contig ID	10126_1.R1084
5'-most EST	LIB3432-001-P1-K1-H5
Method	BLASTX
NCBI GI	g132105
BLAST score	249
E value	2.0e-21
Match length	89
% identity	62
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

	ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	388221
Contig ID	10135_1.R1084
5'-most EST	LIB3431-002-P1-K1-C5
Method	BLASTN
NCBI GI	g6006355
BLAST score	70
E value	6.0e-31
Match length	329
% identity	82
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.	388222
Contig ID	10251_1.R1084
5'-most EST	LIB3432-047-P2-K11-D6
Method	BLASTX
NCBI GI	g1710416
BLAST score	153
E value	1.0e-15
Match length	81
% identity	51
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L1 >gi_2147041_pir__S73259 50S ribosomal protein L1 - Porphyra purpurea chloroplast >gi_1276804 (U38804) 50S ribosomal protein L1 [Porphyra purpurea]
Seq. No.	388223
Contig ID	10262_1.R1084
5'-most EST	g2801125
Seq. No.	388224
Contig ID	10268_1.R1084
5'-most EST	g4714651
Method	BLASTX
NCBI GI	g126888
BLAST score	608
E value	6.0e-63
Match length	121
% identity	94
NCBI Description	MALATE DEHYDROGENASE [NADP], CHLOROPLAST PRECURSOR (NADP-MDH) >gi_319840_pir__DEMZMC malate dehydrogenase (NADP+) (EC 1.1.1.82) precursor, chloroplast - maize >gi_22368_emb_CAA34213_ (X16084) precursor protein (AA -57 to 375) [Zea mays] >gi_226766_prf__1604473A NADP malate dehydrogenase [Zea mays]
Seq. No.	388225
Contig ID	10268_2.R1084
5'-most EST	g3763525
Method	BLASTX
NCBI GI	g126888
BLAST score	849
E value	2.0e-91
Match length	174

% identity	92
NCBI Description	MALATE DEHYDROGENASE [NADP], CHLOROPLAST PRECURSOR (NADP-MDH) >gi_319840_pir__DEMZMC malate dehydrogenase (NADP+) (EC 1.1.1.82) precursor, chloroplast - maize >gi_22368_emb_CAA34213_ (X16084) precursor protein (AA -57 to 375) [Zea mays] >gi_226766_prf__1604473A NADP malate dehydrogenase [Zea mays]

Seq. No.	388226
Contig ID	10271_1.R1084
5'-most EST	LIB3432-034-P2-K1-C7
Method	BLASTX
NCBI GI	g3309086
BLAST score	394
E value	4.0e-66
Match length	141
% identity	91
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana] >gi_4938495_emb_CAB43853.1_ (AL078465) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No.	388227
Contig ID	10281_1.R1084
5'-most EST	uC-osrocyp005b11b1
Method	BLASTX
NCBI GI	g2920587
BLAST score	496
E value	2.0e-51
Match length	151
% identity	65
NCBI Description	(AF038362) TBP-associated factor 172 [Homo sapiens] >gi_2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo sapiens]

Seq. No.	388228
Contig ID	10283_1.R1084
5'-most EST	g3767690
Method	BLASTN
NCBI GI	g2052354
BLAST score	39
E value	4.0e-12
Match length	39
% identity	100
NCBI Description	Human uncoupling protein homolog (UCPH) mRNA, complete cds

Seq. No.	388229
Contig ID	10284_1.R1084
5'-most EST	LIB3432-034-P2-K1-E11

Seq. No.	388230
Contig ID	10286_1.R1084
5'-most EST	LIB3433-028-P1-K1-C9
Method	BLASTX
NCBI GI	g3860323
BLAST score	349
E value	1.0e-32
Match length	77

% identity	83
NCBI Description	(AJ012688) hypothetical protein [Cicer arietinum]

Seq. No.	388231
Contig ID	10286_2.R1084
5'-most EST	uC-osflcyp154e08b1
Method	BLASTX
NCBI GI	g3860323
BLAST score	211
E value	5.0e-27
Match length	77
% identity	81
NCBI Description	(AJ012688) hypothetical protein [Cicer arietinum]

Seq. No.	388232
Contig ID	10289_1.R1084
5'-most EST	LIB3432-034-P2-K1-E7
Method	BLASTX
NCBI GI	g4056456
BLAST score	214
E value	5.0e-17
Match length	60
% identity	68
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	388233
Contig ID	10291_1.R1084
5'-most EST	uC-osflm202106e01b1
Method	BLASTX
NCBI GI	g4874301
BLAST score	689
E value	2.0e-72
Match length	171
% identity	81
NCBI Description	(AC006053) proton-ATPase-like protein [Arabidopsis thaliana]

Seq. No.	388234
Contig ID	10306_1.R1084
5'-most EST	uC-osflcyp154g09b1
Method	BLASTX
NCBI GI	g3024871
BLAST score	443
E value	2.0e-43
Match length	248
% identity	41
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	388235
Contig ID	10321_1.R1084
5'-most EST	LIB3432-034-P2-K1-H6
Method	BLASTX

NCBI GI	g4895183
BLAST score	520
E value	1.0e-52
Match length	175
% identity	57
NCBI Description	(AC007661) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388236
Contig ID	10326_1.R1084
5'-most EST	LIB3432-047-P2-K11-A11
Method	BLASTX
NCBI GI	g480618
BLAST score	256
E value	8.0e-22
Match length	151
% identity	47
NCBI Description	ATAF1 protein - Arabidopsis thaliana (fragment) >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No.	388237
Contig ID	10339_1.R1084
5'-most EST	LIB3432-010-P1-K1-G5
Method	BLASTN
NCBI GI	g3869069
BLAST score	45
E value	2.0e-15
Match length	334
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence

Seq. No.	388238
Contig ID	10341_1.R1084
5'-most EST	LIB3432-047-P2-K11-B6
Method	BLASTX
NCBI GI	g1174867
BLAST score	308
E value	7.0e-28
Match length	72
% identity	75
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf__2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No.	388239
Contig ID	10342_1.R1084
5'-most EST	LIB3432-047-P2-K11-B8

Seq. No.	388240
Contig ID	10346_1.R1084
5'-most EST	g2428954
Method	BLASTX
NCBI GI	g3128218

BLAST score	483
E value	2.0e-48
Match length	127
% identity	70
NCBI Description	(AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No.	388241
Contig ID	10347_1.R1084
5'-most EST	LIB3432-047-P2-K11-C12
Method	BLASTX
NCBI GI	g4539454
BLAST score	215
E value	1.0e-22
Match length	105
% identity	50
NCBI Description	(AL049500) contains EST gb:AA728416 [Arabidopsis thaliana]

Seq. No.	388242
Contig ID	10349_1.R1084
5'-most EST	g3763190
Method	BLASTX
NCBI GI	g4586253
BLAST score	332
E value	7.0e-31
Match length	81
% identity	72
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	388243
Contig ID	10350_1.R1084
5'-most EST	LIB3432-032-P2-K1-A2

Seq. No.	388244
Contig ID	10352_1.R1084
5'-most EST	LIB3432-047-P2-K11-C7
Method	BLASTX
NCBI GI	g5931653
BLAST score	406
E value	2.0e-39
Match length	218
% identity	44
NCBI Description	(AJ011628) squamosa promoter binding protein-like 1 [Arabidopsis thaliana]

Seq. No.	388245
Contig ID	10357_1.R1084
5'-most EST	uC-osflcyp170a01b1

Seq. No.	388246
Contig ID	10360_1.R1084
5'-most EST	g3760380
Method	BLASTX
NCBI GI	g1808686
BLAST score	166
E value	4.0e-11
Match length	160
% identity	39

NCBI Description	(Y10783) hypothetical protein [Sporobolus stapfianus]

Seq. No.	388247
Contig ID	10362_1.R1084
5'-most EST	uC-osflcyp179b11b1
Method	BLASTX
NCBI GI	g4185513
BLAST score	248
E value	2.0e-30
Match length	92
% identity	71
NCBI Description	(AF102823) actin depolymerizing factor 5 [Arabidopsis thaliana] >gi_4185517 (AF102825) actin depolymerizing factor 5 [Arabidopsis thaliana]

Seq. No.	388248
Contig ID	10367_1.R1084
5'-most EST	LIB3432-047-P2-K11-E1
Method	BLASTX
NCBI GI	g3876299
BLAST score	173
E value	3.0e-12
Match length	79
% identity	46
NCBI Description	(Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi... >gi_3880760_emb_CAA16311.1_ (AL021474) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorh

Seq. No.	388249
Contig ID	10374_1.R1084
5'-most EST	uC-osflcyp073h12b1
Method	BLASTX
NCBI GI	g3319776
BLAST score	734
E value	4.0e-86
Match length	171
% identity	87
NCBI Description	(AJ007665) seryl-tRNA synthetase [Zea mays]

Seq. No.	388250
Contig ID	10382_1.R1084
5'-most EST	g2799158
Method	BLASTX
NCBI GI	g4519539
BLAST score	322
E value	2.0e-29
Match length	107
% identity	61
NCBI Description	(AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No.	388251
Contig ID	10382_2.R1084
5'-most EST	g2799162
Method	BLASTX
NCBI GI	g4519539
BLAST score	327
E value	4.0e-30
Match length	85
% identity	75
NCBI Description	(AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No.	388252
Contig ID	10382_3.R1084
5'-most EST	uC-osf1M202070c01a1
Method	BLASTX
NCBI GI	g4519539
BLAST score	585
E value	1.0e-90
Match length	244
% identity	70
NCBI Description	(AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No.	388253
Contig ID	10383_1.R1084
5'-most EST	LIB3432-047-P2-K11-F4
Method	BLASTX
NCBI GI	g4503521
BLAST score	436
E value	8.0e-43
Match length	146
% identity	58
NCBI Description	murine mammary tumor integration site 6 (oncogene homolog) >gi_2498490_sp_Q64252_INT6_MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens]

Seq. No.	388254
Contig ID	10383_2.R1084
5'-most EST	g4716113
Method	BLASTX
NCBI GI	g4503521
BLAST score	275
E value	5.0e-24
Match length	91
% identity	58
NCBI Description	murine mammary tumor integration site 6 (oncogene homolog) >gi_2498490_sp_Q64252_INT6_MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens]

Seq. No.	388255
Contig ID	10385_1.R1084
5'-most EST	LIB3477-008-P1-K1-D8

Seq. No.	388256
Contig ID	10387_1.R1084
5'-most EST	LIB3432-047-P2-K11-F9
Method	BLASTX
NCBI GI	g6056418
BLAST score	520
E value	9.0e-53
Match length	139
% identity	68
NCBI Description	(AC009525) Similar to beta-glucosidases [Arabidopsis thaliana]

Seq. No.	388257
Contig ID	10389_1.R1084
5'-most EST	g4879702
Method	BLASTX
NCBI GI	g6017123
BLAST score	250
E value	4.0e-30
Match length	114
% identity	72
NCBI Description	(AC009895) unknown protein [Arabidopsis thaliana]

Seq. No.	388258
Contig ID	10390_1.R1084
5'-most EST	uC-osflm202110d11b1
Method	BLASTX
NCBI GI	g2252847
BLAST score	336
E value	4.0e-31
Match length	110
% identity	60
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana] >gi_6049889_gb_AAF02804.1_AF195115_24 (AF195115) weak similarity to phthalate permease family [Arabidopsis thaliana]

Seq. No.	388259
Contig ID	10400_1.R1084
5'-most EST	g4968741
Method	BLASTX
NCBI GI	g3452497
BLAST score	753
E value	5.0e-80
Match length	218
% identity	70
NCBI Description	(Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No.	388260
Contig ID	10403_1.R1084
5'-most EST	LIB3432-047-P2-K11-H6
Method	BLASTX

NCBI GI	g1657851
BLAST score	278
E value	4.0e-24
Match length	82
% identity	32
NCBI Description	(U73214) cold acclimation protein WCOR518 [Triticum aestivum]

Seq. No.	388261
Contig ID	10404_1.R1084
5'-most EST	LIB3432-047-P2-K11-H8
Method	BLASTX
NCBI GI	g4539295
BLAST score	461
E value	7.0e-46
Match length	178
% identity	67
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	388262
Contig ID	10407_1.R1084
5'-most EST	g701404

Seq. No.	388263
Contig ID	10410_1.R1084
5'-most EST	LIB3432-007-P1-K1-H10
Method	BLASTX
NCBI GI	g4455256
BLAST score	787
E value	1.0e-83
Match length	179
% identity	78
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	388264
Contig ID	10414_1.R1084
5'-most EST	LIB3432-048-P2-K1-A9
Method	BLASTN
NCBI GI	g5042437
BLAST score	273
E value	1.0e-152
Match length	318
% identity	97
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	388265
Contig ID	10421_1.R1084
5'-most EST	LIB3432-048-P2-K1-B4

Seq. No.	388266
Contig ID	10431_1.R1084
5'-most EST	LIB3432-048-P2-K1-C3
Method	BLASTN
NCBI GI	g1256198
BLAST score	156
E value	4.0e-82

Match length	172
% identity	98
NCBI Description	Rice transposon Tnr3 DNA, complete sequence

Seq. No.	388267
Contig ID	10436_1.R1084
5'-most EST	uC-osflcyp032e01b1

Seq. No.	388268
Contig ID	10437_1.R1084
5'-most EST	LIB3432-048-P2-K1-D1
Method	BLASTX
NCBI GI	g4103635
BLAST score	212
E value	1.0e-16
Match length	73
% identity	53
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	388269
Contig ID	10443_1.R1084
5'-most EST	LIB3434-033-P1-K1-B4
Method	BLASTX
NCBI GI	g4469011
BLAST score	459
E value	2.0e-45
Match length	131
% identity	68
NCBI Description	(AL035602) carbohydrate kinase-like protein [Arabidopsis thaliana]

Seq. No.	388270
Contig ID	10446_1.R1084
5'-most EST	LIB3432-048-P2-K1-D7
Method	BLASTX
NCBI GI	g3335365
BLAST score	195
E value	9.0e-21
Match length	89
% identity	66
NCBI Description	(AC003028) high affinity calcium antiporter [Arabidopsis thaliana]

Seq. No.	388271
Contig ID	10447_1.R1084
5'-most EST	LIB3432-048-P2-K1-D8

Seq. No.	388272
Contig ID	10453_1.R1084
5'-most EST	g2312580
Method	BLASTX
NCBI GI	g4539335
BLAST score	458
E value	8.0e-47
Match length	158
% identity	58
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	388273
Contig ID	10454_1.R1084
5'-most EST	LIB3434-019-P1-K1-F8
Method	BLASTX
NCBI GI	g3786009
BLAST score	1105
E value	1.0e-121
Match length	359
% identity	63
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	388274
Contig ID	10455_1.R1084
5'-most EST	LIB3432-048-P2-K1-E4
Method	BLASTX
NCBI GI	g3024871
BLAST score	240
E value	8.0e-20
Match length	127
% identity	38
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	388275
Contig ID	10475_1.R1084
5'-most EST	uC-osflcyp009e03b1
Method	BLASTX
NCBI GI	g1438883
BLAST score	864
E value	9.0e-93
Match length	257
% identity	64
NCBI Description	(U43840) GmCK3p [Glycine max]

Seq. No.	388276
Contig ID	10482_1.R1084
5'-most EST	g3107617
Method	BLASTX
NCBI GI	g2832898
BLAST score	414
E value	3.0e-40
Match length	134
% identity	63
NCBI Description	(AJ000886) Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus]

Seq. No.	388277
Contig ID	10482_2.R1084
5'-most EST	uC-osflcyp061f09b1
Method	BLASTX
NCBI GI	g2832898
BLAST score	333
E value	6.0e-31
Match length	84
% identity	71

NCBI Description	(AJ000886) Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus]

Seq. No.	388278
Contig ID	10483_1.R1084
5'-most EST	g428049
Method	BLASTX
NCBI GI	g4678941
BLAST score	319
E value	2.0e-29
Match length	145
% identity	48
NCBI Description	(AL049711) gamma response I protein [Arabidopsis thaliana]

Seq. No.	388279
Contig ID	10487_1.R1084
5'-most EST	LIB3432-048-P2-K1-H3

Seq. No.	388280
Contig ID	10494_1.R1084
5'-most EST	LIB3432-059-P1-K1-A12
Method	BLASTN
NCBI GI	g5730046
BLAST score	35
E value	1.0e-09
Match length	37
% identity	64
NCBI Description	Homo sapiens solute carrier family 17 (sodium phosphate), member 3 (SLC17A3) mRNA >gi_2062691_gb_U90545_HSU90545 Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No.	388281
Contig ID	10494_2.R1084
5'-most EST	uC-osf1M202066d10b1

Seq. No.	388282
Contig ID	10505_1.R1084
5'-most EST	LIB3434-048-P1-K1-F3
Method	BLASTX
NCBI GI	g1419088
BLAST score	388
E value	4.0e-37
Match length	83
% identity	77
NCBI Description	(Z71395) calreticulin [Nicotiana plumbaginifolia]

Seq. No.	388283
Contig ID	10509_1.R1084
5'-most EST	g4714841

Seq. No.	388284
Contig ID	10521_1.R1084
5'-most EST	g568663
Method	BLASTX
NCBI GI	g2388911
BLAST score	380

E value	2.0e-36
Match length	144
% identity	49
NCBI Description	(Z98974) hypothetical PSU1-like protein [Schizosaccharomyces pombe]

Seq. No.	388285
Contig ID	10522_1.R1084
5'-most EST	g569941

Seq. No.	388286
Contig ID	10546_1.R1084
5'-most EST	uC-osflm202099d04b1
Method	BLASTX
NCBI GI	g2984005
BLAST score	300
E value	6.0e-37
Match length	178
% identity	48
NCBI Description	(AE000750) ATPase subunit of ATP-dependent protease [Aquifex aeolicus]

Seq. No.	388287
Contig ID	10547_1.R1084
5'-most EST	g2312483
Method	BLASTX
NCBI GI	g1652649
BLAST score	337
E value	2.0e-35
Match length	130
% identity	60
NCBI Description	(D90907) hypothetical protein [Synechocystis sp.]

Seq. No.	388288
Contig ID	10551_1.R1084
5'-most EST	g5455383
Method	BLASTX
NCBI GI	g4006872
BLAST score	448
E value	2.0e-58
Match length	175
% identity	66
NCBI Description	(Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	388289
Contig ID	10556_1.R1084
5'-most EST	g4715726
Method	BLASTX
NCBI GI	g3834303
BLAST score	291
E value	6.0e-26
Match length	146
% identity	49
NCBI Description	(AC005679) F9K20.3 [Arabidopsis thaliana]

Seq. No.	388290

Contig ID	10557_1.R1084
5'-most EST	uC-osrocyp013f12b1
Method	BLASTX
NCBI GI	g1416514
BLAST score	395
E value	5.0e-38
Match length	99
% identity	75
NCBI Description	(D63168) CTP:phosphocholine cytidylyltransferase [Brassica napus]

Seq. No.	388291
Contig ID	10569_1.R1084
5'-most EST	g5005279
Method	BLASTX
NCBI GI	g134022
BLAST score	350
E value	3.0e-33
Match length	72
% identity	99
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70914_pir__R3RZ8 ribosomal protein S8 - rice chloroplast >gi_12022_emb_CAA33931_ (X15901) ribosomal protein S8 [Oryza sativa] >gi_226643_prf__1603356BT ribosomal protein S8 [Oryza sativa]

Seq. No.	388292
Contig ID	10573_1.R1084
5'-most EST	LIB3432-059-P1-K1-H7
Method	BLASTX
NCBI GI	g2281115
BLAST score	772
E value	5.0e-82
Match length	225
% identity	68
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	388293
Contig ID	10584_1.R1084
5'-most EST	LIB3432-060-P1-K1-A6

Seq. No.	388294
Contig ID	10591_1.R1084
5'-most EST	g3761798

Seq. No.	388295
Contig ID	10591_2.R1084
5'-most EST	LIB3432-012-P1-K1-E8
Method	BLASTX
NCBI GI	g4836881
BLAST score	792
E value	2.0e-84
Match length	225
% identity	69
NCBI Description	(AC007260) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	388296
Contig ID	10594_1.R1084
5'-most EST	g428590
Method	BLASTX
NCBI GI	g3341443
BLAST score	341
E value	2.0e-31
Match length	218
% identity	29
NCBI Description	(AJ223074) acid phosphatase [Glycine max]

Seq. No.	388297
Contig ID	10605_1.R1084
5'-most EST	LIB3434-047-P1-K1-G1
Method	BLASTX
NCBI GI	g445612
BLAST score	485
E value	2.0e-48
Match length	121
% identity	77
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	388298
Contig ID	10605_2.R1084
5'-most EST	LIB3477-003-P1-K1-C11
Method	BLASTX
NCBI GI	g445612
BLAST score	544
E value	2.0e-55
Match length	121
% identity	85
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	388299
Contig ID	10605_3.R1084
5'-most EST	LIB3432-060-P1-K1-C8
Method	BLASTX
NCBI GI	g445612
BLAST score	533
E value	4.0e-54
Match length	116
% identity	86
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	388300
Contig ID	10611_1.R1084
5'-most EST	g3759819
Method	BLASTX
NCBI GI	g4217999
BLAST score	712
E value	6.0e-75
Match length	183
% identity	72
NCBI Description	(AC006135) putative ubiquitin--protein ligase (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]

Seq. No.	388301
Contig ID	10616_1.R1084
5'-most EST	LIB3474-008-P1-K1-C9
Method	BLASTX
NCBI GI	g5042435
BLAST score	467
E value	3.0e-84
Match length	221
% identity	67
NCBI Description	(AC006193) Unknown protein [Arabidopsis thaliana]

Seq. No.	388302
Contig ID	10616_2.R1084
5'-most EST	g4878593
Method	BLASTX
NCBI GI	g5042435
BLAST score	371
E value	8.0e-68
Match length	171
% identity	71
NCBI Description	(AC006193) Unknown protein [Arabidopsis thaliana]

Seq. No.	388303
Contig ID	10619_1.R1084
5'-most EST	g5005515
Method	BLASTX
NCBI GI	g732003
BLAST score	212
E value	2.0e-16
Match length	150
% identity	39
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2125977_pir__I84534 outer membrane lipoprotein - Escherichia coli >gi_536993 (U14003) ORF_f177 [Escherichia coli] >gi_717134 (U21726) lipocalin precursor [Escherichia coli] >gi_1790592 (AE000487) outer membrane lipoprotein (lipocalin) [Escherichia coli]

Seq. No.	388304
Contig ID	10634_1.R1084
5'-most EST	uC-osroM202008a02a1
Method	BLASTX
NCBI GI	g6006853
BLAST score	374
E value	1.0e-62
Match length	178
% identity	69
NCBI Description	(AC009540) unknown protein [Arabidopsis thaliana]

Seq. No.	388305
Contig ID	10634_2.R1084
5'-most EST	LIB3432-042-P2-K1-H4
Method	BLASTX
NCBI GI	g6006853
BLAST score	472
E value	3.0e-47
Match length	126

% identity	69
NCBI Description	(AC009540) unknown protein [Arabidopsis thaliana]
Seq. No.	388306
Contig ID	10638_1.R1084
5'-most EST	LIB3432-060-P1-K1-G1
Seq. No.	388307
Contig ID	10639_1.R1084
5'-most EST	g2311868
Seq. No.	388308
Contig ID	10643_1.R1084
5'-most EST	uC-osflcyp029c06b1
Method	BLASTX
NCBI GI	g2388564
BLAST score	231
E value	8.0e-19
Match length	221
% identity	31
NCBI Description	(AC000098) ESTs gb_AA042402,gb_ATTS1380 come from this gene. [Arabidopsis thaliana]
Seq. No.	388309
Contig ID	10646_1.R1084
5'-most EST	LIB3432-028-P1-K1-H3
Method	BLASTX
NCBI GI	g4850271
BLAST score	598
E value	7.0e-62
Match length	202
% identity	62
NCBI Description	(AJ238244) putative high affinity sulfate transporter [Aegilops tauschii]
Seq. No.	388310
Contig ID	10664_1.R1084
5'-most EST	g287214
Seq. No.	388311
Contig ID	10668_1.R1084
5'-most EST	LIB3432-005-P1-K1-A5
Method	BLASTX
NCBI GI	g4006910
BLAST score	488
E value	1.0e-48
Match length	178
% identity	55
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	388312
Contig ID	10672_1.R1084
5'-most EST	uC-osflM202089b12b1
Method	BLASTX
NCBI GI	g82264
BLAST score	1197
E value	1.0e-132

Match length	250
% identity	90
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)8I) - potato (fragment) >gi_498789_emb_CAA56109_ (X79597) cytochrome c1 [Solanum tuberosum]

Seq. No.	388313
Contig ID	10673_1.R1084
5'-most EST	g2796421

Seq. No.	388314
Contig ID	10675_1.R1084
5'-most EST	uC-osf1cyp088b11b1
Method	BLASTX
NCBI GI	g2739044
BLAST score	666
E value	1.0e-69
Match length	185
% identity	68
NCBI Description	(AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max]

Seq. No.	388315
Contig ID	10677_1.R1084
5'-most EST	LIB3432-005-P1-K1-B4
Method	BLASTX
NCBI GI	g2586083
BLAST score	182
E value	2.0e-13
Match length	121
% identity	37
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	388316
Contig ID	10681_1.R1084
5'-most EST	g2312687
Method	BLASTX
NCBI GI	g951427
BLAST score	538
E value	6.0e-71
Match length	160
% identity	83
NCBI Description	(M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]

Seq. No.	388317
Contig ID	10685_1.R1084
5'-most EST	g428306

Seq. No.	388318
Contig ID	10689_1.R1084
5'-most EST	LIB3432-005-P1-K1-C5
Method	BLASTX
NCBI GI	g2499924
BLAST score	329

E value	2.0e-30
Match length	159
% identity	42
NCBI Description	POLYPEPTIDE DEFORMYLASE (PDF) (FORMYLMETHIONINE DEFORMYLASE) >gi_1652560_dbj_BAA17481_ (D90906) polypeptide deformylase [Synechocystis sp.]

Seq. No.	388319
Contig ID	10694_1.R1084
5'-most EST	LIB3432-005-P1-K1-D10
Method	BLASTX
NCBI GI	g4539452
BLAST score	494
E value	8.0e-50
Match length	124
% identity	68
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	388320
Contig ID	10695_1.R1084
5'-most EST	LIB3432-005-P1-K1-D11
Method	BLASTX
NCBI GI	g2702281
BLAST score	480
E value	4.0e-48
Match length	118
% identity	38
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	388321
Contig ID	10698_1.R1084
5'-most EST	g4879912
Method	BLASTX
NCBI GI	g5080769
BLAST score	164
E value	7.0e-11
Match length	68
% identity	53
NCBI Description	(AC007576) Unknown protein [Arabidopsis thaliana]

Seq. No.	388322
Contig ID	10707_1.R1084
5'-most EST	LIB3433-019-P1-K1-E4
Method	BLASTX
NCBI GI	g1001355
BLAST score	297
E value	5.0e-53
Match length	315
% identity	44
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	388323
Contig ID	10716_1.R1084
5'-most EST	LIB3432-005-P1-K1-F10
Method	BLASTX

NCBI GI	g3548803
BLAST score	404
E value	9.0e-62
Match length	223
% identity	68
NCBI Description	(AC005313) putative DNA-binding protein [Arabidopsis thaliana] >gi_4335770_gb_AAD17447_ (AC006284) putative SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

Seq. No.	388324
Contig ID	10719_1.R1084
5'-most EST	LIB3433-007-Q6-K1-H2
Method	BLASTX
NCBI GI	g2832633
BLAST score	533
E value	1.0e-104
Match length	207
% identity	92
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	388325
Contig ID	10723_1.R1084
5'-most EST	uC-osf1cyp172f02b1
Method	BLASTX
NCBI GI	g2129927
BLAST score	533
E value	1.0e-108
Match length	248
% identity	77
NCBI Description	zeta-carotene desaturase precursor - pepper >gi_1176437_bbs_171885 zeta-carotene desaturase, CapZDS=phytoene desaturase homolog [Capsicum annuum, early ripening fruit, Peptide, 588 aa] >gi_6006401_emb_CAA61985.1_ (X89897) zeta-carotene /neurosporene dehydrogenase (desaturase) [Capsicum annuum]

Seq. No.	388326
Contig ID	10726_2.R1084
5'-most EST	LIB3432-005-P1-K1-G11
Method	BLASTX
NCBI GI	g1169198
BLAST score	195
E value	7.0e-15
Match length	69
% identity	58
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR >gi_479738_pir__S35270 hypothetical protein - Arabidopsis thaliana >gi_166926 (L11367) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]

Seq. No.	388327
Contig ID	10742_1.R1084
5'-most EST	LIB3432-005-P1-K1-H9
Method	BLASTN
NCBI GI	g5852170
BLAST score	360

E value	0.0e+00
Match length	387
% identity	98
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No.	388328
Contig ID	10743_1.R1084
5'-most EST	LIB3432-005-P1-K1-H7
Method	BLASTX
NCBI GI	g100294
BLAST score	203
E value	8.0e-16
Match length	46
% identity	43
NCBI Description	ribonucleoprotein B, 29K - wood tobacco >gi_14135_emb_CAA43428_ (X61114) 29kD B ribonucleoprotein [Nicotiana sylvestris]

Seq. No.	388329
Contig ID	10751_1.R1084
5'-most EST	LIB3432-006-P1-K1-A4

Seq. No.	388330
Contig ID	10759_1.R1084
5'-most EST	uC-osflcyp037e04b1
Method	BLASTX
NCBI GI	g5031275
BLAST score	808
E value	3.0e-86
Match length	202
% identity	73
NCBI Description	(AF139496) unknown [Prunus armeniaca]

Seq. No.	388331
Contig ID	10760_1.R1084
5'-most EST	LIB3432-006-P1-K1-B3
Method	BLASTX
NCBI GI	g2654870
BLAST score	256
E value	7.0e-22
Match length	55
% identity	84
NCBI Description	(AF015302) RbohAOsp [Oryza sativa]

Seq. No.	388332
Contig ID	10762_1.R1084
5'-most EST	LIB3477-002-P1-K1-G4
Method	BLASTX
NCBI GI	g1928991
BLAST score	985
E value	1.0e-125
Match length	326
% identity	74
NCBI Description	(U92815) heat shock protein 70 precursor [Citrullus lanatus]

Seq. No.	388333
Contig ID	10770_1.R1084
5'-most EST	LIB3432-006-P1-K1-C4
Method	BLASTX
NCBI GI	g4566614
BLAST score	504
E value	9.0e-54
Match length	137
% identity	78
NCBI Description	(AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No.	388334
Contig ID	10774_1.R1084
5'-most EST	uC-osf1cyp081c01b1
Method	BLASTX
NCBI GI	g2443329
BLAST score	611
E value	5.0e-63
Match length	166
% identity	70
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	388335
Contig ID	10776_1.R1084
5'-most EST	g5607473

Seq. No.	388336
Contig ID	10779_1.R1084
5'-most EST	g701900
Method	BLASTX
NCBI GI	g4582787
BLAST score	1168
E value	1.0e-128
Match length	231
% identity	96
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No.	388337
Contig ID	10780_1.R1084
5'-most EST	LIB3432-006-P1-K1-D2

Seq. No.	388338
Contig ID	10793_1.R1084
5'-most EST	g2431343
Method	BLASTX
NCBI GI	g3831441
BLAST score	188
E value	5.0e-14
Match length	95
% identity	53
NCBI Description	(AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388339
Contig ID	10810_1.R1084
5'-most EST	LIB3432-006-P1-K1-G1
Method	BLASTX

NCBI GI	g4512432
BLAST score	163
E value	6.0e-11
Match length	62
% identity	56
NCBI Description	(AB017508) rplQ homologue (identity of 84% to B. subtilis) [Bacillus halodurans]

Seq. No.	388340
Contig ID	10816_1.R1084
5'-most EST	uC-osflcyp152e04b1
Method	BLASTX
NCBI GI	g3928543
BLAST score	156
E value	4.0e-10
Match length	116
% identity	34
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	388341
Contig ID	10816_2.R1084
5'-most EST	uC-osflM202068e06b1

Seq. No.	388342
Contig ID	10825_1.R1084
5'-most EST	g4879227
Method	BLASTX
NCBI GI	g4895249
BLAST score	612
E value	3.0e-75
Match length	200
% identity	64
NCBI Description	(AC007659) unknown protein [Arabidopsis thaliana]

Seq. No.	388343
Contig ID	10827_1.R1084
5'-most EST	LIB3432-036-P2-K1-A2
Method	BLASTX
NCBI GI	g4981935
BLAST score	251
E value	5.0e-21
Match length	187
% identity	33
NCBI Description	(AE001791) phosphoglycerate mutase [Thermotoga maritima]

Seq. No.	388344
Contig ID	10832_1.R1084
5'-most EST	g2310010
Method	BLASTX
NCBI GI	g3319340
BLAST score	657
E value	2.0e-68
Match length	206
% identity	62
NCBI Description	(AF077407) contains similarity to E. coli cation transport protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No.	388345
Contig ID	10836_1.R1084
5'-most EST	uC-osflcyp029e09b1
Seq. No.	388346
Contig ID	10838_1.R1084
5'-most EST	LIB3432-007-P1-K1-A3
Seq. No.	388347
Contig ID	10839_1.R1084
5'-most EST	g427236
Method	BLASTN
NCBI GI	g3925236
BLAST score	69
E value	7.0e-30
Match length	241
% identity	90
NCBI Description	Zea mays 6-phosphogluconate dehydrogenase gene, partial cds
Seq. No.	388348
Contig ID	10840_1.R1084
5'-most EST	LIB3479-001-Q6-K1-F9
Seq. No.	388349
Contig ID	10844_1.R1084
5'-most EST	LIB3432-027-P1-K1-B11
Seq. No.	388350
Contig ID	10855_1.R1084
5'-most EST	uC-osroM202034g06b1
Method	BLASTX
NCBI GI	g2244865
BLAST score	156
E value	4.0e-10
Match length	128
% identity	38
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	388351
Contig ID	10865_1.R1084
5'-most EST	uC-osflcyp065b07b1
Method	BLASTX
NCBI GI	g4538959
BLAST score	426
E value	1.0e-41
Match length	102
% identity	75
NCBI Description	(AL049488) putative protein [Arabidopsis thaliana]
Seq. No.	388352
Contig ID	10871_1.R1084
5'-most EST	uC-osflcyp159f05b1
Seq. No.	388353
Contig ID	10871_2.R1084
5'-most EST	uC-osrocyp013d09b1

Method	BLASTX
NCBI GI	g559330
BLAST score	189
E value	5.0e-14
Match length	169
% identity	34
NCBI Description	(D38521) The ha0919 gene product is novel. [Homo sapiens]

Seq. No.	388354
Contig ID	10880_1.R1084
5'-most EST	LIB3434-034-P1-K1-F11
Method	BLASTX
NCBI GI	g3980378
BLAST score	397
E value	2.0e-38
Match length	154
% identity	52
NCBI Description	(AC004561) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	388355
Contig ID	10882_1.R1084
5'-most EST	LIB3434-015-P1-K1-C3

Seq. No.	388356
Contig ID	10883_1.R1084
5'-most EST	LIB3432-007-P1-K1-E9

Seq. No.	388357
Contig ID	10888_1.R1084
5'-most EST	LIB3432-022-P1-K1-G6
Method	BLASTX
NCBI GI	g3786001
BLAST score	527
E value	1.0e-53
Match length	123
% identity	76
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	388358
Contig ID	10898_1.R1084
5'-most EST	LIB3432-007-P1-K1-G12
Method	BLASTX
NCBI GI	g5911167
BLAST score	431
E value	3.0e-42
Match length	159
% identity	52
NCBI Description	(AF136221) putative transposase protein [Zea mays]

Seq. No.	388359
Contig ID	10909_2.R1084
5'-most EST	g4880374

Seq. No.	388360
Contig ID	10910_1.R1084
5'-most EST	LIB3434-010-P1-K1-A12

Method	BLASTX
NCBI GI	g1805654
BLAST score	613
E value	2.0e-63
Match length	217
% identity	55
NCBI Description	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]

Seq. No.	388361
Contig ID	10912_1.R1084
5'-most EST	uC-osflcyp021d07b1
Method	BLASTN
NCBI GI	g5902191
BLAST score	40
E value	8.0e-13
Match length	110
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F12M16 from chromosome I, complete sequence

Seq. No.	388362
Contig ID	10918_1.R1084
5'-most EST	LIB3432-008-P1-K1-A11
Method	BLASTX
NCBI GI	g2190543
BLAST score	513
E value	1.0e-51
Match length	252
% identity	49
NCBI Description	(AC001229) EST gb_N37484 comes from this gene. [Arabidopsis thaliana]

Seq. No.	388363
Contig ID	10924_1.R1084
5'-most EST	uC-osflcyp173c12b1
Method	BLASTX
NCBI GI	g4454472
BLAST score	439
E value	7.0e-43
Match length	175
% identity	55
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	388364
Contig ID	10924_3.R1084
5'-most EST	uC-osflcyp098a09a1

Seq. No.	388365
Contig ID	10926_1.R1084
5'-most EST	g2309936
Method	BLASTX
NCBI GI	g4741844
BLAST score	420
E value	4.0e-86
Match length	196
% identity	92

NCBI Description	(AF112964) small GTP-binding protein [Triticum aestivum]

Seq. No.	388366
Contig ID	10932_1.R1084
5'-most EST	LIB3432-008-P1-K1-B6
Method	BLASTX
NCBI GI	g3075391
BLAST score	482
E value	7.0e-79
Match length	306
% identity	58
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	388367
Contig ID	10939_1.R1084
5'-most EST	g1631600
Method	BLASTX
NCBI GI	g3269293
BLAST score	572
E value	1.0e-58
Match length	181
% identity	61
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	388368
Contig ID	10940_1.R1084
5'-most EST	g2431522
Method	BLASTX
NCBI GI	g4678376
BLAST score	333
E value	1.0e-30
Match length	70
% identity	89
NCBI Description	(AL049656) putative protein [Arabidopsis thaliana]

Seq. No.	388369
Contig ID	10942_1.R1084
5'-most EST	LIB3433-021-P1-K1-E11
Method	BLASTX
NCBI GI	g584892
BLAST score	807
E value	2.0e-86
Match length	147
% identity	99
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) >gi_629805_pir__S43516 serine carboxypeptidase I - rice >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I [Oryza sativa]

Seq. No.	388370
Contig ID	10946_1.R1084
5'-most EST	g2801291
Method	BLASTX
NCBI GI	g4972052
BLAST score	168
E value	2.0e-12
Match length	257

% identity	25
NCBI Description	(AL078470) putative protein [Arabidopsis thaliana]
Seq. No.	388371
Contig ID	10947_1.R1084
5'-most EST	LIB3432-008-P1-K1-C9
Seq. No.	388372
Contig ID	10962_1.R1084
5'-most EST	g569263
Seq. No.	388373
Contig ID	10963_1.R1084
5'-most EST	LIB3432-008-P1-K1-E6
Method	BLASTX
NCBI GI	g5360754
BLAST score	731
E value	2.0e-77
Match length	150
% identity	91
NCBI Description	(AB011441) glucose-6-phosphate dehydrogenase [Triticum aestivum]
Seq. No.	388374
Contig ID	10968_1.R1084
5'-most EST	uC-osflcyp144b04b1
Method	BLASTX
NCBI GI	g4220521
BLAST score	696
E value	1.0e-72
Match length	420
% identity	41
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]
Seq. No.	388375
Contig ID	10968_3.R1084
5'-most EST	LIB3474-009-P1-K1-C3
Method	BLASTX
NCBI GI	g4220521
BLAST score	234
E value	2.0e-19
Match length	89
% identity	46
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]
Seq. No.	388376
Contig ID	10972_1.R1084
5'-most EST	LIB3479-004-Q6-K2-G7
Seq. No.	388377
Contig ID	10973_1.R1084
5'-most EST	LIB3432-008-P1-K1-F4
Method	BLASTX
NCBI GI	g4115379
BLAST score	280
E value	9.0e-25
Match length	141

% identity	45
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	388378
Contig ID	10973_2.R1084
5'-most EST	g1632003
Method	BLASTX
NCBI GI	g4115379
BLAST score	197
E value	4.0e-15
Match length	82
% identity	50
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	388379
Contig ID	10978_1.R1084
5'-most EST	g2800283
Method	BLASTX
NCBI GI	g5734720
BLAST score	159
E value	2.0e-10
Match length	91
% identity	33
NCBI Description	(AC008075) Contains PF_01426 BAH (bromo-adjacent homology) domain. ESTs gb_N96349, gb_T42710, gb_H77084, gb_AA395147 and gb_AA605500 come from this gene. [Arabidopsis thaliana]

Seq. No.	388380
Contig ID	10981_1.R1084
5'-most EST	LIB3432-008-P1-K1-G11
Method	BLASTX
NCBI GI	g4467359
BLAST score	455
E value	4.0e-45
Match length	196
% identity	50
NCBI Description	(AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

Seq. No.	388381
Contig ID	10982_1.R1084
5'-most EST	g701853

Seq. No.	388382
Contig ID	10987_1.R1084
5'-most EST	LIB3432-008-P1-K1-G6

Seq. No.	388383
Contig ID	10994_1.R1084
5'-most EST	uC-osroM202016a12b1
Method	BLASTX
NCBI GI	g4467145
BLAST score	315
E value	7.0e-29
Match length	119

% identity	52
NCBI Description	(AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]
Seq. No.	388384
Contig ID	10996_1.R1084
5'-most EST	g5667609
Seq. No.	388385
Contig ID	10998_1.R1084
5'-most EST	LIB3432-009-P1-K1-A1
Seq. No.	388386
Contig ID	10999_1.R1084
5'-most EST	uC-osrocyp012h07b1
Method	BLASTX
NCBI GI	g3757522
BLAST score	568
E value	3.0e-58
Match length	155
% identity	79
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]
Seq. No.	388387
Contig ID	11000_1.R1084
5'-most EST	LIB3432-009-P1-K1-A11
Method	BLASTX
NCBI GI	g5731763
BLAST score	250
E value	3.0e-21
Match length	92
% identity	60
NCBI Description	(X92419) SNAP25A protein [Arabidopsis thaliana] >gi_5731764_emb_CAB52583.1_ (X92420) SNAP25AB protein [Arabidopsis thaliana]
Seq. No.	388388
Contig ID	11001_1.R1084
5'-most EST	LIB3432-009-P1-K1-A2
Method	BLASTX
NCBI GI	g3367594
BLAST score	194
E value	2.0e-14
Match length	70
% identity	53
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]
Seq. No.	388389
Contig ID	11016_1.R1084
5'-most EST	LIB3432-009-P1-K1-B6
Method	BLASTN
NCBI GI	g4680189
BLAST score	34
E value	2.0e-09
Match length	42
% identity	95
NCBI Description	Oryza sativa subsp. indica putative dnaJ-like protein,

	putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds
Seq. No.	388390
Contig ID	11021_1.R1084
5'-most EST	uC-osrocyp028g06a1
Seq. No.	388391
Contig ID	11021_2.R1084
5'-most EST	uC-osrocyp028b07b1
Seq. No.	388392
Contig ID	11021_4.R1084
5'-most EST	g3767074
Method	BLASTX
NCBI GI	g773414
BLAST score	119
E value	1.0e-14
Match length	44
% identity	85
NCBI Description	(U23751) beta galactosidase [Cloning vector pBBR1MCS-2] >gi_833819 (U25059) LacZ alpha peptide [Cloning vector pBBR1MCS-3] >gi_833823 (U25060) LacZ alpha peptide [Cloning vector pBBR1MCS-4] >gi_833827 (U25061) LacZ alpha peptide [Cloning vector pBBR1MCS-5]
Seq. No.	388393
Contig ID	11027_1.R1084
5'-most EST	LIB3432-009-P1-K1-C6
Method	BLASTX
NCBI GI	g4587572
BLAST score	423
E value	4.0e-41
Match length	134
% identity	60
NCBI Description	(AC006550) Similar to gb_U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF_00400 WD40, G-beta repeats. ESTs gb_T43386 and gb_AA395236 come from this gene. [Arabidopsis thaliana]
Seq. No.	388394
Contig ID	11028_1.R1084
5'-most EST	g2442377
Seq. No.	388395
Contig ID	11030_1.R1084
5'-most EST	LIB3434-037-P1-K1-C7
Seq. No.	388396
Contig ID	11033_1.R1084
5'-most EST	LIB3434-016-P1-K1-H1
Seq. No.	388397
Contig ID	11034_1.R1084
5'-most EST	LIB3432-009-P1-K1-D12

Seq. No.	388398
Contig ID	11039_2.R1084
5'-most EST	LIB3474-003-P1-K1-A7
Method	BLASTX
NCBI GI	g3746067
BLAST score	612
E value	3.0e-63
Match length	166
% identity	72
NCBI Description	(AC005311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388399
Contig ID	11066_1.R1084
5'-most EST	LIB3432-009-P1-K1-G5
Method	BLASTX
NCBI GI	g549732
BLAST score	221
E value	1.0e-17
Match length	73
% identity	52
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION >gi_481110_pir__S37791 hypothetical protein YKL160w - yeast (Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_ (Z26877) unknown [Saccharomyces cerevisiae] >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w [Saccharomyces cerevisiae] >gi_1582545_prf__2118404F ORF [Saccharomyces cerevisiae]

Seq. No.	388400
Contig ID	11070_1.R1084
5'-most EST	LIB3432-009-P1-K1-H1
Method	BLASTX
NCBI GI	g2911052
BLAST score	454
E value	7.0e-45
Match length	134
% identity	66
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	388401
Contig ID	11078_1.R1084
5'-most EST	g5771110

Seq. No.	388402
Contig ID	11079_1.R1084
5'-most EST	LIB3432-009-P1-K1-H8
Method	BLASTX
NCBI GI	g4262140
BLAST score	340
E value	8.0e-32
Match length	118
% identity	61
NCBI Description	(AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]

Seq. No.	388403
Contig ID	11081_1.R1084
5'-most EST	LIB3432-010-P1-K1-A1

Seq. No.	388404
Contig ID	11091_1.R1084
5'-most EST	LIB3432-010-P1-K1-B11
Method	BLASTX
NCBI GI	g940288
BLAST score	410
E value	1.0e-39
Match length	151
% identity	56
NCBI Description	(L43510) protein localized in the nucleoli of pea nuclei; ORF; putative [Pisum sativum]

Seq. No.	388405
Contig ID	11092_1.R1084
5'-most EST	LIB3432-010-P1-K1-B12
Method	BLASTX
NCBI GI	g1778149
BLAST score	443
E value	1.0e-43
Match length	135
% identity	64
NCBI Description	(U66404) phosphate/phosphoenolpyruvate translocator precursor [Zea mays]

Seq. No.	388406
Contig ID	11098_1.R1084
5'-most EST	g2310428
Method	BLASTX
NCBI GI	g2970556
BLAST score	393
E value	2.0e-37
Match length	236
% identity	40
NCBI Description	(AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]

Seq. No.	388407
Contig ID	11099_1.R1084
5'-most EST	g3768015

Seq. No.	388408
Contig ID	11106_1.R1084
5'-most EST	LIB3432-010-P1-K1-C6
Method	BLASTX
NCBI GI	g1076668
BLAST score	1186
E value	1.0e-130
Match length	238
% identity	93
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	388409
Contig ID	11107_1.R1084
5'-most EST	LIB3432-010-P1-K1-C7

Seq. No.	388410
Contig ID	11108_1.R1084
5'-most EST	g5667494
Method	BLASTX
NCBI GI	g4455256
BLAST score	446
E value	7.0e-44
Match length	149
% identity	60
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	388411
Contig ID	11111_1.R1084
5'-most EST	LIB3434-005-P1-K1-F3

Seq. No.	388412
Contig ID	11117_1.R1084
5'-most EST	uC-osflcyp045h01b1
Method	BLASTX
NCBI GI	g2262105
BLAST score	209
E value	1.0e-34
Match length	188
% identity	41
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	388413
Contig ID	11122_1.R1084
5'-most EST	g569618
Method	BLASTX
NCBI GI	g5231113
BLAST score	116
E value	9.0e-14
Match length	199
% identity	36
NCBI Description	(AF141202) EIN2 [Arabidopsis thaliana] >gi_5231115_gb_AAD41077.1_AF141203_1 (AF141203) EIN2 [Arabidopsis thaliana]

Seq. No.	388414
Contig ID	11124_1.R1084
5'-most EST	uC-osflcyp085d04b1
Method	BLASTX
NCBI GI	g2275199
BLAST score	243
E value	1.0e-42
Match length	217
% identity	51
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388415
Contig ID	11131_1.R1084
5'-most EST	uC-osflcyp157c06a1

Seq. No.	388416

Contig ID	11137_1.R1084
5'-most EST	LIB3432-010-P1-K1-F3
Method	BLASTX
NCBI GI	g416564
BLAST score	277
E value	2.0e-24
Match length	78
% identity	72
NCBI Description	ABCISIC ACID-INDUCIBLE PROTEIN KINASE >gi_422013_pir__A46408 abscisic acid-inducible serine/threonine protein kinase homolog - wheat (fragment) >gi_170664_gb_AAA96325.1_AAA96325 (M94726) protein kinase [Triticum aestivum]

Seq. No.	388417
Contig ID	11139_1.R1084
5'-most EST	LIB3479-002-Q6-K1-D8

Seq. No.	388418
Contig ID	11144_1.R1084
5'-most EST	LIB3479-003-Q6-K2-F8
Method	BLASTX
NCBI GI	g2702270
BLAST score	849
E value	4.0e-91
Match length	293
% identity	53
NCBI Description	(AC003033) unknown protein [Arabidopsis thaliana]

Seq. No.	388419
Contig ID	11153_1.R1084
5'-most EST	LIB3432-010-P1-K1-G7

Seq. No.	388420
Contig ID	11156_1.R1084
5'-most EST	LIB3432-010-P1-K1-H1
Method	BLASTX
NCBI GI	g4049342
BLAST score	331
E value	1.0e-30
Match length	163
% identity	17
NCBI Description	(AL034567) adenylate translocator (brittle-1)-like protein [Arabidopsis thaliana]

Seq. No.	388421
Contig ID	11159_1.R1084
5'-most EST	LIB3432-039-P1-K1-F8
Method	BLASTN
NCBI GI	g2264315
BLAST score	37
E value	5.0e-11
Match length	129
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence

Seq. No.	388422
Contig ID	11170_1.R1084
5'-most EST	LIB3432-011-P1-K1-A11

Seq. No.	388423
Contig ID	11173_1.R1084
5'-most EST	LIB3432-011-P1-K1-A3
Method	BLASTX
NCBI GI	g5596996
BLAST score	971
E value	1.0e-105
Match length	249
% identity	77
NCBI Description	(Y14600) putative protein serine /threonine kinase [Sorghum bicolor]

Seq. No.	388424
Contig ID	11174_1.R1084
5'-most EST	LIB3432-016-P1-K1-F11
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	6.0e-11
Match length	37
% identity	60
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388425
Contig ID	11174_2.R1084
5'-most EST	g2427558

Seq. No.	388426
Contig ID	11179_1.R1084
5'-most EST	LIB3477-004-P1-K1-B11
Method	BLASTX
NCBI GI	g2117937
BLAST score	2122
E value	0.0e+00
Match length	468
% identity	89
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No.	388427
Contig ID	11179_2.R1084
5'-most EST	g3763379
Method	BLASTX
NCBI GI	g136739
BLAST score	256
E value	6.0e-34
Match length	92
% identity	75
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	388428
Contig ID	11192_1.R1084
5'-most EST	LIB3433-050-P1-K1-F12
Method	BLASTX
NCBI GI	g3892056
BLAST score	544
E value	2.0e-55
Match length	124
% identity	83
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	388429
Contig ID	11192_2.R1084
5'-most EST	LIB3432-011-P1-K1-C2
Method	BLASTX
NCBI GI	g3892056
BLAST score	536
E value	1.0e-54
Match length	126
% identity	82
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	388430
Contig ID	11194_1.R1084
5'-most EST	LIB3433-043-P1-K1-F3
Method	BLASTX
NCBI GI	g4960150
BLAST score	296
E value	9.0e-40
Match length	93
% identity	95
NCBI Description	(AF153277) DNA-directed RNA polymerase IIa [Nicotiana tabacum] >gi_4960152_gb_AAD34614.1_AF153278_1 (AF153278) DNA-directed RNA polymerase IIb [Nicotiana tabacum]

Seq. No.	388431
Contig ID	11197_1.R1084
5'-most EST	LIB3432-011-P1-K1-C7
Method	BLASTX
NCBI GI	g3851005
BLAST score	253
E value	2.0e-21
Match length	61
% identity	84
NCBI Description	(AF069911) pyruvate dehydrogenase E1 alpha subunit [Zea mays]

Seq. No.	388432
Contig ID	11197_2.R1084
5'-most EST	LIB3433-022-P1-K1-B5
Method	BLASTX
NCBI GI	g1709446
BLAST score	672
E value	8.0e-77
Match length	214

% identity	67
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT, MITOCHONDRIAL PRECURSOR (PDHE1-A) >gi_2117533_pir__JC4358 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha chain - Arabidopsis thaliana mitochondrion >gi_710400 (U21214) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	388433
Contig ID	11204_1.R1084
5'-most EST	g2431209
Method	BLASTX
NCBI GI	g3738323
BLAST score	400
E value	8.0e-39
Match length	125
% identity	57
NCBI Description	(AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388434
Contig ID	11206_1.R1084
5'-most EST	g454454
Method	BLASTX
NCBI GI	g4584358
BLAST score	253
E value	1.0e-41
Match length	135
% identity	79
NCBI Description	(AC006420) unknown protein [Arabidopsis thaliana]

Seq. No.	388435
Contig ID	11206_2.R1084
5'-most EST	g5002841
Method	BLASTX
NCBI GI	g4584358
BLAST score	288
E value	1.0e-25
Match length	102
% identity	67
NCBI Description	(AC006420) unknown protein [Arabidopsis thaliana]

Seq. No.	388436
Contig ID	11208_1.R1084
5'-most EST	LIB3432-011-P1-K1-D7

Seq. No.	388437
Contig ID	11210_1.R1084
5'-most EST	uC-osroM202026g05b1
Method	BLASTX
NCBI GI	g4038034
BLAST score	322
E value	2.0e-29
Match length	92
% identity	68
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	388438

Contig ID	11211_1.R1084
5'-most EST	LIB3432-011-P1-K1-E1
Method	BLASTX
NCBI GI	g2934902
BLAST score	960
E value	1.0e-104
Match length	213
% identity	90
NCBI Description	(AF039304) cpSecY [Zea mays]

Seq. No.	388439
Contig ID	11212_1.R1084
5'-most EST	uC-osflcyp067c10a1

Seq. No.	388440
Contig ID	11214_1.R1084
5'-most EST	LIB3434-011-P1-K1-G8

Seq. No.	388441
Contig ID	11216_1.R1084
5'-most EST	uC-osflM202046f04b1
Method	BLASTX
NCBI GI	g4514655
BLAST score	909
E value	1.0e-100
Match length	266
% identity	67
NCBI Description	(AB024058) IDS3 [Hordeum vulgare]

Seq. No.	388442
Contig ID	11216_3.R1084
5'-most EST	uC-osflM202037a04b1
Method	BLASTX
NCBI GI	g520582
BLAST score	353
E value	2.0e-33
Match length	107
% identity	59
NCBI Description	(D37796) Ids3 [Hordeum vulgare]

Seq. No.	388443
Contig ID	11221_1.R1084
5'-most EST	g4716196
Method	BLASTX
NCBI GI	g2558660
BLAST score	304
E value	2.0e-27
Match length	139
% identity	26
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	388444
Contig ID	11224_1.R1084
5'-most EST	uC-osflm202111d04b1
Method	BLASTX
NCBI GI	g4982509
BLAST score	517

E value 2.0e-52
Match length 141
% identity 76
NCBI Description (AC000107) F17F8.15 [Arabidopsis thaliana]

Seq. No. 388445
Contig ID 11238_1.R1084
5'-most EST LIB3432-026-P1-K1-D1
Method BLASTN
NCBI GI g4680488
BLAST score 204
E value 1.0e-111
Match length 385
% identity 99
NCBI Description Oryza sativa BAC clone 1.H19, complete sequence

Seq. No. 388446
Contig ID 11240_1.R1084
5'-most EST LIB3432-011-P1-K1-G6
Method BLASTX
NCBI GI g3650033
BLAST score 283
E value 1.0e-26
Match length 163
% identity 48
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 388447
Contig ID 11240_2.R1084
5'-most EST LIB3432-028-P1-K1-A12
Method BLASTX
NCBI GI g3650033
BLAST score 374
E value 1.0e-35
Match length 119
% identity 63
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 388448
Contig ID 11246_1.R1084
5'-most EST g2800879
Method BLASTX
NCBI GI g4468813
BLAST score 241
E value 4.0e-20
Match length 54
% identity 80
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 388449
Contig ID 11249_1.R1084
5'-most EST g5005353

Seq. No. 388450
Contig ID 11251_1.R1084
5'-most EST LIB3432-011-P1-K1-H7

Seq. No.	388451
Contig ID	11253_1.R1084
5'-most EST	g2312616

Seq. No.	388452
Contig ID	11253_2.R1084
5'-most EST	LIB3432-011-P1-K1-H9

Seq. No.	388453
Contig ID	11259_1.R1084
5'-most EST	g700912
Method	BLASTX
NCBI GI	g4220531
BLAST score	161
E value	3.0e-10
Match length	99
% identity	41
NCBI Description	(AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388454
Contig ID	11260_1.R1084
5'-most EST	LIB3432-012-P1-K1-A4
Method	BLASTX
NCBI GI	g6016697
BLAST score	488
E value	1.0e-74
Match length	200
% identity	73
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	388455
Contig ID	11262_1.R1084
5'-most EST	uC-osflcyp110a06a1

Seq. No.	388456
Contig ID	11264_1.R1084
5'-most EST	uC-osroM202037e09b1
Method	BLASTX
NCBI GI	g3702323
BLAST score	767
E value	1.0e-106
Match length	420
% identity	52
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	388457
Contig ID	11273_1.R1084
5'-most EST	g427641
Method	BLASTX
NCBI GI	g3861189
BLAST score	158
E value	2.0e-10
Match length	54
% identity	65
NCBI Description	(AJ235272) 50S RIBOSOMAL PROTEIN L14 (rplN) [Rickettsia prowazekii]

Seq. No.	388458
Contig ID	11279_1.R1084
5'-most EST	LIB3432-012-P1-K1-C4

Seq. No.	388459
Contig ID	11284_1.R1084
5'-most EST	LIB3432-012-P1-K1-C9

Seq. No.	388460
Contig ID	11290_1.R1084
5'-most EST	LIB3434-012-P1-K1-E10
Method	BLASTX
NCBI GI	g3256035
BLAST score	614
E value	2.0e-63
Match length	259
% identity	48
NCBI Description	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No.	388461
Contig ID	11300_1.R1084
5'-most EST	uC-osroM202019e08a1

Seq. No.	388462
Contig ID	11301_1.R1084
5'-most EST	g4715483

Seq. No.	388463
Contig ID	11308_1.R1084
5'-most EST	LIB3432-012-P1-K1-E9
Method	BLASTN
NCBI GI	g6015437
BLAST score	34
E value	2.0e-09
Match length	34
% identity	58
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388464
Contig ID	11310_1.R1084
5'-most EST	LIB3432-012-P1-K1-F11
Method	BLASTX
NCBI GI	g1877183
BLAST score	178
E value	1.0e-12
Match length	98
% identity	39
NCBI Description	(Y11586) putative mitochondrial matrix protein [Chlamydomonas reinhardtii]

Seq. No.	388465
Contig ID	11312_1.R1084
5'-most EST	g2799003
Method	BLASTX
NCBI GI	g4662632
BLAST score	226

E value	3.0e-18
Match length	60
% identity	80
NCBI Description	(AC007267) unknown protein [Arabidopsis thaliana]

Seq. No.	388466
Contig ID	11316_1.R1084
5'-most EST	LIB3432-012-P1-K1-F8
Method	BLASTX
NCBI GI	g3522929
BLAST score	743
E value	9.0e-79
Match length	151
% identity	91
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	388467
Contig ID	11323_1.R1084
5'-most EST	g4879503
Method	BLASTX
NCBI GI	g3786008
BLAST score	205
E value	8.0e-16
Match length	91
% identity	48
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	388468
Contig ID	11331_1.R1084
5'-most EST	LIB3432-012-P1-K1-H2
Method	BLASTX
NCBI GI	g1362055
BLAST score	618
E value	4.0e-64
Match length	168
% identity	70
NCBI Description	phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - alfalfa >gi_603221 (U18239) 6-phosphogluconate dehydrogenase [Medicago sativa subsp. sativa]

Seq. No.	388469
Contig ID	11341_1.R1084
5'-most EST	LIB3432-013-P1-K1-A11
Method	BLASTX
NCBI GI	g4115949
BLAST score	259
E value	2.0e-22
Match length	114
% identity	51
NCBI Description	(AF118223) contains similarity to adenosine deaminases [Arabidopsis thaliana]

Seq. No.	388470
Contig ID	11343_1.R1084
5'-most EST	LIB3432-013-P1-K1-A2

Method	BLASTX
NCBI GI	g2224663
BLAST score	636
E value	5.0e-74
Match length	288
% identity	58
NCBI Description	(AB002359) KIAA0361 [Homo sapiens]

Seq. No.	388471
Contig ID	11345_1.R1084
5'-most EST	LIB3432-013-P1-K1-A4
Method	BLASTX
NCBI GI	g4204294
BLAST score	679
E value	3.0e-71
Match length	210
% identity	69
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	388472
Contig ID	11350_1.R1084
5'-most EST	LIB3433-047-P1-K1-C6
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	1.0e-09
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	388473
Contig ID	11373_1.R1084
5'-most EST	LIB3432-013-P1-K1-C9
Method	BLASTX
NCBI GI	g5091620
BLAST score	485
E value	1.0e-48
Match length	188
% identity	57
NCBI Description	(AC007454) Contains similarity to gi_836774 FAB1 protein from Saccharomyces cerevisiae genome gb_D50617. [Arabidopsis thaliana]

Seq. No.	388474
Contig ID	11375_1.R1084
5'-most EST	uC-osflcyp171e09b1
Method	BLASTX
NCBI GI	g4895198
BLAST score	161
E value	2.0e-10
Match length	132
% identity	35
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No.	388475
Contig ID	11381_1.R1084

5'-most EST	LIB3432-013-P1-K1-D8
Method	BLASTX
NCBI GI	g5669650
BLAST score	292
E value	3.0e-26
Match length	153
% identity	42
NCBI Description	(AF096260) ER66 protein [Lycopersicon esculentum]

Seq. No.	388476
Contig ID	11389_1.R1084
5'-most EST	LIB3432-013-P1-K1-E4

Seq. No.	388477
Contig ID	11394_1.R1084
5'-most EST	LIB3434-029-P1-K1-H5
Method	BLASTX
NCBI GI	g2494041
BLAST score	518
E value	2.0e-52
Match length	208
% identity	51
NCBI Description	DIAMINOPIMELATE EPIMERASE (DAP EPIMERASE) >gi_1653875_dbj_BAA18785_ (D90917) diaminopimelate epimerase [Synechocystis sp.]

Seq. No.	388478
Contig ID	11394_2.R1084
5'-most EST	LIB3432-013-P1-K1-E9
Method	BLASTX
NCBI GI	g2494041
BLAST score	211
E value	2.0e-16
Match length	83
% identity	48
NCBI Description	DIAMINOPIMELATE EPIMERASE (DAP EPIMERASE) >gi_1653875_dbj_BAA18785_ (D90917) diaminopimelate epimerase [Synechocystis sp.]

Seq. No.	388479
Contig ID	11397_1.R1084
5'-most EST	uC-osflcyp024e12b1
Method	BLASTX
NCBI GI	g4895186
BLAST score	465
E value	9.0e-56
Match length	162
% identity	64
NCBI Description	(AC007661) putative growth regulator protein [Arabidopsis thaliana]

Seq. No.	388480
Contig ID	11409_1.R1084
5'-most EST	g2311579
Method	BLASTX
NCBI GI	g1085650
BLAST score	949

E value	1.0e-103
Match length	214
% identity	87
NCBI Description	aspartate transcarbomoylase - wheat >gi_688218_bbs_156442 aspartate carbamoyltransferase {C-terminal} {EC 2.1.3.2} [Triticum aestivum=wheat, avalon, seedlings, Peptide Partial, 233 aa]

Seq. No.	388481
Contig ID	11414_1.R1084
5'-most EST	LIB3432-013-P1-K1-G7
Method	BLASTX
NCBI GI	g3024363
BLAST score	462
E value	6.0e-46
Match length	125
% identity	74
NCBI Description	PHENYLALANINE AMMONIA-LYASE >gi_1483610_emb_CAA68036_ (X99705) phenylalanine ammonia-lyase [Triticum aestivum]

Seq. No.	388482
Contig ID	11419_1.R1084
5'-most EST	g4880880
Method	BLASTX
NCBI GI	g5257221
BLAST score	689
E value	2.0e-72
Match length	266
% identity	53
NCBI Description	(AF117887) protein arginine methyltransferase [Mus musculus]

Seq. No.	388483
Contig ID	11426_1.R1084
5'-most EST	LIB3432-043-P1-K1-A11

Seq. No.	388484
Contig ID	11429_1.R1084
5'-most EST	LIB3432-014-P1-K1-A10

Seq. No.	388485
Contig ID	11438_1.R1084
5'-most EST	g3763614

Seq. No.	388486
Contig ID	11446_1.R1084
5'-most EST	LIB3432-014-P1-K1-B6
Method	BLASTX
NCBI GI	g5830788
BLAST score	474
E value	2.0e-47
Match length	136
% identity	68
NCBI Description	(AL117188) thioredoxin reductase (NADPH) 2 [Arabidopsis thaliana]

Seq. No. 388487

Contig ID	11451_1.R1084
5'-most EST	LIB3432-014-P1-K1-C10
Method	BLASTX
NCBI GI	g4204265
BLAST score	632
E value	7.0e-66
Match length	163
% identity	67
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	388488
Contig ID	11461_1.R1084
5'-most EST	g5607380
Method	BLASTX
NCBI GI	g5738376
BLAST score	602
E value	7.0e-67
Match length	169
% identity	75
NCBI Description	(AL021889) N-acetylornithine deacetylase-like protein, fragment [Arabidopsis thaliana]

Seq. No.	388489
Contig ID	11466_1.R1084
5'-most EST	LIB3432-014-P1-K1-D3
Method	BLASTX
NCBI GI	g2369766
BLAST score	371
E value	3.0e-35
Match length	76
% identity	87
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	388490
Contig ID	11471_1.R1084
5'-most EST	LIB3432-014-P1-K1-D9
Method	BLASTX
NCBI GI	g3927825
BLAST score	1545
E value	1.0e-172
Match length	342
% identity	85
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	388491
Contig ID	11484_1.R1084
5'-most EST	uC-osrocyp030b09b1
Method	BLASTX
NCBI GI	g1351856
BLAST score	2568
E value	0.0e+00
Match length	551
% identity	90
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

Seq. No.	388492
Contig ID	11488_1.R1084
5'-most EST	LIB3474-007-P1-K1-C4
Method	BLASTX
NCBI GI	g4580456
BLAST score	350
E value	1.0e-32
Match length	215
% identity	41
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	388493
Contig ID	11491_1.R1084
5'-most EST	g3761587
Method	BLASTX
NCBI GI	g4263704
BLAST score	160
E value	2.0e-26
Match length	170
% identity	46
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	388494
Contig ID	11491_2.R1084
5'-most EST	LIB3432-014-P1-K1-F5
Method	BLASTX
NCBI GI	g4263704
BLAST score	250
E value	5.0e-27
Match length	168
% identity	43
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	388495
Contig ID	11496_1.R1084
5'-most EST	uC-osflcyp125b12b1
Method	BLASTX
NCBI GI	g3096910
BLAST score	1144
E value	1.0e-125
Match length	284
% identity	77
NCBI Description	(AJ005813) neoxanthin cleavage enzyme [Arabidopsis thaliana]

Seq. No.	388496
Contig ID	11503_1.R1084
5'-most EST	LIB3432-014-P1-K1-G7
Method	BLASTX
NCBI GI	g6093660
BLAST score	156
E value	1.0e-09
Match length	107
% identity	36

NCBI Description	PYRROLIDONE-CARBOXYLATE PEPTIDASE (5-OXOPROLYL-PEPTIDASE) (PYROGLUTAMYL-PEPTIDASE I) (PGP-I) (PYRASE) >gi_3551425_dbj_BAA32989_ (AB015291) pyrrolidone carboxyl peptidase [Pyrococcus furiosus]
Seq. No.	388497
Contig ID	11505_1.R1084
5'-most EST	LIB3432-014-P1-K1-G9
Seq. No.	388498
Contig ID	11509_1.R1084
5'-most EST	LIB3433-058-P1-K1-C4
Method	BLASTX
NCBI GI	g294845
BLAST score	934
E value	1.0e-101
Match length	248
% identity	70
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]
Seq. No.	388499
Contig ID	11514_1.R1084
5'-most EST	LIB3434-057-P1-K1-C10
Method	BLASTX
NCBI GI	g2961358
BLAST score	178
E value	1.0e-12
Match length	55
% identity	64
NCBI Description	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]
Seq. No.	388500
Contig ID	11536_1.R1084
5'-most EST	g4715694
Method	BLASTX
NCBI GI	g5123948
BLAST score	325
E value	3.0e-35
Match length	183
% identity	48
NCBI Description	(AL079349) putative protein [Arabidopsis thaliana]
Seq. No.	388501
Contig ID	11544_1.R1084
5'-most EST	LIB3432-015-P1-K1-C7
Seq. No.	388502
Contig ID	11553_1.R1084
5'-most EST	g428828
Method	BLASTX
NCBI GI	g2281115
BLAST score	1173
E value	1.0e-129
Match length	292
% identity	76

NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	388503
Contig ID	11560_1.R1084
5'-most EST	uC-osflcyp097a07b1
Method	BLASTX
NCBI GI	g3184283
BLAST score	1711
E value	0.0e+00
Match length	469
% identity	74
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]

Seq. No.	388504
Contig ID	11566_1.R1084
5'-most EST	g3462566

Seq. No.	388505
Contig ID	11571_1.R1084
5'-most EST	LIB3432-015-P1-K1-F11
Method	BLASTX
NCBI GI	g5911326
BLAST score	485
E value	1.0e-48
Match length	206
% identity	49
NCBI Description	(AF108387) transporter associated with antigen processing 1 [Heterodontus francisci]

Seq. No.	388506
Contig ID	11575_1.R1084
5'-most EST	g5771183
Method	BLASTX
NCBI GI	g6006362
BLAST score	271
E value	2.0e-23
Match length	66
% identity	91
NCBI Description	(AP000559) Similar to Arabidopsis thaliana chromosome II BAC T32F12, hypothetical protein (AC005314) [Oryza sativa]

Seq. No.	388507
Contig ID	11577_1.R1084
5'-most EST	LIB3599-001-P1-K6-H11
Method	BLASTX
NCBI GI	g3193301
BLAST score	504
E value	2.0e-51
Match length	169
% identity	62
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No. 388508

Contig ID	11579_1.R1084
5'-most EST	LIB3434-019-P1-K1-B8
Method	BLASTX
NCBI GI	g2443857
BLAST score	714
E value	3.0e-75
Match length	146
% identity	88
NCBI Description	(U79961) vacuolar sorting receptor homolog [Zea mays]

Seq. No.	388509
Contig ID	11584_1.R1084
5'-most EST	g3759110
Method	BLASTX
NCBI GI	g1907270
BLAST score	726
E value	1.0e-76
Match length	191
% identity	76
NCBI Description	(X96761) sulphate transporter protein [Sporobolus stapfianus]

Seq. No.	388510
Contig ID	11600_1.R1084
5'-most EST	LIB3474-003-P1-K1-E9
Method	BLASTX
NCBI GI	g466160
BLAST score	361
E value	3.0e-34
Match length	81
% identity	86
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	388511
Contig ID	11602_1.R1084
5'-most EST	uC-osroM202003f04a2

Seq. No.	388512
Contig ID	11605_1.R1084
5'-most EST	uC-osflcyp082f09b1

Seq. No.	388513
Contig ID	11614_1.R1084
5'-most EST	LIB3432-016-P1-K1-B11

Seq. No.	388514
Contig ID	11619_1.R1084
5'-most EST	LIB3432-016-P1-K1-B5
Method	BLASTX
NCBI GI	g4678934
BLAST score	250
E value	2.0e-21
Match length	139
% identity	42

NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	388515
Contig ID	11622_1.R1084
5'-most EST	LIB3434-016-P1-K1-A10
Method	BLASTX
NCBI GI	g1174870
BLAST score	235
E value	2.0e-19
Match length	61
% identity	70
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN >gi_633685_emb_CAA55861_ (X79274) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	388516
Contig ID	11623_1.R1084
5'-most EST	LIB3432-016-P1-K1-B9
Method	BLASTX
NCBI GI	g1215812
BLAST score	560
E value	2.0e-57
Match length	160
% identity	68
NCBI Description	(D38170) probenazole-inducible protein PBZ1 [Oryza sativa] >gi_2780343_dbj_BAA24277_ (D82066) PBZ1 [Oryza sativa]

Seq. No.	388517
Contig ID	11628_1.R1084
5'-most EST	g4716084
Method	BLASTX
NCBI GI	g2576361
BLAST score	396
E value	4.0e-38
Match length	122
% identity	59
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	388518
Contig ID	11631_1.R1084
5'-most EST	LIB3432-016-P1-K1-C5
Method	BLASTX
NCBI GI	g4959731
BLAST score	405
E value	3.0e-44
Match length	209
% identity	43
NCBI Description	(AF136446) chaperonin-containing-TCP1 theta subunit [Tetrahymena pyriformis]

Seq. No.	388519
Contig ID	11646_1.R1084
5'-most EST	g3761224
Method	BLASTX
NCBI GI	g4539459
BLAST score	153

E value	2.0e-17
Match length	54
% identity	69
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	388520
Contig ID	11657_1.R1084
5'-most EST	LIB3432-016-P1-K1-E7
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	3.0e-10
Match length	36
% identity	59
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388521
Contig ID	11658_1.R1084
5'-most EST	g5004164

Seq. No.	388522
Contig ID	11660_1.R1084
5'-most EST	g702471

Seq. No.	388523
Contig ID	11667_1.R1084
5'-most EST	LIB3432-016-P1-K1-F6
Method	BLASTX
NCBI GI	g1705677
BLAST score	335
E value	4.0e-31
Match length	75
% identity	85
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	388524
Contig ID	11672_1.R1084
5'-most EST	LIB3432-016-P1-K1-G10

Seq. No.	388525
Contig ID	11675_1.R1084
5'-most EST	g2310012
Method	BLASTX
NCBI GI	g4567249
BLAST score	368
E value	3.0e-45
Match length	141
% identity	67
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388526
Contig ID	11688_1.R1084
5'-most EST	LIB3432-016-P1-K1-H3
Method	BLASTX

NCBI GI	g3068713
BLAST score	531
E value	6.0e-54
Match length	151
% identity	68
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	388527
Contig ID	11703_1.R1084
5'-most EST	g2312013
Method	BLASTX
NCBI GI	g4127348
BLAST score	398
E value	3.0e-43
Match length	138
% identity	69
NCBI Description	(AJ010449) glutathione transferase [Alopecurus myosuroides]

Seq. No.	388528
Contig ID	11703_2.R1084
5'-most EST	g286888
Method	BLASTX
NCBI GI	g2190992
BLAST score	528
E value	1.0e-53
Match length	151
% identity	68
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No.	388529
Contig ID	11703_3.R1084
5'-most EST	LIB3432-017-P1-K1-B1
Method	BLASTX
NCBI GI	g2982262
BLAST score	174
E value	3.0e-12
Match length	101
% identity	27
NCBI Description	(AF051214) probable glutathione S-transferase [Picea mariana]

Seq. No.	388530
Contig ID	11703_4.R1084
5'-most EST	g4878790
Method	BLASTX
NCBI GI	g4127350
BLAST score	305
E value	2.0e-36
Match length	111
% identity	72
NCBI Description	(AJ010450) glutathione transferase [Alopecurus myosuroides]

Seq. No.	388531
Contig ID	11703_5.R1084
5'-most EST	g701948
Method	BLASTX

NCBI GI	g2190992
BLAST score	345
E value	2.0e-32
Match length	88
% identity	69
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No.	388532
Contig ID	11703_6.R1084
5'-most EST	g700747
Method	BLASTX
NCBI GI	g4127348
BLAST score	375
E value	4.0e-36
Match length	99
% identity	70
NCBI Description	(AJ010449) glutathione transferase [Alopecurus myosuroides]

Seq. No.	388533
Contig ID	11703_7.R1084
5'-most EST	g700317
Method	BLASTX
NCBI GI	g2190992
BLAST score	345
E value	2.0e-32
Match length	113
% identity	58
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No.	388534
Contig ID	11712_1.R1084
5'-most EST	LIB3432-017-P1-K1-B7

Seq. No.	388535
Contig ID	11714_1.R1084
5'-most EST	LIB3432-017-P1-K1-B9
Method	BLASTX
NCBI GI	g4335756
BLAST score	205
E value	3.0e-29
Match length	137
% identity	26
NCBI Description	(AC006284) putative ankyrin [Arabidopsis thaliana]

Seq. No.	388536
Contig ID	11720_1.R1084
5'-most EST	g4716625
Method	BLASTX
NCBI GI	g4510346
BLAST score	279
E value	3.0e-24
Match length	79
% identity	70
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388537
Contig ID	11730_1.R1084
5'-most EST	LIB3432-017-P1-K1-D12

Seq. No.	388538
Contig ID	11732_1.R1084
5'-most EST	uC-osflm202107g08b1
Method	BLASTX
NCBI GI	g4101703
BLAST score	831
E value	1.0e-103
Match length	424
% identity	46
NCBI Description	(AF006078) glucose acyltransferase [Solanum berthaultii]

Seq. No.	388539
Contig ID	11740_1.R1084
5'-most EST	LIB3432-017-P1-K1-E10
Method	BLASTX
NCBI GI	g2244971
BLAST score	239
E value	7.0e-20
Match length	58
% identity	74
NCBI Description	(Z97340) galactokinase like protein [Arabidopsis thaliana]

Seq. No.	388540
Contig ID	11753_1.R1084
5'-most EST	g4878759

Seq. No.	388541
Contig ID	11756_1.R1084
5'-most EST	LIB3432-017-P1-K1-F6

Seq. No.	388542
Contig ID	11786_1.R1084
5'-most EST	LIB3432-018-P1-K1-A7

Seq. No.	388543
Contig ID	11793_1.R1084
5'-most EST	g569695

Seq. No.	388544
Contig ID	11797_1.R1084
5'-most EST	uC-osflcyp071c05b1
Method	BLASTX
NCBI GI	g2245125
BLAST score	159
E value	2.0e-10
Match length	74
% identity	47
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388545
Contig ID	11797_2.R1084
5'-most EST	LIB3434-054-P1-K1-C10
Method	BLASTX

NCBI GI	g2245125
BLAST score	156
E value	6.0e-10
Match length	52
% identity	60
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388546
Contig ID	11819_1.R1084
5'-most EST	uC-osroM202028e04b1
Method	BLASTX
NCBI GI	g3935181
BLAST score	1209
E value	1.0e-133
Match length	241
% identity	88
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	388547
Contig ID	11827_1.R1084
5'-most EST	uC-osflcyp174g02b1
Method	BLASTX
NCBI GI	g3702321
BLAST score	474
E value	2.0e-47
Match length	113
% identity	55
NCBI Description	(AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No.	388548
Contig ID	11827_2.R1084
5'-most EST	g427350
Method	BLASTX
NCBI GI	g3702321
BLAST score	282
E value	6.0e-35
Match length	83
% identity	88
NCBI Description	(AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No.	388549
Contig ID	11833_1.R1084
5'-most EST	LIB3432-018-P1-K1-F12

Seq. No.	388550
Contig ID	11838_1.R1084
5'-most EST	uC-osrocyp016g03b1
Method	BLASTX
NCBI GI	g5777631
BLAST score	615
E value	3.0e-82
Match length	253
% identity	65
NCBI Description	(AJ245900) CAA303719.1 protein [Oryza sativa]

Seq. No.	388551
Contig ID	11844_1.R1084
5'-most EST	uC-osflcyp109c02b1
Method	BLASTX
NCBI GI	g2340166
BLAST score	1112
E value	1.0e-122
Match length	345
% identity	63
NCBI Description	(AF008124) glutathione S-conjugate transporting ATPase [Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug resistance-associated protein homolog [Arabidopsis thaliana]

Seq. No.	388552
Contig ID	11844_2.R1084
5'-most EST	LIB3432-018-P1-K1-G2
Method	BLASTX
NCBI GI	g2340166
BLAST score	271
E value	1.0e-23
Match length	82
% identity	61
NCBI Description	(AF008124) glutathione S-conjugate transporting ATPase [Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug resistance-associated protein homolog [Arabidopsis thaliana]

Seq. No.	388553
Contig ID	11849_1.R1084
5'-most EST	LIB3474-012-P1-K1-D5
Method	BLASTX
NCBI GI	g3287270
BLAST score	899
E value	5.0e-97
Match length	197
% identity	84
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	388554
Contig ID	11859_1.R1084
5'-most EST	LIB3432-018-P1-K1-H6
Method	BLASTX
NCBI GI	g130187
BLAST score	731
E value	1.0e-77
Match length	143
% identity	99
NCBI Description	PHYTOCHROME A >gi_82499_pir__S03728 phytochrome (clone phy18) - rice >gi_20288_emb_CAA32375_ (X14172) phytochrome [Oryza sativa]

Seq. No.	388555
Contig ID	11861_1.R1084
5'-most EST	LIB3432-018-P1-K1-H8

Seq. No.	388556

Contig ID	11862_1.R1084
5'-most EST	LIB3433-038-P1-K1-B2
Method	BLASTX
NCBI GI	g3717946
BLAST score	259
E value	4.0e-22
Match length	110
% identity	52
NCBI Description	(AJ005901) vag1 [Arabidopsis thaliana] >gi_5853315_gb_AAD54418.1_ (AF181688) vacuolar membrane ATPase subunit G [Arabidopsis thaliana]

Seq. No.	388557
Contig ID	11864_1.R1084
5'-most EST	uC-osflcyp156b12b1
Method	BLASTX
NCBI GI	g2244935
BLAST score	195
E value	9.0e-15
Match length	94
% identity	40
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388558
Contig ID	11866_1.R1084
5'-most EST	uC-osflcyp109g06b1

Seq. No.	388559
Contig ID	11881_1.R1084
5'-most EST	LIB3432-019-P1-K1-B8
Method	BLASTX
NCBI GI	g2791806
BLAST score	510
E value	2.0e-51
Match length	165
% identity	57
NCBI Description	(AF041433) bet3 [Mus musculus]

Seq. No.	388560
Contig ID	11887_1.R1084
5'-most EST	uC-osflM202056c12a1
Method	BLASTX
NCBI GI	g1311479
BLAST score	1490
E value	1.0e-166
Match length	305
% identity	95
NCBI Description	(D45890) sucrose phosphate synthase [Oryza sativa]

Seq. No.	388561
Contig ID	11890_1.R1084
5'-most EST	LIB3432-019-P1-K1-C6

Seq. No.	388562
Contig ID	11895_1.R1084
5'-most EST	uC-osflM202061h12b1

Seq. No.	388563
Contig ID	11896_1.R1084
5'-most EST	g2312702
Method	BLASTX
NCBI GI	g2980789
BLAST score	427
E value	6.0e-42
Match length	189
% identity	49
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388564
Contig ID	11899_1.R1084
5'-most EST	LIB3432-019-P1-K1-D4

Seq. No.	388565
Contig ID	11900_1.R1084
5'-most EST	uC-osflcyp080c12b1
Method	BLASTX
NCBI GI	g2224901
BLAST score	211
E value	2.0e-16
Match length	56
% identity	68
NCBI Description	(U67134) PcMYB1 protein [Petroselinum crispum]

Seq. No.	388566
Contig ID	11903_1.R1084
5'-most EST	LIB3432-019-P1-K1-D8
Method	BLASTX
NCBI GI	g854731
BLAST score	926
E value	1.0e-100
Match length	212
% identity	81
NCBI Description	(U19183) acetyl-coenzyme A carboxylase [Zea mays]

Seq. No.	388567
Contig ID	11904_1.R1084
5'-most EST	g3462545
Method	BLASTX
NCBI GI	g1418990
BLAST score	291
E value	1.0e-25
Match length	147
% identity	42
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]

Seq. No.	388568
Contig ID	11905_1.R1084
5'-most EST	LIB3432-029-P1-K1-C9
Method	BLASTX
NCBI GI	g20385
BLAST score	171
E value	8.0e-12
Match length	43
% identity	84

NCBI Description	(X06612) put. rps7 [Oryza sativa]

Seq. No.	388569
Contig ID	11912_1.R1084
5'-most EST	uC-osrocyp010f02b1

Seq. No.	388570
Contig ID	11919_1.R1084
5'-most EST	g2427874

Seq. No.	388571
Contig ID	11928_1.R1084
5'-most EST	g700459
Method	BLASTX
NCBI GI	g549010
BLAST score	887
E value	1.0e-107
Match length	211
% identity	91
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir__S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No.	388572
Contig ID	11941_1.R1084
5'-most EST	g3090522

Seq. No.	388573
Contig ID	11944_1.R1084
5'-most EST	LIB3432-025-P1-K1-F5
Method	BLASTX
NCBI GI	g3980396
BLAST score	605
E value	1.0e-62
Match length	117
% identity	89
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	388574
Contig ID	11954_1.R1084
5'-most EST	LIB3432-020-P1-K1-A2
Method	BLASTX
NCBI GI	g5042446
BLAST score	247
E value	5.0e-21
Match length	95
% identity	61
NCBI Description	(AC007789) putative WRKY DNA binding protein [Oryza sativa]

Seq. No.	388575
Contig ID	11958_1.R1084
5'-most EST	LIB3432-020-P1-K1-A7
Method	BLASTX
NCBI GI	g3935150
BLAST score	606
E value	5.0e-63
Match length	153
% identity	41
NCBI Description	(AC005106) T25N20.14 [Arabidopsis thaliana]

Seq. No.	388576
Contig ID	11963_1.R1084
5'-most EST	LIB3479-002-Q6-K1-B11

Seq. No.	388577
Contig ID	11963_2.R1084
5'-most EST	g4715310
Method	BLASTX
NCBI GI	g4914333
BLAST score	193
E value	1.0e-14
Match length	55
% identity	64
NCBI Description	(AC005489) F14N23.19 [Arabidopsis thaliana]

Seq. No.	388578
Contig ID	11968_1.R1084
5'-most EST	LIB3432-020-P1-K1-B6

Seq. No.	388579
Contig ID	11974_1.R1084
5'-most EST	LIB3432-020-P1-K1-D4
Method	BLASTN
NCBI GI	g5852170
BLAST score	560
E value	0.0e+00
Match length	564
% identity	100
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No.	388580
Contig ID	11978_1.R1084
5'-most EST	g2312296
Method	BLASTX
NCBI GI	g584825
BLAST score	544
E value	2.0e-55
Match length	123
% identity	80
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	388581
Contig ID	11985_1.R1084

5'-most EST	LIB3433-035-P1-K1-G6
Method	BLASTX
NCBI GI	g5453902
BLAST score	228
E value	2.0e-18
Match length	99
% identity	49
NCBI Description	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) >gi_4689436_gb_AAD27893.1_AF143096_1 (AF143096) peptidyl-prolyl cis-trans isomerase EPVH [Homo sapiens] >gi_5420453_dbj_BAA82320.1_ (AB009690) parvulin [Homo sapiens]

Seq. No.	388582
Contig ID	11986_1.R1084
5'-most EST	g1631696
Method	BLASTX
NCBI GI	g1705678
BLAST score	1574
E value	1.0e-176
Match length	333
% identity	48
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No.	388583
Contig ID	11987_1.R1084
5'-most EST	uC-osroM202013a11b1
Method	BLASTX
NCBI GI	g3281853
BLAST score	1078
E value	1.0e-117
Match length	264
% identity	83
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	388584
Contig ID	11987_2.R1084
5'-most EST	uC-osflcyp011f06b1

Seq. No.	388585
Contig ID	11988_1.R1084
5'-most EST	uC-osflM202086h02a1
Method	BLASTX
NCBI GI	g4104056
BLAST score	281
E value	6.0e-25
Match length	75
% identity	69
NCBI Description	(AF031194) S276 [Triticum aestivum]

Seq. No.	388586
Contig ID	12000_1.R1084
5'-most EST	uC-osflcyp099g02b1
Method	BLASTX

NCBI GI	g940288
BLAST score	280
E value	1.0e-24
Match length	89
% identity	30
NCBI Description	(L43510) protein localized in the nucleoli of pea nuclei; ORF; putative [Pisum sativum]

Seq. No.	388587
Contig ID	12003_1.R1084
5'-most EST	LIB3432-020-P1-K1-E8
Method	BLASTX
NCBI GI	g4105180
BLAST score	426
E value	8.0e-42
Match length	147
% identity	56
NCBI Description	(AF043905) plastoglobule associated protein PG1 precursor [Pisum sativum]

Seq. No.	388588
Contig ID	12007_1.R1084
5'-most EST	g1631948
Method	BLASTX
NCBI GI	g5360595
BLAST score	234
E value	2.0e-19
Match length	65
% identity	62
NCBI Description	(AB022330) nClpP5 [Arabidopsis thaliana]

Seq. No.	388589
Contig ID	12020_1.R1084
5'-most EST	LIB3432-020-P1-K1-G2
Method	BLASTN
NCBI GI	g1667606
BLAST score	45
E value	6.0e-16
Match length	146
% identity	85
NCBI Description	Triticum aestivum Tap mRNA, partial cds

Seq. No.	388590
Contig ID	12022_1.R1084
5'-most EST	LIB3433-021-P1-K1-B2

Seq. No.	388591
Contig ID	12023_1.R1084
5'-most EST	LIB3432-020-P1-K1-G6
Method	BLASTX
NCBI GI	g2832692
BLAST score	213
E value	2.0e-25
Match length	114
% identity	53
NCBI Description	(AL021713) putative protein [Arabidopsis thaliana]

Seq. No.	388592
Contig ID	12034_1.R1084
5'-most EST	LIB3477-004-P1-K1-E6

Seq. No.	388593
Contig ID	12048_1.R1084
5'-most EST	LIB3432-021-P1-K1-B10
Method	BLASTX
NCBI GI	g3757521
BLAST score	263
E value	3.0e-38
Match length	147
% identity	56
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	388594
Contig ID	12055_1.R1084
5'-most EST	LIB3479-012-Q6-K1-H10
Method	BLASTX
NCBI GI	g2589162
BLAST score	776
E value	8.0e-83
Match length	190
% identity	77
NCBI Description	(D88451) aldehyde oxidase [Zea mays]

Seq. No.	388595
Contig ID	12059_1.R1084
5'-most EST	LIB3432-021-P1-K1-C11

Seq. No.	388596
Contig ID	12066_1.R1084
5'-most EST	LIB3432-021-P1-K1-C8
Method	BLASTX
NCBI GI	g5103813
BLAST score	209
E value	1.0e-16
Match length	79
% identity	63
NCBI Description	(AC007591) Contains a PF_00175 Oxidoreductase FAD/NADH-binding domain. ESTs gb_H76345 and gb_AA651465 come from this gene. [Arabidopsis thaliana]

Seq. No.	388597
Contig ID	12067_1.R1084
5'-most EST	LIB3432-021-P1-K1-C9

Seq. No.	388598
Contig ID	12078_1.R1084
5'-most EST	LIB3432-021-P1-K1-E1
Method	BLASTX
NCBI GI	g2245005
BLAST score	270
E value	2.0e-49
Match length	211
% identity	21
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388599
Contig ID	12082_1.R1084
5'-most EST	LIB3432-021-P1-K1-E2
Method	BLASTX
NCBI GI	g2827635
BLAST score	604
E value	1.0e-62
Match length	177
% identity	70
NCBI Description	(AL021636) predicted protein [Arabidopsis thaliana]

Seq. No.	388600
Contig ID	12084_1.R1084
5'-most EST	LIB3434-045-P1-K1-B9
Method	BLASTX
NCBI GI	g3786006
BLAST score	506
E value	4.0e-51
Match length	136
% identity	69
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388601
Contig ID	12085_1.R1084
5'-most EST	uC-osflcyp075h07b1

Seq. No.	388602
Contig ID	12087_1.R1084
5'-most EST	uC-osflM202051g02b1
Method	BLASTX
NCBI GI	g4966344
BLAST score	364
E value	1.0e-69
Match length	229
% identity	60
NCBI Description	(AC006341) ESTs gb_F15498, gb_H37515, gb_T41906, gb_T22448, gb_W43356 and gb_T20739 come from this gene. [Arabidopsis thaliana]

Seq. No.	388603
Contig ID	12098_1.R1084
5'-most EST	g4880789
Method	BLASTX
NCBI GI	g5733089
BLAST score	892
E value	1.0e-123
Match length	271
% identity	77
NCBI Description	(AF172681) amine oxidase [Canavalia lineata]

Seq. No.	388604
Contig ID	12099_1.R1084
5'-most EST	g5667196
Method	BLASTX
NCBI GI	g3096930
BLAST score	797

E value	1.0e-84
Match length	436
% identity	45
NCBI Description	(AL023094) Homeodomain-like protein [Arabidopsis thaliana]

Seq. No.	388605
Contig ID	12101_1.R1084
5'-most EST	g3107516
Method	BLASTX
NCBI GI	g3413511
BLAST score	1569
E value	1.0e-175
Match length	351
% identity	84
NCBI Description	(AJ000265) glucose-6-phosphate isomerase [Spinacia oleracea]

Seq. No.	388606
Contig ID	12107_1.R1084
5'-most EST	LIB3432-021-P1-K1-G4
Method	BLASTX
NCBI GI	g5123925
BLAST score	303
E value	5.0e-57
Match length	158
% identity	64
NCBI Description	(AL079350) putative protein [Arabidopsis thaliana]

Seq. No.	388607
Contig ID	12114_1.R1084
5'-most EST	g3061141
Method	BLASTX
NCBI GI	g3482918
BLAST score	1931
E value	0.0e+00
Match length	420
% identity	88
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	388608
Contig ID	12117_1.R1084
5'-most EST	LIB3479-011-Q6-K1-E4
Method	BLASTX
NCBI GI	g584825
BLAST score	636
E value	7.0e-66
Match length	149
% identity	79
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	388609
Contig ID	12117_2.R1084
5'-most EST	LIB3479-007-Q6-K1-E10

Seq. No.	388610
Contig ID	12120_1.R1084
5'-most EST	g2442218
Method	BLASTN
NCBI GI	g6063530
BLAST score	442
E value	0.0e+00
Match length	662
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	388611
Contig ID	12123_1.R1084
5'-most EST	uC-osrocyp013c04b1
Method	BLASTX
NCBI GI	g5080793
BLAST score	199
E value	5.0e-15
Match length	83
% identity	51
NCBI Description	(AC007576) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	388612
Contig ID	12127_1.R1084
5'-most EST	uC-osrocyp008g05b1

Seq. No.	388613
Contig ID	12131_1.R1084
5'-most EST	g701436
Method	BLASTX
NCBI GI	g2505868
BLAST score	251
E value	2.0e-21
Match length	87
% identity	27
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388614
Contig ID	12132_1.R1084
5'-most EST	LIB3432-022-P1-K1-A7
Method	BLASTX
NCBI GI	g2674203
BLAST score	416
E value	2.0e-40
Match length	140
% identity	61
NCBI Description	(AF036328) CLP protease regulatory subunit CLPX [Arabidopsis thaliana]

Seq. No.	388615
Contig ID	12138_1.R1084
5'-most EST	LIB3432-035-P2-K1-G9
Method	BLASTX
NCBI GI	g4996842
BLAST score	388
E value	1.0e-50
Match length	209

% identity	47
NCBI Description	(AB027501) Dcarg-1 [Daucus carota]

Seq. No.	388616
Contig ID	12143_1.R1084
5'-most EST	g4879414
Method	BLASTX
NCBI GI	g4539292
BLAST score	417
E value	2.0e-40
Match length	95
% identity	80
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	388617
Contig ID	12147_1.R1084
5'-most EST	LIB3477-004-P1-K1-A6

Seq. No.	388618
Contig ID	12151_1.R1084
5'-most EST	LIB3432-022-P1-K1-C8
Method	BLASTX
NCBI GI	g4455244
BLAST score	227
E value	2.0e-39
Match length	198
% identity	45
NCBI Description	(AL035523) MtN3-like protein [Arabidopsis thaliana]

Seq. No.	388619
Contig ID	12151_2.R1084
5'-most EST	uC-osflcyp110e02b1

Seq. No.	388620
Contig ID	12155_1.R1084
5'-most EST	g3766800
Method	BLASTX
NCBI GI	g2245378
BLAST score	436
E value	3.0e-43
Match length	128
% identity	70
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana] >gi_5080809_gb_AAD39318.1_AC007258_7 (AC007258) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	388621
Contig ID	12156_1.R1084
5'-most EST	LIB3432-022-P1-K1-D2

Seq. No.	388622
Contig ID	12167_1.R1084
5'-most EST	LIB3599-001-P1-N6-G1
Method	BLASTX
NCBI GI	g4115379
BLAST score	257

E value	5.0e-22
Match length	124
% identity	43
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	388623
Contig ID	12170_1.R1084
5'-most EST	LIB3434-053-P1-K1-G4

Seq. No.	388624
Contig ID	12181_1.R1084
5'-most EST	LIB3432-022-P1-K1-F5
Method	BLASTX
NCBI GI	g3036796
BLAST score	271
E value	2.0e-23
Match length	125
% identity	43
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805858_emb_CAA21478.1_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	388625
Contig ID	12185_1.R1084
5'-most EST	LIB3432-022-P1-K1-F9
Method	BLASTX
NCBI GI	g5902382
BLAST score	219
E value	1.0e-17
Match length	75
% identity	55
NCBI Description	(AC009322) Unknown protein [Arabidopsis thaliana]

Seq. No.	388626
Contig ID	12186_1.R1084
5'-most EST	LIB3433-049-P1-K1-B2

Seq. No.	388627
Contig ID	12187_1.R1084
5'-most EST	LIB3432-022-P1-K1-G10
Method	BLASTX
NCBI GI	g3914667
BLAST score	339
E value	1.0e-31
Match length	82
% identity	83
NCBI Description	50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR >gi_2459427 (AC002332) putative chloroplast 50S ribosomal protein L28 [Arabidopsis thaliana]

Seq. No.	388628
Contig ID	12188_1.R1084
5'-most EST	LIB3432-022-P1-K1-G11
Method	BLASTN
NCBI GI	g58067
BLAST score	111

E value	5.0e-55
Match length	128
% identity	98
NCBI Description	pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP

Seq. No.	388629
Contig ID	12200_1.R1084
5'-most EST	g3758936

Seq. No.	388630
Contig ID	12203_1.R1084
5'-most EST	LIB3432-022-P1-K1-H7
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	4.0e-10
Match length	35
% identity	38
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	388631
Contig ID	12214_1.R1084
5'-most EST	LIB3433-007-Q6-K1-F11
Method	BLASTX
NCBI GI	g1711618
BLAST score	241
E value	3.0e-20
Match length	96
% identity	44
NCBI Description	LOW AFFINITY SULPHATE TRANSPORTER 3 >gi_1085993_pir__S51765 low affinity sulphate transporter - Stylosanthes hamata >gi_607188_emb_CAA57831_ (X82454) low affinity sulphate transporter [Stylosanthes hamata]

Seq. No.	388632
Contig ID	12222_1.R1084
5'-most EST	LIB3433-026-P1-K1-B8

Seq. No.	388633
Contig ID	12225_1.R1084
5'-most EST	g3761535

Seq. No.	388634
Contig ID	12230_1.R1084
5'-most EST	LIB3474-001-P1-K1-F6
Method	BLASTX
NCBI GI	g2894599
BLAST score	324
E value	1.0e-29
Match length	114
% identity	57
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	388635
Contig ID	12230_2.R1084
5'-most EST	uC-osrocyp014g05b1

Method	BLASTX
NCBI GI	g2894599
BLAST score	302
E value	3.0e-45
Match length	119
% identity	76
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	388636
Contig ID	12231_1.R1084
5'-most EST	g702828
Method	BLASTX
NCBI GI	g3880441
BLAST score	158
E value	2.0e-10
Match length	53
% identity	51
NCBI Description	(Z82062) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D76353 comes from this gene; cDNA EST EMBL:D71838 comes from this gene; cDNA EST EMBL:D74561 comes from this gene; cDNA EST EMBL:D73319 comes from this

Seq. No.	388637
Contig ID	12232_1.R1084
5'-most EST	g3768576
Method	BLASTX
NCBI GI	g3063444
BLAST score	167
E value	3.0e-11
Match length	37
% identity	81
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana] >gi_4973256_gb_AAD35005.1_AF144387_1 (AF144387) thioredoxin-like 1 [Arabidopsis thaliana]

Seq. No.	388638
Contig ID	12232_2.R1084
5'-most EST	LIB3432-049-P1-K1-E11
Method	BLASTX
NCBI GI	g3063444
BLAST score	685
E value	6.0e-72
Match length	153
% identity	82
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana] >gi_4973256_gb_AAD35005.1_AF144387_1 (AF144387) thioredoxin-like 1 [Arabidopsis thaliana]

Seq. No.	388639
Contig ID	12237_1.R1084
5'-most EST	LIB3432-023-P1-K1-D2
Method	BLASTX
NCBI GI	g585451
BLAST score	90
E value	3.0e-10
Match length	62
% identity	66

NCBI Description	MALATE OXIDOREDUCTASE [NAD] 62 KD ISOFORM, MITOCHONDRIAL PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi_1076667_pir__B53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 62K chain precursor, mitochondrial - potato >gi_438249_emb_CAA80559_ (Z23023) malate dehydrogenase [Solanum tuberosum]

Seq. No.	388640
Contig ID	12241_1.R1084
5'-most EST	uC-osflm202109h10b1
Method	BLASTX
NCBI GI	g2911072
BLAST score	225
E value	4.0e-18
Match length	96
% identity	55
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	388641
Contig ID	12252_1.R1084
5'-most EST	uC-osflcyp111f02b1
Method	BLASTX
NCBI GI	g3047104
BLAST score	284
E value	8.0e-25
Match length	132
% identity	56
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	388642
Contig ID	12268_1.R1084
5'-most EST	LIB3432-031-P1-K1-E1
Method	BLASTX
NCBI GI	g1076660
BLAST score	198
E value	6.0e-15
Match length	52
% identity	69
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	388643
Contig ID	12270_1.R1084
5'-most EST	LIB3432-023-P1-K1-G3

Seq. No.	388644
Contig ID	12270_2.R1084
5'-most EST	g5803417

Seq. No.	388645
Contig ID	12281_1.R1084
5'-most EST	LIB3474-006-P1-K1-G6
Method	BLASTX
NCBI GI	g4115388
BLAST score	485

E value	4.0e-70
Match length	211
% identity	61
NCBI Description	(AC005967) putative prolylcarboxypeptidase [Arabidopsis thaliana]

Seq. No.	388646
Contig ID	12283_1.R1084
5'-most EST	g572482
Method	BLASTX
NCBI GI	g1652297
BLAST score	196
E value	5.0e-24
Match length	214
% identity	39
NCBI Description	(D90904) hypothetical protein [Synechocystis sp.]

Seq. No.	388647
Contig ID	12285_1.R1084
5'-most EST	g2428527

Seq. No.	388648
Contig ID	12291_1.R1084
5'-most EST	LIB3432-024-P1-K1-A12

Seq. No.	388649
Contig ID	12293_1.R1084
5'-most EST	g2280606
Method	BLASTX
NCBI GI	g2443886
BLAST score	907
E value	8.0e-98
Match length	239
% identity	75
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	388650
Contig ID	12296_1.R1084
5'-most EST	LIB3434-057-P1-K1-G11
Method	BLASTX
NCBI GI	g5304837
BLAST score	402
E value	8.0e-39
Match length	126
% identity	58
NCBI Description	(AJ243483) ATP citrate lyase [Cyanophora paradoxa]

Seq. No.	388651
Contig ID	12313_1.R1084
5'-most EST	LIB3432-024-P1-K1-C8
Method	BLASTX
NCBI GI	g731675
BLAST score	247
E value	5.0e-30
Match length	123
% identity	58
NCBI Description	HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION

>gi_626631_pir__S46811 hypothetical protein YHR074w - yeast (Saccharomyces cerevisiae) >gi_500832 (U10556) Yhr074wp [Saccharomyces cerevisiae]

Seq. No.	388652
Contig ID	12314_1.R1084
5'-most EST	g3106945

Seq. No.	388653
Contig ID	12317_1.R1084
5'-most EST	g427796

Seq. No.	388654
Contig ID	12317_2.R1084
5'-most EST	g5005218

Seq. No.	388655
Contig ID	12319_1.R1084
5'-most EST	g701370

Seq. No.	388656
Contig ID	12324_1.R1084
5'-most EST	LIB3433-031-P1-K1-H9
Method	BLASTX
NCBI GI	g4103635
BLAST score	161
E value	1.0e-10
Match length	75
% identity	35
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	388657
Contig ID	12330_1.R1084
5'-most EST	LIB3432-024-P1-K1-E5

Seq. No.	388658
Contig ID	12331_1.R1084
5'-most EST	g2801245
Method	BLASTN
NCBI GI	g5566583
BLAST score	94
E value	4.0e-45
Match length	114
% identity	97
NCBI Description	Lepilemur dorsalis genomic fragment, RAPD with primer operon OPH4, clone A10a

Seq. No.	388659
Contig ID	12334_1.R1084
5'-most EST	LIB3434-038-P1-K1-H9

Seq. No.	388660
Contig ID	12336_1.R1084
5'-most EST	uC-osroM202003c01a2
Method	BLASTX
NCBI GI	g5668813
BLAST score	211

E value	4.0e-20
Match length	140
% identity	42
NCBI Description	(AC007519) Similar to gb_X77136 HSR203J protein from Nicotiana tabacum and is a member of the PF_00135 Carboxylesterase family. ESTs gb_Z25688 and gb_F14025 come from this gene. [Arabidopsis thaliana]

Seq. No.	388661
Contig ID	12339_1.R1084
5'-most EST	LIB3432-024-P1-K1-F3
Method	BLASTX
NCBI GI	g119355
BLAST score	1119
E value	1.0e-123
Match length	226
% identity	96
NCBI Description	ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1) >gi_100869_pir__S16257 phosphopyruvate hydratase (EC 4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase [Zea mays]

Seq. No.	388662
Contig ID	12340_1.R1084
5'-most EST	LIB3432-024-P1-K1-F5

Seq. No.	388663
Contig ID	12352_1.R1084
5'-most EST	g3762400
Method	BLASTX
NCBI GI	g400578
BLAST score	278
E value	3.0e-24
Match length	109
% identity	48
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi_346531_pir__S28240 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-18(IP) - bovine >gi_226_emb_CAA44900_ (X63215) NADH dehydrogenase [Bos taurus]

Seq. No.	388664
Contig ID	12356_1.R1084
5'-most EST	g3763813
Method	BLASTX
NCBI GI	g4154673
BLAST score	164
E value	9.0e-11
Match length	58
% identity	59
NCBI Description	(AE001454) PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) [Helicobacter pylori J99]

Seq. No.	388665
Contig ID	12380_1.R1084
5'-most EST	uC-osflcyp017f01b1

Method	BLASTX
NCBI GI	g5302797
BLAST score	374
E value	8.0e-71
Match length	229
% identity	62
NCBI Description	(Z97341) HSP like protein [Arabidopsis thaliana]

Seq. No.	388666
Contig ID	12381_1.R1084
5'-most EST	LIB3432-032-P2-K1-B4

Seq. No.	388667
Contig ID	12385_1.R1084
5'-most EST	uC-osflcyp159g08b1
Method	BLASTX
NCBI GI	g2642213
BLAST score	389
E value	3.0e-37
Match length	80
% identity	88
NCBI Description	(AF030385) nitrate-induced NOI protein [Zea mays] >gi_2895781 (AF045033) nitrate-induced NOI protein [Zea mays]

Seq. No.	388668
Contig ID	12388_1.R1084
5'-most EST	g5803393
Method	BLASTN
NCBI GI	g4091079
BLAST score	35
E value	7.0e-10
Match length	77
% identity	86
NCBI Description	Oryza sativa nucleic acid binding protein mRNA, complete cds

Seq. No.	388669
Contig ID	12398_1.R1084
5'-most EST	LIB3432-032-P2-K1-C9
Method	BLASTX
NCBI GI	g4895187
BLAST score	207
E value	7.0e-16
Match length	163
% identity	45
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No.	388670
Contig ID	12408_1.R1084
5'-most EST	uC-osflcyp034d03b1
Method	BLASTX
NCBI GI	g2257756
BLAST score	229
E value	2.0e-18
Match length	193
% identity	31

NCBI Description	(U82815) nucleolar histone deacetylase HD2-p39 [Zea mays] >gi_3650466 (AF026917) histone deacetylase HD2-p39 [Zea mays]

Seq. No.	388671
Contig ID	12417_1.R1084
5'-most EST	LIB3434-048-P1-K1-F1
Method	BLASTX
NCBI GI	g3201680
BLAST score	573
E value	6.0e-59
Match length	224
% identity	50
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	388672
Contig ID	12420_1.R1084
5'-most EST	g3763694
Method	BLASTX
NCBI GI	g4586449
BLAST score	374
E value	1.0e-35
Match length	78
% identity	82
NCBI Description	(AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]

Seq. No.	388673
Contig ID	12435_1.R1084
5'-most EST	LIB3432-032-P2-K1-G2
Method	BLASTX
NCBI GI	g3043712
BLAST score	429
E value	6.0e-42
Match length	151
% identity	57
NCBI Description	(AB011166) KIAA0594 protein [Homo sapiens]

Seq. No.	388674
Contig ID	12439_1.R1084
5'-most EST	LIB3433-043-P1-K1-C9
Method	BLASTX
NCBI GI	g4454032
BLAST score	788
E value	8.0e-84
Match length	247
% identity	61
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	388675
Contig ID	12443_1.R1084
5'-most EST	g4715930

Seq. No.	388676
Contig ID	12450_1.R1084
5'-most EST	LIB3432-032-P2-K1-H5
Method	BLASTX
NCBI GI	g4309758

BLAST score	250
E value	3.0e-21
Match length	64
% identity	73
NCBI Description	(AC006217) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388677
Contig ID	12452_2.R1084
5'-most EST	g3090593
Method	BLASTX
NCBI GI	g3935185
BLAST score	199
E value	4.0e-15
Match length	96
% identity	43
NCBI Description	(AC004557) F17L21.28 [Arabidopsis thaliana]

Seq. No.	388678
Contig ID	12453_1.R1084
5'-most EST	uC-osflcyp177c02b1
Method	BLASTX
NCBI GI	g6014701
BLAST score	830
E value	1.0e-91
Match length	251
% identity	68
NCBI Description	(AF190450) enoyl-CoA-hydratase [Avicennia marina]

Seq. No.	388679
Contig ID	12455_1.R1084
5'-most EST	LIB3432-035-P2-K1-A1
Method	BLASTX
NCBI GI	g4006872
BLAST score	328
E value	4.0e-32
Match length	110
% identity	66
NCBI Description	(Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	388680
Contig ID	12457_1.R1084
5'-most EST	LIB3475-003-P1-K2-D3
Method	BLASTX
NCBI GI	g5042408
BLAST score	685
E value	5.0e-72
Match length	214
% identity	62
NCBI Description	(AC006193) very similar to alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	388681
Contig ID	12463_1.R1084
5'-most EST	g3061133
Method	BLASTX
NCBI GI	g2129726

BLAST score	552
E value	1.0e-56
Match length	135
% identity	79
NCBI Description	RNA polymerase II third largest chain RPB35.5A - Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II third largest subunit [Arabidopsis thaliana] >gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA polymerase II, third largest subunit [Arabidopsis thaliana]

Seq. No.	388682
Contig ID	12464_1.R1084
5'-most EST	g4716488
Method	BLASTX
NCBI GI	g3482967
BLAST score	293
E value	2.0e-36
Match length	164
% identity	57
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	388683
Contig ID	12464_2.R1084
5'-most EST	LIB3432-035-P2-K1-A8
Method	BLASTN
NCBI GI	g5730046
BLAST score	35
E value	6.0e-10
Match length	35
% identity	62
NCBI Description	Homo sapiens solute carrier family 17 (sodium phosphate), member 3 (SLC17A3) mRNA >gi_2062691_gb_U90545_HSU90545 Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No.	388684
Contig ID	12469_1.R1084
5'-most EST	LIB3432-035-P2-K1-B12
Method	BLASTX
NCBI GI	g20290
BLAST score	1225
E value	1.0e-153
Match length	289
% identity	98
NCBI Description	(X57563) phytochrome B [Oryza sativa]

Seq. No.	388685
Contig ID	12481_1.R1084
5'-most EST	LIB3432-035-P2-K1-C4
Method	BLASTX
NCBI GI	g5733886
BLAST score	422
E value	2.0e-41
Match length	111
% identity	77

NCBI Description	(AC007932) F11A17.20 [Arabidopsis thaliana]

Seq. No.	388686
Contig ID	12482_1.R1084
5'-most EST	LIB3432-035-P2-K1-C5
Method	BLASTX
NCBI GI	g4544447
BLAST score	356
E value	1.0e-38
Match length	142
% identity	58
NCBI Description	(AC006592) putative GTP cyclohydrolase [Arabidopsis thaliana]

Seq. No.	388687
Contig ID	12484_1.R1084
5'-most EST	LIB3477-006-P1-K1-D6
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36
% identity	59
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388688
Contig ID	12485_1.R1084
5'-most EST	LIB3477-007-P1-K1-D9

Seq. No.	388689
Contig ID	12487_1.R1084
5'-most EST	g4714859
Method	BLASTX
NCBI GI	g2462754
BLAST score	165
E value	5.0e-21
Match length	115
% identity	47
NCBI Description	(AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	388690
Contig ID	12492_1.R1084
5'-most EST	LIB3432-040-P1-K1-H8
Method	BLASTX
NCBI GI	g1707878
BLAST score	721
E value	2.0e-76
Match length	157
% identity	84
NCBI Description	AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T PROTEIN) >gi_2129976_pir__S59948 aminomethyltransferase (EC 2.1.2.10) precursor - potato >gi_438254_emb_CAA81081_ (Z25862) T-protein [Solanum tuberosum]

Seq. No.	388691
Contig ID	12497_1.R1084
5'-most EST	LIB3433-049-P1-K1-A8

Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	1.0e-09
Match length	36
% identity	38
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	388692
Contig ID	12507_1.R1084
5'-most EST	LIB3474-002-P1-K1-F2
Method	BLASTX
NCBI GI	g1169238
BLAST score	1011
E value	1.0e-110
Match length	264
% identity	72
NCBI Description	GLUTAMATE DECARBOXYLASE (GAD) >gi_1076648_pir__A48767 glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia >gi_294112 (L16797) glutamate decarboxylase [Petunia hybrida] >gi_309680 (L16977) glutamate decarboxylase [Petunia hybrida]

Seq. No.	388693
Contig ID	12523_1.R1084
5'-most EST	uC-osf1M202095b02b1
Method	BLASTX
NCBI GI	g2760327
BLAST score	995
E value	1.0e-108
Match length	218
% identity	53
NCBI Description	(AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No.	388694
Contig ID	12526_1.R1084
5'-most EST	LIB3432-035-P2-K1-G5
Method	BLASTX
NCBI GI	g3201477
BLAST score	325
E value	6.0e-30
Match length	112
% identity	59
NCBI Description	(AJ006021) putative PRL1 associated protein [Arabidopsis thaliana]

Seq. No.	388695
Contig ID	12536_1.R1084
5'-most EST	g2309638
Method	BLASTX
NCBI GI	g3643594
BLAST score	897
E value	1.0e-96
Match length	245
% identity	70
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	388696
Contig ID	12536_2.R1084
5'-most EST	LIB3433-060-P1-K1-E8
Method	BLASTX
NCBI GI	g1888551
BLAST score	360
E value	9.0e-38
Match length	152
% identity	59
NCBI Description	(U89895) pathogenesis-related protein class 1 [Oryza sativa]

Seq. No.	388697
Contig ID	12542_1.R1084
5'-most EST	LIB3432-035-P2-K1-H9
Method	BLASTX
NCBI GI	g2183249
BLAST score	340
E value	2.0e-33
Match length	101
% identity	75
NCBI Description	(AF002211) glutathione-S-transferase [Triticum aestivum] >gi_4185800 (AF109714) glutathione S-transferase [Triticum aestivum]

Seq. No.	388698
Contig ID	12543_1.R1084
5'-most EST	LIB3477-004-P1-K1-G12
Method	BLASTX
NCBI GI	g3341511
BLAST score	719
E value	6.0e-76
Match length	142
% identity	96
NCBI Description	(AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]

Seq. No.	388699
Contig ID	12543_2.R1084
5'-most EST	LIB3432-036-P2-K1-A1
Method	BLASTX
NCBI GI	g3341511
BLAST score	550
E value	2.0e-56
Match length	137
% identity	77
NCBI Description	(AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]

Seq. No.	388700
Contig ID	12556_1.R1084
5'-most EST	LIB3434-021-P1-K1-G3
Method	BLASTX
NCBI GI	g1931647
BLAST score	253
E value	2.0e-21
Match length	48
% identity	96
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog

[Arabidopsis thaliana]

Seq. No.	388701
Contig ID	12561_1.R1084
5'-most EST	LIB3432-036-P2-K1-B7

Seq. No.	388702
Contig ID	12563_2.R1084
5'-most EST	LIB3432-036-P2-K1-B9
Method	BLASTX
NCBI GI	g4102839
BLAST score	218
E value	3.0e-17
Match length	189
% identity	30
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	388703
Contig ID	12573_1.R1084
5'-most EST	LIB3432-036-P2-K1-C7
Method	BLASTX
NCBI GI	g4885481
BLAST score	258
E value	6.0e-22
Match length	130
% identity	45
NCBI Description	RNA polymerase II transcriptional regulation mediator (Med6, S. cerevisiae, homolog of) >gi_2618738 (U78082) RNA polymerase transcriptional regulation mediator [Homo sapiens]

Seq. No.	388704
Contig ID	12582_1.R1084
5'-most EST	LIB3432-036-P2-K1-D6
Method	BLASTX
NCBI GI	g5882718
BLAST score	340
E value	1.0e-31
Match length	128
% identity	52
NCBI Description	(AC008263) ESTs gb_AA067482 and gb_AI100542 come from this gene. [Arabidopsis thaliana]

Seq. No.	388705
Contig ID	12583_1.R1084
5'-most EST	LIB3432-036-P2-K1-D7

Seq. No.	388706
Contig ID	12586_1.R1084
5'-most EST	g702441
Method	BLASTX
NCBI GI	g2494075
BLAST score	1171
E value	1.0e-129
Match length	249
% identity	91
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE [NADP+]) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1084478_pir__S43833 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - maize >gi_474408_emb_CAA53075_ (X75326) glyceraldehyde-3-phosphate dehydrogenase (GAPN) [Zea mays]

Seq. No.	388707
Contig ID	12596_1.R1084
5'-most EST	LIB3433-046-P1-K1-F2

Seq. No.	388708
Contig ID	12622_1.R1084
5'-most EST	LIB3432-036-P2-K1-H5
Method	BLASTX
NCBI GI	g3790188
BLAST score	817
E value	2.0e-87
Match length	197
% identity	81
NCBI Description	(Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana tabacum]

Seq. No.	388709
Contig ID	12650_1.R1084
5'-most EST	LIB3432-042-P2-K1-C12
Method	BLASTN
NCBI GI	g5803242
BLAST score	59
E value	2.0e-24
Match length	143
% identity	21
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	388710
Contig ID	12651_1.R1084
5'-most EST	uC-osflcyp126a05b1
Method	BLASTN
NCBI GI	g6016845
BLAST score	98
E value	1.0e-47
Match length	173
% identity	77
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	388711
Contig ID	12651_2.R1084
5'-most EST	LIB3432-042-P2-K1-C2

Seq. No.	388712
Contig ID	12656_1.R1084
5'-most EST	LIB3432-042-P2-K1-C7

Seq. No.	388713
Contig ID	12659_1.R1084
5'-most EST	LIB3432-042-P2-K1-D1

Method	BLASTX
NCBI GI	g3540182
BLAST score	139
E value	3.0e-12
Match length	77
% identity	63
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	388714
Contig ID	12662_1.R1084
5'-most EST	g3106513
Method	BLASTX
NCBI GI	g4467144
BLAST score	599
E value	7.0e-62
Match length	195
% identity	59
NCBI Description	(AL035540) putative phosphatidylinositol synthase [Arabidopsis thaliana]

Seq. No.	388715
Contig ID	12663_1.R1084
5'-most EST	LIB3432-042-P2-K1-D2

Seq. No.	388716
Contig ID	12664_1.R1084
5'-most EST	LIB3432-042-P2-K1-D3

Seq. No.	388717
Contig ID	12664_2.R1084
5'-most EST	g286698

Seq. No.	388718
Contig ID	12664_3.R1084
5'-most EST	LIB3479-001-Q6-K1-F6

Seq. No.	388719
Contig ID	12667_1.R1084
5'-most EST	g3445011
Method	BLASTX
NCBI GI	g1808694
BLAST score	282
E value	9.0e-25
Match length	87
% identity	66
NCBI Description	(Y10787) hypothetical protein [Sporobolus stapfianus]

Seq. No.	388720
Contig ID	12667_3.R1084
5'-most EST	g2310841
Method	BLASTX
NCBI GI	g1808694
BLAST score	524
E value	1.0e-53
Match length	117
% identity	87
NCBI Description	(Y10787) hypothetical protein [Sporobolus stapfianus]

Seq. No.	388721
Contig ID	12677_1.R1084
5'-most EST	g428777
Method	BLASTX
NCBI GI	g3874271
BLAST score	832
E value	4.0e-89
Match length	208
% identity	69
NCBI Description	(Z81467) predicted using Genefinder; Similarity to Drosophila UDP-glucose:glycoprotein glucosyltransferase (TR:Q09332); cDNA EST yk250b10.3 comes from this gene; cDNA EST yk250b10.5 comes from this gene [Caenorhabditis elegans] >gi_3876437_emb_CAB04207.1_ (Z81516) predicted using Genefinder; Similarity to Drosophila UDP-glucose:glycoprotein glucosyltransferase (TR:Q09332); cDNA EST yk250b10.3 comes from this gene; cDNA EST yk250b10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	388722
Contig ID	12678_1.R1084
5'-most EST	g2800990

Seq. No.	388723
Contig ID	12687_1.R1084
5'-most EST	g4880972
Method	BLASTX
NCBI GI	g4519938
BLAST score	747
E value	1.0e-106
Match length	391
% identity	58
NCBI Description	(AB019240) RPR1h [Oryza sativa]

Seq. No.	388724
Contig ID	12688_1.R1084
5'-most EST	g2311648
Method	BLASTX
NCBI GI	g3212852
BLAST score	239
E value	3.0e-21
Match length	151
% identity	44
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	388725
Contig ID	12690_1.R1084
5'-most EST	uC-osflcyp055h05b1

Seq. No.	388726
Contig ID	12693_1.R1084
5'-most EST	LIB3434-034-P1-K1-B12
Method	BLASTN
NCBI GI	g4733953
BLAST score	36
E value	1.0e-10

Match length	101
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	388727
Contig ID	12698_1.R1084
5'-most EST	g702701

Seq. No.	388728
Contig ID	12716_1.R1084
5'-most EST	LIB3432-043-P1-K1-B10
Method	BLASTX
NCBI GI	g2262172
BLAST score	426
E value	1.0e-41
Match length	126
% identity	66
NCBI Description	(AC002329) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	388729
Contig ID	12723_1.R1084
5'-most EST	g287110
Method	BLASTX
NCBI GI	g3986289
BLAST score	760
E value	8.0e-81
Match length	240
% identity	61
NCBI Description	(AB017357) L-Galactono-1,4-lactone dehydrogenase [Ipomoea batatas]

Seq. No.	388730
Contig ID	12733_1.R1084
5'-most EST	LIB3432-043-P1-K1-C6

Seq. No.	388731
Contig ID	12742_1.R1084
5'-most EST	g427600
Method	BLASTX
NCBI GI	g3461820
BLAST score	589
E value	2.0e-60
Match length	219
% identity	57
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	388732
Contig ID	12743_1.R1084
5'-most EST	LIB3432-043-P1-K1-D4

Seq. No.	388733
Contig ID	12752_1.R1084
5'-most EST	LIB3433-049-P1-K1-G5
Method	BLASTX
NCBI GI	g3021357

BLAST score	661
E value	2.0e-88
Match length	210
% identity	79
NCBI Description	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	388734
Contig ID	12756_1.R1084
5'-most EST	g4716465

Seq. No.	388735
Contig ID	12768_1.R1084
5'-most EST	g3768394
Method	BLASTX
NCBI GI	g5006855
BLAST score	488
E value	8.0e-49
Match length	264
% identity	49
NCBI Description	(AF145729) homeodomain leucine zipper protein [Oryza sativa]

Seq. No.	388736
Contig ID	12780_1.R1084
5'-most EST	g702916

Seq. No.	388737
Contig ID	12781_1.R1084
5'-most EST	uC-osroM202020g02b1
Method	BLASTX
NCBI GI	g6016720
BLAST score	635
E value	4.0e-66
Match length	192
% identity	62
NCBI Description	(AC009325) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388738
Contig ID	12782_1.R1084
5'-most EST	uC-osflM202055f06b1
Method	BLASTX
NCBI GI	g3335345
BLAST score	182
E value	1.0e-17
Match length	63
% identity	76
NCBI Description	(AC004512) Contains similarity to ABC transporter gb_1651790 from Synechocystis sp. gb_D90900. [Arabidopsis thaliana]

Seq. No.	388739
Contig ID	12784_1.R1084
5'-most EST	LIB3432-043-P1-K1-H12
Method	BLASTN
NCBI GI	g6063530
BLAST score	435

E value	0.0e+00
Match length	643
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	388740
Contig ID	12793_1.R1084
5'-most EST	g6024941
Method	BLASTX
NCBI GI	g5915837
BLAST score	495
E value	1.0e-49
Match length	202
% identity	48
NCBI Description	CYTOCHROME P450 71D8 (P450 CP7) >gi_3334667_emb_CAA71517_ (Y10493) putative cytochrome P450 [Glycine max]

Seq. No.	388741
Contig ID	12794_1.R1084
5'-most EST	LIB3432-044-P1-K1-A11
Method	BLASTX
NCBI GI	g4680206
BLAST score	559
E value	3.0e-57
Match length	159
% identity	74
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	388742
Contig ID	12799_1.R1084
5'-most EST	LIB3432-044-P1-K1-A5
Method	BLASTX
NCBI GI	g1354466
BLAST score	361
E value	3.0e-34
Match length	94
% identity	71
NCBI Description	(U52910) U1 snRNP 70K truncated protein [Arabidopsis thaliana] >gi_1354468 (U52909) U1 snRNP 70K truncated protein [Arabidopsis thaliana]

Seq. No.	388743
Contig ID	12800_1.R1084
5'-most EST	LIB3432-044-P1-K1-A6
Method	BLASTX
NCBI GI	g132580
BLAST score	275
E value	3.0e-24
Match length	102
% identity	58
NCBI Description	PROTEIN SYNTHESIS INHIBITOR II (RIBOSOME-INACTIVATING PROTEIN II) (RRNA N-GLYCOSIDASE) >gi_72360_pir__RLBH protein synthesis inhibitor II - barley >gi_225420_prf__1303209A translation inhibitor II [Hordeum vulgare var. distichum]

Seq. No.	388744

Contig ID	12801_1.R1084
5'-most EST	LIB3434-010-P1-K1-E12

Seq. No.	388745
Contig ID	12826_1.R1084
5'-most EST	g568426
Method	BLASTX
NCBI GI	g3043612
BLAST score	221
E value	1.0e-17
Match length	197
% identity	37
NCBI Description	(AB011116) KIAA0544 protein [Homo sapiens]

Seq. No.	388746
Contig ID	12843_1.R1084
5'-most EST	LIB3432-044-P1-K1-E5
Method	BLASTX
NCBI GI	g4803944
BLAST score	225
E value	3.0e-18
Match length	66
% identity	61
NCBI Description	(AC006264) putative C2-domain protein (prosite: PD0C00380) [Arabidopsis thaliana]

Seq. No.	388747
Contig ID	12845_1.R1084
5'-most EST	LIB3432-044-P1-K1-E7
Method	BLASTX
NCBI GI	g5091545
BLAST score	175
E value	2.0e-12
Match length	69
% identity	55
NCBI Description	(AC007067) T10O24.14 [Arabidopsis thaliana]

Seq. No.	388748
Contig ID	12850_1.R1084
5'-most EST	LIB3432-044-P1-K1-F2
Method	BLASTX
NCBI GI	g2911067
BLAST score	963
E value	1.0e-116
Match length	284
% identity	76
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No.	388749
Contig ID	12853_1.R1084
5'-most EST	LIB3432-044-P1-K1-F6
Method	BLASTX
NCBI GI	g3123295
BLAST score	158
E value	1.0e-10
Match length	46

% identity	59
NCBI Description	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169 (AF026473) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	388750
Contig ID	12859_1.R1084
5'-most EST	LIB3433-040-P1-K1-D5
Method	BLASTX
NCBI GI	g3367596
BLAST score	673
E value	2.0e-70
Match length	182
% identity	70
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	388751
Contig ID	12860_2.R1084
5'-most EST	LIB3432-044-P1-K1-G2

Seq. No.	388752
Contig ID	12863_1.R1084
5'-most EST	g5004280
Method	BLASTX
NCBI GI	g3540183
BLAST score	602
E value	1.0e-115
Match length	320
% identity	63
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	388753
Contig ID	12863_2.R1084
5'-most EST	g2312897
Method	BLASTX
NCBI GI	g2827709
BLAST score	297
E value	2.0e-29
Match length	104
% identity	73
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	388754
Contig ID	12864_1.R1084
5'-most EST	g287133

Seq. No.	388755
Contig ID	12868_1.R1084
5'-most EST	g5004458
Method	BLASTX
NCBI GI	g5912424
BLAST score	541
E value	4.0e-55
Match length	154
% identity	72
NCBI Description	(AJ242970) BTF3b-like factor [Arabidopsis thaliana]

Seq. No.	388756
Contig ID	12871_1.R1084
5'-most EST	LIB3432-044-P1-K1-H12

Seq. No.	388757
Contig ID	12888_1.R1084
5'-most EST	LIB3432-045-P1-K1-B10
Method	BLASTX
NCBI GI	g4432844
BLAST score	298
E value	7.0e-27
Match length	143
% identity	41
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	388758
Contig ID	12892_1.R1084
5'-most EST	LIB3432-045-P1-K1-B3

Seq. No.	388759
Contig ID	12893_1.R1084
5'-most EST	g3768237

Seq. No.	388760
Contig ID	12904_1.R1084
5'-most EST	LIB3432-045-P1-K1-C4

Seq. No.	388761
Contig ID	12908_1.R1084
5'-most EST	LIB3432-045-P1-K1-C9
Method	BLASTX
NCBI GI	g5453607
BLAST score	490
E value	4.0e-49
Match length	134
% identity	69
NCBI Description	chaperonin containing TCP1, subunit 7 (eta); CCT-eta >gi_3041738_sp_Q99832_TCPH_HUMAN T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF INTERACTING PROTEIN) >gi_2559010 (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens]

Seq. No.	388762
Contig ID	12911_1.R1084
5'-most EST	LIB3432-045-P1-K1-D11
Method	BLASTN
NCBI GI	g5734616
BLAST score	384
E value	0.0e+00
Match length	440
% identity	97
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No.	388763
Contig ID	12913_1.R1084

5'-most EST	g5005531
Seq. No.	388764
Contig ID	12917_1.R1084
5'-most EST	LIB3432-045-P1-K1-D7
Seq. No.	388765
Contig ID	12923_1.R1084
5'-most EST	LIB3432-045-P1-K1-E2
Seq. No.	388766
Contig ID	12944_1.R1084
5'-most EST	g3759061
Seq. No.	388767
Contig ID	12945_1.R1084
5'-most EST	LIB3432-045-P1-K1-G8
Seq. No.	388768
Contig ID	12948_1.R1084
5'-most EST	g2442706
Method	BLASTX
NCBI GI	g3386621
BLAST score	793
E value	2.0e-84
Match length	224
% identity	68
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.	388769
Contig ID	12954_1.R1084
5'-most EST	g4715677
Method	BLASTX
NCBI GI	g4646206
BLAST score	1638
E value	0.0e+00
Match length	403
% identity	76
NCBI Description	(AC007230) Contains similarity to gb_D13630 KIAA0005 gene from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene. [Arabidopsis thaliana]
Seq. No.	388770
Contig ID	12961_1.R1084
5'-most EST	LIB3432-046-P1-K1-A2
Method	BLASTX
NCBI GI	g6091763
BLAST score	214
E value	7.0e-17
Match length	63
% identity	63
NCBI Description	(AC009327) hypothetical protein [Arabidopsis thaliana]
Seq. No.	388771
Contig ID	12964_1.R1084
5'-most EST	uC-osflcyp175h03b1

Method	BLASTX
NCBI GI	g4538929
BLAST score	201
E value	5.0e-15
Match length	192
% identity	43
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	388772
Contig ID	12967_1.R1084
5'-most EST	LIB3432-046-P1-K1-B11
Method	BLASTX
NCBI GI	g4539417
BLAST score	449
E value	2.0e-44
Match length	120
% identity	66
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	388773
Contig ID	12967_2.R1084
5'-most EST	g3761028
Method	BLASTX
NCBI GI	g4539417
BLAST score	247
E value	8.0e-30
Match length	99
% identity	63
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	388774
Contig ID	12969_1.R1084
5'-most EST	uC-osflM202095b12b1
Method	BLASTX
NCBI GI	g3935141
BLAST score	565
E value	1.0e-57
Match length	348
% identity	38
NCBI Description	(AC005106) T25N20.5 [Arabidopsis thaliana]

Seq. No.	388775
Contig ID	12972_1.R1084
5'-most EST	LIB3432-026-P1-K1-A1
Method	BLASTX
NCBI GI	g4335771
BLAST score	238
E value	3.0e-40
Match length	127
% identity	72
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	388776
Contig ID	12973_1.R1084
5'-most EST	g2801082

Seq. No.	388777
Contig ID	12974_1.R1084
5'-most EST	uC-osf1cyp082b03b1

Seq. No.	388778
Contig ID	12975_1.R1084
5'-most EST	LIB3432-046-P1-K1-B9
Method	BLASTX
NCBI GI	g6006872
BLAST score	333
E value	7.0e-31
Match length	131
% identity	56
NCBI Description	(AC009540) s-syntaxin-like protein [Arabidopsis thaliana]

Seq. No.	388779
Contig ID	12976_1.R1084
5'-most EST	uC-osroM202018f08b1
Method	BLASTX
NCBI GI	g6056196
BLAST score	320
E value	2.0e-40
Match length	267
% identity	35
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	388780
Contig ID	12985_1.R1084
5'-most EST	LIB3432-046-P1-K1-C8

Seq. No.	388781
Contig ID	12987_1.R1084
5'-most EST	g2312919
Method	BLASTX
NCBI GI	g3142331
BLAST score	232
E value	9.0e-19
Match length	192
% identity	33
NCBI Description	(U97327) calcyclin binding protein [Mus musculus]

Seq. No.	388782
Contig ID	12993_1.R1084
5'-most EST	LIB3477-011-P1-K1-G4
Method	BLASTX
NCBI GI	g4204265
BLAST score	428
E value	5.0e-42
Match length	194
% identity	47
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	388783
Contig ID	12998_1.R1084
5'-most EST	LIB3474-001-P1-K1-E3
Method	BLASTX
NCBI GI	g4567286

BLAST score	1483
E value	1.0e-165
Match length	462
% identity	64
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	388784
Contig ID	12998_2.R1084
5'-most EST	g427702
Method	BLASTX
NCBI GI	g3367534
BLAST score	516
E value	5.0e-63
Match length	190
% identity	66
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	388785
Contig ID	12998_3.R1084
5'-most EST	LIB3479-001-Q6-K1-A12
Method	BLASTX
NCBI GI	g3367534
BLAST score	182
E value	2.0e-13
Match length	42
% identity	74
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	388786
Contig ID	12999_1.R1084
5'-most EST	g571947
Method	BLASTX
NCBI GI	g4337025
BLAST score	947
E value	1.0e-169
Match length	468
% identity	63
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana] >gi_4972047_emb_CAB43915.1_ (AL078470) AIM1 protein [Arabidopsis thaliana]

Seq. No.	388787
Contig ID	13023_1.R1084
5'-most EST	g2280993
Method	BLASTX
NCBI GI	g4510363
BLAST score	642
E value	6.0e-67
Match length	134
% identity	87
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	388788
Contig ID	13026_1.R1084
5'-most EST	LIB3432-046-P1-K1-G3

Seq. No.	388789
Contig ID	13029_1.R1084
5'-most EST	uC-osflcyp152a10b1
Method	BLASTX
NCBI GI	g3850823
BLAST score	234
E value	4.0e-19
Match length	89
% identity	60
NCBI Description	(Y18351) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]

Seq. No.	388790
Contig ID	13038_2.R1084
5'-most EST	g703016
Method	BLASTX
NCBI GI	g2213621
BLAST score	183
E value	1.0e-13
Match length	99
% identity	38
NCBI Description	(AC000103) F21J9.26 [Arabidopsis thaliana]

Seq. No.	388791
Contig ID	13052_1.R1084
5'-most EST	g4715364

Seq. No.	388792
Contig ID	13056_1.R1084
5'-most EST	LIB3477-003-P1-K1-E1
Method	BLASTX
NCBI GI	g113178
BLAST score	273
E value	9.0e-24
Match length	137
% identity	36
NCBI Description	ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE) (APH) (ACYLAMINOACYL-PEPTIDASE) >gi_91923_pir__S07624 acylaminoacyl-peptidase (EC 3.4.19.1) - rat >gi_202932 (J04733) acyl-peptide hydrolase [Rattus norvegicus]

Seq. No.	388793
Contig ID	13076_1.R1084
5'-most EST	uC-osroM202003c06a2
Method	BLASTX
NCBI GI	g4758922
BLAST score	187
E value	2.0e-28
Match length	251
% identity	35
NCBI Description	phosphatidylinositol glycan, class L >gi_4239986_dbj_BAA74775.1_ (AB017165) PIG-L [Homo sapiens]

Seq. No.	388794
Contig ID	13094_1.R1084
5'-most EST	uC-osflcyp172g11b1
Method	BLASTX
NCBI GI	g5524756
BLAST score	763
E value	1.0e-123
Match length	242
% identity	47
NCBI Description	(AJ243528) putative glyoxalase I [Triticum aestivum]

Seq. No.	388795
Contig ID	13096_1.R1084
5'-most EST	LIB3432-052-P1-K1-D11

Seq. No.	388796
Contig ID	13105_1.R1084
5'-most EST	LIB3432-049-P1-K1-G11
Method	BLASTX
NCBI GI	g2911358
BLAST score	180
E value	7.0e-13
Match length	49
% identity	71
NCBI Description	(AF041043) NADPH HC toxin reductase [Zea mays]

Seq. No.	388797
Contig ID	13114_2.R1084
5'-most EST	g5003476

Seq. No.	388798
Contig ID	13114_3.R1084
5'-most EST	g2801142

Seq. No.	388799
Contig ID	13116_1.R1084
5'-most EST	g3768682

Seq. No.	388800
Contig ID	13116_2.R1084
5'-most EST	LIB3432-049-P1-K1-H11
Method	BLASTX
NCBI GI	g4803951
BLAST score	984
E value	1.0e-128
Match length	307
% identity	69
NCBI Description	(AC006202) unknown protein [Arabidopsis thaliana]

Seq. No.	388801
Contig ID	13124_1.R1084
5'-most EST	g428485
Method	BLASTX
NCBI GI	g2342683
BLAST score	449
E value	2.0e-44

Match length	232
% identity	43
NCBI Description	(AC000106) Contains similarity to Bos beta-mannosidase (gb_U46067). [Arabidopsis thaliana]

Seq. No.	388802
Contig ID	13125_1.R1084
5'-most EST	LIB3434-021-P1-K1-G12
Method	BLASTX
NCBI GI	g1709129
BLAST score	1230
E value	1.0e-135
Match length	249
% identity	90
NCBI Description	GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3 >gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) - alfalfa >gi_313148_emb_CAA48472_ (X68409) protein kinase [Medicago sativa]

Seq. No.	388803
Contig ID	13131_1.R1084
5'-most EST	LIB3432-050-P1-K1-C4

Seq. No.	388804
Contig ID	13133_1.R1084
5'-most EST	LIB3432-050-P1-K1-B9
Method	BLASTX
NCBI GI	g4415931
BLAST score	782
E value	3.0e-83
Match length	217
% identity	68
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	388805
Contig ID	13141_1.R1084
5'-most EST	uC-osf1M202098e04b1
Method	BLASTX
NCBI GI	g3913791
BLAST score	973
E value	1.0e-106
Match length	231
% identity	79
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2407615 (AF017983) gamma-glutamylcysteine synthetase [Lycopersicon esculentum]

Seq. No.	388806
Contig ID	13141_2.R1084
5'-most EST	g4879008
Method	BLASTX
NCBI GI	g3913791
BLAST score	801
E value	3.0e-99

Match length	194
% identity	91
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2407615 (AF017983) gamma-glutamylcysteine synthetase [Lycopersicon esculentum]

Seq. No.	388807
Contig ID	13145_2.R1084
5'-most EST	LIB3432-050-P1-K1-D1
Method	BLASTX
NCBI GI	g5824665
BLAST score	324
E value	8.0e-30
Match length	142
% identity	47
NCBI Description	(AL110479) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans]

Seq. No.	388808
Contig ID	13147_1.R1084
5'-most EST	LIB3432-050-P1-K1-D12
Method	BLASTX
NCBI GI	g4538903
BLAST score	160
E value	2.0e-10
Match length	90
% identity	39
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	388809
Contig ID	13162_1.R1084
5'-most EST	LIB3477-003-P1-K1-G8

Seq. No.	388810
Contig ID	13164_1.R1084
5'-most EST	LIB3433-007-Q6-K1-E9

Seq. No.	388811
Contig ID	13165_1.R1084
5'-most EST	g427211

Seq. No.	388812
Contig ID	13169_1.R1084
5'-most EST	g3767174

Seq. No.	388813
Contig ID	13176_1.R1084
5'-most EST	g568550
Method	BLASTX
NCBI GI	g3342800
BLAST score	657
E value	5.0e-69
Match length	132
% identity	96
NCBI Description	(AF061837) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	388814
Contig ID	13176_2.R1084
5'-most EST	g3090472
Method	BLASTX
NCBI GI	g3342802
BLAST score	586
E value	7.0e-61
Match length	193
% identity	76
NCBI Description	(AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	388815
Contig ID	13188_1.R1084
5'-most EST	LIB3433-060-P1-K1-H8

Seq. No.	388816
Contig ID	13198_1.R1084
5'-most EST	LIB3432-051-P1-K1-B1

Seq. No.	388817
Contig ID	13204_1.R1084
5'-most EST	LIB3432-051-P1-K1-B4
Method	BLASTX
NCBI GI	g3152582
BLAST score	272
E value	1.0e-23
Match length	71
% identity	66
NCBI Description	(AC002986) YUP8H12R.20 [Arabidopsis thaliana]

Seq. No.	388818
Contig ID	13209_1.R1084
5'-most EST	LIB3432-051-P1-K1-B9
Method	BLASTX
NCBI GI	g4468980
BLAST score	766
E value	1.0e-81
Match length	191
% identity	72
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	388819
Contig ID	13212_1.R1084
5'-most EST	g2443071
Method	BLASTX
NCBI GI	g2959370
BLAST score	275
E value	1.0e-23
Match length	132
% identity	39
NCBI Description	(AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	388820
Contig ID	13220_1.R1084
5'-most EST	g2427679

Method	BLASTX
NCBI GI	g1877480
BLAST score	270
E value	8.0e-50
Match length	184
% identity	65
NCBI Description	(U89270) short-chain alcohol dehydrogenase [Tripsacum dactyloides]

Seq. No.	388821
Contig ID	13226_1.R1084
5'-most EST	LIB3432-051-P1-K1-D6
Method	BLASTX
NCBI GI	g3152605
BLAST score	343
E value	4.0e-37
Match length	141
% identity	60
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388822
Contig ID	13229_1.R1084
5'-most EST	LIB3432-051-P1-K1-D9
Method	BLASTX
NCBI GI	g4519671
BLAST score	353
E value	5.0e-33
Match length	127
% identity	61
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No.	388823
Contig ID	13232_1.R1084
5'-most EST	uC-osflcyp017f02b1
Method	BLASTX
NCBI GI	g399333
BLAST score	206
E value	1.0e-22
Match length	81
% identity	68
NCBI Description	CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8) precursor - pepper >gi_17944_emb_CAA46086_ (X64874) O-acetylserine (thiol)-lyase [Capsicum annuum]

Seq. No.	388824
Contig ID	13238_1.R1084
5'-most EST	LIB3432-051-P1-K1-E7
Method	BLASTX
NCBI GI	g3786005
BLAST score	428
E value	6.0e-42
Match length	104
% identity	46
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	388825
Contig ID	13240_1.R1084
5'-most EST	LIB3433-025-P1-K1-B3
Method	BLASTX
NCBI GI	g2832717
BLAST score	1463
E value	0.0e+00
Match length	372
% identity	95
NCBI Description	(AJ003114) alkaline/neutral invertase [Lolium temulentum]

Seq. No.	388826
Contig ID	13244_1.R1084
5'-most EST	LIB3432-051-P1-K1-F3
Method	BLASTX
NCBI GI	g5107829
BLAST score	610
E value	3.0e-63
Match length	146
% identity	73
NCBI Description	(AF149413) contains similarity to several Arabidopsis thaliana hypothetical proteins including GB:U95973 and GB:AC002392

Seq. No.	388827
Contig ID	13245_1.R1084
5'-most EST	LIB3432-051-P1-K1-F4

Seq. No.	388828
Contig ID	13257_1.R1084
5'-most EST	uC-osflcyp123b11b1
Method	BLASTX
NCBI GI	g2104681
BLAST score	178
E value	2.0e-12
Match length	170
% identity	44
NCBI Description	(X97907) transcription factor [Vicia faba]

Seq. No.	388829
Contig ID	13258_1.R1084
5'-most EST	LIB3432-051-P1-K1-G6
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	1.0e-09
Match length	35
% identity	38
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	388830
Contig ID	13267_1.R1084
5'-most EST	LIB3433-025-P1-K1-G11
Method	BLASTX
NCBI GI	g1669341
BLAST score	233

E value	5.0e-19
Match length	166
% identity	42
NCBI Description	(D45066) AOBP (ascorbate oxidase promoter-binding protein) [Cucurbita maxima]

Seq. No.	388831
Contig ID	13276_1.R1084
5'-most EST	LIB3432-052-P1-K1-A3

Seq. No.	388832
Contig ID	13283_1.R1084
5'-most EST	g3759885
Method	BLASTX
NCBI GI	g5729708
BLAST score	635
E value	5.0e-66
Match length	159
% identity	72
NCBI Description	(AC007927) putative phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	388833
Contig ID	13283_2.R1084
5'-most EST	LIB3433-005-Q6-K1-A10
Method	BLASTX
NCBI GI	g5139541
BLAST score	244
E value	3.0e-20
Match length	75
% identity	55
NCBI Description	(AJ243308) nodulin26-like major intrinsic protein [Pisum sativum]

Seq. No.	388834
Contig ID	13283_3.R1084
5'-most EST	LIB3434-030-P1-K1-B8
Method	BLASTX
NCBI GI	g1076748
BLAST score	556
E value	9.0e-57
Match length	239
% identity	48
NCBI Description	major intrinsic protein - rice >gi_440869_dbj_BAA04257_ (D17443) major intrinsic protein [Oryza sativa]

Seq. No.	388835
Contig ID	13284_1.R1084
5'-most EST	LIB3432-052-P1-K1-B11
Method	BLASTN
NCBI GI	g310320
BLAST score	209
E value	1.0e-113
Match length	534
% identity	93
NCBI Description	Oryza sativa cytosolic copper/zinc-superoxide dismutase (SodCc2) gene, complete cds

Seq. No.	388836
Contig ID	13289_1.R1084
5'-most EST	g3768625

Seq. No.	388837
Contig ID	13291_1.R1084
5'-most EST	g427347
Method	BLASTX
NCBI GI	g730461
BLAST score	214
E value	7.0e-17
Match length	56
% identity	68
NCBI Description	40S RIBOSOMAL PROTEIN YS29A >gi_626904_pir__S48503 ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi_287628_dbj_BAA03507_ (D14676) ribosomal protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729) Ylr388wp [Saccharomyces cerevisiae]

Seq. No.	388838
Contig ID	13291_2.R1084
5'-most EST	LIB3434-042-P1-K1-C12
Method	BLASTX
NCBI GI	g730461
BLAST score	201
E value	2.0e-15
Match length	52
% identity	69
NCBI Description	40S RIBOSOMAL PROTEIN YS29A >gi_626904_pir__S48503 ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi_287628_dbj_BAA03507_ (D14676) ribosomal protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729) Ylr388wp [Saccharomyces cerevisiae]

Seq. No.	388839
Contig ID	13296_1.R1084
5'-most EST	LIB3432-052-P1-K1-C12

Seq. No.	388840
Contig ID	13299_1.R1084
5'-most EST	LIB3432-003-P1-K1-H2
Method	BLASTX
NCBI GI	g3261775
BLAST score	340
E value	7.0e-32
Match length	137
% identity	46
NCBI Description	(Z95584) hypothetical protein Rv1165 [Mycobacterium tuberculosis]

Seq. No.	388841
Contig ID	13300_1.R1084
5'-most EST	LIB3477-010-P1-K1-H7
Method	BLASTX
NCBI GI	g2462826
BLAST score	488

E value	7.0e-49
Match length	272
% identity	38
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	388842
Contig ID	13302_1.R1084
5'-most EST	g3760349
Method	BLASTX
NCBI GI	g6041803
BLAST score	204
E value	2.0e-15
Match length	128
% identity	43
NCBI Description	(AC009755) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388843
Contig ID	13315_1.R1084
5'-most EST	LIB3433-035-P1-K1-B2
Method	BLASTX
NCBI GI	g2880047
BLAST score	770
E value	9.0e-82
Match length	305
% identity	50
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388844
Contig ID	13327_1.R1084
5'-most EST	g427855
Method	BLASTX
NCBI GI	g4426627
BLAST score	658
E value	8.0e-69
Match length	131
% identity	86
NCBI Description	(AF099969) sterol-C5(6)-desaturase homolog [Nicotiana tabacum]

Seq. No.	388845
Contig ID	13336_1.R1084
5'-most EST	g427652
Method	BLASTX
NCBI GI	g5306242
BLAST score	213
E value	3.0e-20
Match length	60
% identity	80
NCBI Description	(AC006438) unknown protein [Arabidopsis thaliana]

Seq. No.	388846
Contig ID	13340_1.R1084
5'-most EST	LIB3433-051-P1-K1-B11
Method	BLASTX
NCBI GI	g4504909
BLAST score	407
E value	3.0e-39

Match length	234
% identity	35
NCBI Description	karyopherin (importin) beta 3 >gi_2102696 (U72761) karyopherin beta 3 [Homo sapiens]

Seq. No.	388847
Contig ID	13341_1.R1084
5'-most EST	LIB3432-052-P1-K1-G3
Method	BLASTX
NCBI GI	g3193301
BLAST score	604
E value	2.0e-62
Match length	223
% identity	57
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No.	388848
Contig ID	13350_1.R1084
5'-most EST	LIB3432-052-P1-K1-H3
Method	BLASTX
NCBI GI	g3128234
BLAST score	759
E value	6.0e-81
Match length	160
% identity	86
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388849
Contig ID	13354_1.R1084
5'-most EST	uC-osflcyp051g11b1

Seq. No.	388850
Contig ID	13362_1.R1084
5'-most EST	g569872
Method	BLASTX
NCBI GI	g4106395
BLAST score	786
E value	6.0e-85
Match length	188
% identity	78
NCBI Description	(AF073744) raffinose synthase [Cucumis sativus]

Seq. No.	388851
Contig ID	13366_1.R1084
5'-most EST	LIB3433-037-P1-K1-A3
Method	BLASTX
NCBI GI	g2765140
BLAST score	828
E value	1.0e-88
Match length	211
% identity	70
NCBI Description	(Y11931) 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase [Nicotiana rustica]

Seq. No.	388852

Contig ID	13376_1.R1084
5'-most EST	g2796914
Seq. No.	388853
Contig ID	13380_1.R1084
5'-most EST	LIB3474-012-P1-K1-G4
Method	BLASTX
NCBI GI	g1001449
BLAST score	167
E value	1.0e-11
Match length	80
% identity	44
NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]
Seq. No.	388854
Contig ID	13390_1.R1084
5'-most EST	g699737
Method	BLASTX
NCBI GI	g3941289
BLAST score	835
E value	3.0e-89
Match length	269
% identity	58
NCBI Description	(AF018093) similarity to SCAMP37 [Pisum sativum]
Seq. No.	388855
Contig ID	13398_1.R1084
5'-most EST	uC-osroM202018b06b1
Method	BLASTX
NCBI GI	g2149640
BLAST score	1237
E value	1.0e-137
Match length	281
% identity	86
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana] >gi_5733867_gb_AAD49755.1_AC007932_3 (AC007932) Identical to gb_U91995 Argonaute protein from Arabidopsis thaliana. ESTs gb_H76075, gb_AA720232, gb_N65911 and gb_AA651494 come from this gene
Seq. No.	388856
Contig ID	13406_1.R1084
5'-most EST	LIB3432-056-P1-K1-B10
Method	BLASTX
NCBI GI	g2731443
BLAST score	195
E value	1.0e-14
Match length	99
% identity	42
NCBI Description	(U96923) [prot= cDNA of the glycoamidase gene [Aspergillus niger]
Seq. No.	388857
Contig ID	13407_1.R1084
5'-most EST	LIB3433-038-P1-K1-D4
Method	BLASTX
NCBI GI	g115587

BLAST score	1126
E value	1.0e-178
Match length	351
% identity	89
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) (CP21) >gi_418801_pir__S31159 phosphoenolpyruvate carboxylase (EC 4.1.1.31) CP21 - sorghum >gi_21630_emb_CAA39197_ (X55664) phosphoenolpyruvate carboxylase [Sorghum bicolor] >gi_22615_emb_CAA46267_ (X65137) phosphoenolpyruvate carboxylase [Sorghum bicolor]

Seq. No.	388858
Contig ID	13408_1.R1084
5'-most EST	LIB3432-057-P1-K1-F11
Method	BLASTX
NCBI GI	g3298538
BLAST score	322
E value	2.0e-29
Match length	209
% identity	30
NCBI Description	(AC004681) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388859
Contig ID	13409_2.R1084
5'-most EST	uC-osroM202030a05a1

Seq. No.	388860
Contig ID	13411_1.R1084
5'-most EST	uC-osflM202048g10b1
Method	BLASTX
NCBI GI	g4239845
BLAST score	1002
E value	1.0e-109
Match length	236
% identity	81
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	388861
Contig ID	13412_1.R1084
5'-most EST	LIB3432-056-P1-K1-B5
Method	BLASTX
NCBI GI	g4996842
BLAST score	347
E value	2.0e-32
Match length	139
% identity	47
NCBI Description	(AB027501) Dcarg-1 [Daucus carota]

Seq. No.	388862
Contig ID	13419_1.R1084
5'-most EST	uC-osflcyp153e04b1
Method	BLASTX
NCBI GI	g4530611
BLAST score	700
E value	1.0e-138
Match length	319
% identity	81

NCBI Description	(AF134552) serine/threonine protein phosphatase PP2A-2 catalytic subunit [Oryza sativa subsp. indica]

Seq. No.	388863
Contig ID	13419_2.R1084
5'-most EST	g2800539

Seq. No.	388864
Contig ID	13446_1.R1084
5'-most EST	LIB3432-056-P1-K1-E6
Method	BLASTX
NCBI GI	g5725443
BLAST score	432
E value	2.0e-42
Match length	159
% identity	62
NCBI Description	(AL109787) putative protein [Arabidopsis thaliana]

Seq. No.	388865
Contig ID	13447_1.R1084
5'-most EST	g3445012

Seq. No.	388866
Contig ID	13449_1.R1084
5'-most EST	LIB3433-039-P1-K1-E11
Method	BLASTX
NCBI GI	g4314378
BLAST score	541
E value	5.0e-55
Match length	233
% identity	44
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana] >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative lipase [Arabidopsis thaliana]

Seq. No.	388867
Contig ID	13452_1.R1084
5'-most EST	LIB3432-056-P1-K1-F11

Seq. No.	388868
Contig ID	13453_1.R1084
5'-most EST	LIB3432-056-P1-K1-F2
Method	BLASTX
NCBI GI	g3451072
BLAST score	579
E value	2.0e-59
Match length	155
% identity	67
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	388869
Contig ID	13458_1.R1084
5'-most EST	g571573
Method	BLASTX
NCBI GI	g4566505
BLAST score	222
E value	2.0e-37

Match length	109
% identity	68
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	388870
Contig ID	13462_1.R1084
5'-most EST	uC-osroM202001h05b1

Seq. No.	388871
Contig ID	13469_1.R1084
5'-most EST	g2799994
Method	BLASTX
NCBI GI	g5922624
BLAST score	257
E value	8.0e-22
Match length	85
% identity	68
NCBI Description	(AP000492) ESTs C97742(C62458),AU078102(C62458) correspond to a region of the predicted gene.; similar to syntaxin related protein AtVam3p (U88045) [Oryza sativa] >gi_6016857_dbj_BAA85200.1_ (AP000570) ESTs C97742(C62458),AU078102(C62458) correspond to a region of the predicted gene.; Similar to syntaxin related protein AtVam3p (U88045) [Oryza sativa]

Seq. No.	388872
Contig ID	13469_2.R1084
5'-most EST	g5039039
Method	BLASTX
NCBI GI	g5922624
BLAST score	1126
E value	1.0e-123
Match length	258
% identity	90
NCBI Description	(AP000492) ESTs C97742(C62458),AU078102(C62458) correspond to a region of the predicted gene.; similar to syntaxin related protein AtVam3p (U88045) [Oryza sativa] >gi_6016857_dbj_BAA85200.1_ (AP000570) ESTs C97742(C62458),AU078102(C62458) correspond to a region of the predicted gene.; Similar to syntaxin related protein AtVam3p (U88045) [Oryza sativa]

Seq. No.	388873
Contig ID	13474_1.R1084
5'-most EST	LIB3432-056-P1-K1-H10
Method	BLASTX
NCBI GI	g5042155
BLAST score	273
E value	6.0e-24
Match length	74
% identity	72
NCBI Description	(AL078620) putative protein [Arabidopsis thaliana]

Seq. No.	388874
Contig ID	13480_1.R1084
5'-most EST	uC-osroM202008e10a1

Method	BLASTX
NCBI GI	g3879734
BLAST score	368
E value	1.0e-34
Match length	230
% identity	39
NCBI Description	(Z93388) predicted using Genefinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D7

Seq. No.	388875
Contig ID	13483_1.R1084
5'-most EST	uC-osroM202018a06b1
Method	BLASTX
NCBI GI	g1351904
BLAST score	778
E value	1.0e-135
Match length	294
% identity	89
NCBI Description	BIFUNCTIONAL ASPARTOKINASE/HOMOSERINE DEHYDROGENASE 1, CHLOROPLAST PRECURSOR (AK-HD 1) (AK-HSDH 1) [INCLUDES: ASPARTOKINASE ; HOMOSERINE DEHYDROGENASE] >gi_500851 (L33912) aspartate kinase-homoserine dehydrogenase [Zea mays]

Seq. No.	388876
Contig ID	13484_1.R1084
5'-most EST	LIB3432-056-P1-K1-H9

Seq. No.	388877
Contig ID	13489_1.R1084
5'-most EST	LIB3477-007-P1-K1-H12
Method	BLASTN
NCBI GI	g5441876
BLAST score	43
E value	1.0e-14
Match length	87
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	388878
Contig ID	13490_1.R1084
5'-most EST	g2800108
Method	BLASTX
NCBI GI	g123530
BLAST score	156
E value	8.0e-10
Match length	172
% identity	2
NCBI Description	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR >gi_72400_pir__KGZQHL histidine-rich glycoprotein precursor - Plasmodium lophurae >gi_9999_emb_CAA25698_ (X01469) histidine-rich protein [Plasmodium lophurae] >gi_224316_prf__1101401A protein,His rich [Plasmodium sp.]

Seq. No.	388879
Contig ID	13499_1.R1084
5'-most EST	uC-osflcyp139h12a1

Seq. No.	388880
Contig ID	13509_1.R1084
5'-most EST	g4969036

Seq. No.	388881
Contig ID	13510_1.R1084
5'-most EST	LIB3432-057-P1-K1-C12
Method	BLASTX
NCBI GI	g1709804
BLAST score	377
E value	6.0e-70
Match length	201
% identity	72
NCBI Description	26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi_2213932 (AF006305) 26S proteasome regulatory subunit [Homo sapiens]

Seq. No.	388882
Contig ID	13512_1.R1084
5'-most EST	LIB3432-057-P1-K1-C3
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	38
% identity	60
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388883
Contig ID	13523_1.R1084
5'-most EST	LIB3432-057-P1-K1-D4

Seq. No.	388884
Contig ID	13534_1.R1084
5'-most EST	LIB3432-057-P1-K1-E6
Method	BLASTX
NCBI GI	g4926827
BLAST score	427
E value	5.0e-42
Match length	150
% identity	60
NCBI Description	(AC004135) T17H7.12 [Arabidopsis thaliana]

Seq. No.	388885
Contig ID	13556_1.R1084
5'-most EST	g571762
Method	BLASTX
NCBI GI	g4567260
BLAST score	596
E value	1.0e-123
Match length	292

% identity	76
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] >gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative NADPH-dependent mannose-6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	388886
Contig ID	13564_1.R1084
5'-most EST	LIB3432-057-P1-K1-H7
Method	BLASTX
NCBI GI	g100226
BLAST score	369
E value	7.0e-35
Match length	170
% identity	45
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	388887
Contig ID	13573_1.R1084
5'-most EST	LIB3432-058-P1-K1-A5
Method	BLASTX
NCBI GI	g2231046
BLAST score	205
E value	1.0e-15
Match length	54
% identity	70
NCBI Description	(Y12618) PPF-1 protein [Pisum sativum]

Seq. No.	388888
Contig ID	13588_1.R1084
5'-most EST	LIB3432-058-P1-K1-B9

Seq. No.	388889
Contig ID	13594_1.R1084
5'-most EST	LIB3432-058-P1-K1-C3
Method	BLASTX
NCBI GI	g1352469
BLAST score	710
E value	8.0e-75
Match length	177
% identity	82
NCBI Description	BETA-FRUCTOFURANOSIDASE, CELL WALL ISOZYME PRECURSOR (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) >gi_736359 (U17695) invertase [Zea mays] >gi_1582380_prf__2118364A cell wall invertase [Zea mays]

Seq. No.	388890
Contig ID	13595_1.R1084
5'-most EST	g4716399
Method	BLASTX
NCBI GI	g132918
BLAST score	320
E value	3.0e-29

Match length	70
% identity	87
NCBI Description	50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35) >gi_81486_pir__A36107 ribosomal protein L35 precursor, chloroplast - spinach >gi_170139 (M60449) ribosomal protein L35 [Spinacia oleracea]

Seq. No.	388891
Contig ID	13601_1.R1084
5'-most EST	LIB3432-058-P1-K1-D1
Method	BLASTX
NCBI GI	g6056199
BLAST score	283
E value	5.0e-40
Match length	173
% identity	49
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	388892
Contig ID	13604_1.R1084
5'-most EST	uC-osrocyp036b03b1
Method	BLASTX
NCBI GI	g2244898
BLAST score	996
E value	1.0e-108
Match length	209
% identity	89
NCBI Description	(Z97338) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	388893
Contig ID	13605_1.R1084
5'-most EST	uC-osflcyp175c04b1
Method	BLASTX
NCBI GI	g3873647
BLAST score	254
E value	2.0e-21
Match length	182
% identity	35
NCBI Description	(Z71177) Similarity with 39.2kd yeast protein (Swiss Prot accession number P42836) [Caenorhabditis elegans]

Seq. No.	388894
Contig ID	13608_1.R1084
5'-most EST	LIB3432-058-P1-K1-D5
Method	BLASTX
NCBI GI	g3080425
BLAST score	609
E value	6.0e-85
Match length	185
% identity	86
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	388895
Contig ID	13614_1.R1084
5'-most EST	LIB3432-058-P1-K1-E10
Method	BLASTX
NCBI GI	g1143427

BLAST score	753
E value	7.0e-80
Match length	195
% identity	77
NCBI Description	(X73961) heat shock protein 70 [Cucumis sativus]

Seq. No.	388896
Contig ID	13624_1.R1084
5'-most EST	g3763372
Method	BLASTX
NCBI GI	g6094211
BLAST score	357
E value	1.0e-33
Match length	76
% identity	91
NCBI Description	PROBABLE SMALL NUCLEAR RIBONUCLEOPROTEIN G (SNRNP-G) (SM PROTEIN G) >gi_3738322 (AC005170) putative small nuclear ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	388897
Contig ID	13626_1.R1084
5'-most EST	g2427237

Seq. No.	388898
Contig ID	13629_1.R1084
5'-most EST	g3761365
Method	BLASTX
NCBI GI	g5306238
BLAST score	251
E value	4.0e-21
Match length	103
% identity	47
NCBI Description	(AC006438) putative cold acclimation protein WCOR413 [Triticum aestivum] [Arabidopsis thaliana]

Seq. No.	388899
Contig ID	13635_1.R1084
5'-most EST	g5004178
Method	BLASTX
NCBI GI	g2213882
BLAST score	1532
E value	1.0e-171
Match length	438
% identity	69
NCBI Description	(AF004165) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	388900
Contig ID	13655_1.R1084
5'-most EST	g1711291
Method	BLASTX
NCBI GI	g2924779
BLAST score	888
E value	1.0e-118
Match length	296
% identity	73
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis

thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	388901
Contig ID	13661_1.R1084
5'-most EST	LIB3432-002-P1-K1-A5

Seq. No.	388902
Contig ID	13663_1.R1084
5'-most EST	LIB3475-002-P1-K2-H6
Method	BLASTX
NCBI GI	g3522950
BLAST score	265
E value	6.0e-23
Match length	79
% identity	57
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388903
Contig ID	13665_1.R1084
5'-most EST	g2431283
Method	BLASTX
NCBI GI	g4678225
BLAST score	665
E value	1.0e-69
Match length	159
% identity	79
NCBI Description	(AC007135) unknown protein [Arabidopsis thaliana]

Seq. No.	388904
Contig ID	13672_1.R1084
5'-most EST	LIB3432-002-P1-K1-B5
Method	BLASTX
NCBI GI	g730450
BLAST score	763
E value	5.0e-81
Match length	192
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B) >gi_480649_pir__S37134 cold-induced protein BnC24B - rape >gi_398922_emb_CAA80343_ (Z22620) cold induced protein (BnC24B) [Brassica napus]

Seq. No.	388905
Contig ID	13672_2.R1084
5'-most EST	LIB3432-039-P1-K1-G10
Method	BLASTX
NCBI GI	g730526
BLAST score	781
E value	4.0e-83
Match length	197
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein

[Arabidopsis thaliana]

Seq. No.	388906
Contig ID	13677_1.R1084
5'-most EST	LIB3432-002-P1-K1-C10
Method	BLASTX
NCBI GI	g4914384
BLAST score	196
E value	5.0e-15
Match length	63
% identity	59
NCBI Description	(AC007167) putative APG protein [Arabidopsis thaliana]

Seq. No.	388907
Contig ID	13678_1.R1084
5'-most EST	LIB3432-002-P1-K1-C12
Method	BLASTX
NCBI GI	g1215812
BLAST score	511
E value	6.0e-53
Match length	146
% identity	72
NCBI Description	(D38170) probenazole-inducible protein PBZ1 [Oryza sativa] >gi_2780343_dbj_BAA24277_ (D82066) PBZ1 [Oryza sativa]

Seq. No.	388908
Contig ID	13679_1.R1084
5'-most EST	g4880923
Method	BLASTX
NCBI GI	g3763932
BLAST score	243
E value	6.0e-23
Match length	98
% identity	63
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	388909
Contig ID	13686_1.R1084
5'-most EST	LIB3432-002-P1-K1-D1

Seq. No.	388910
Contig ID	13689_1.R1084
5'-most EST	LIB3432-002-P1-K1-D3
Method	BLASTX
NCBI GI	g3297816
BLAST score	167
E value	3.0e-11
Match length	76
% identity	46
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	388911
Contig ID	13690_1.R1084
5'-most EST	LIB3433-003-Q6-K6-G5
Method	BLASTX
NCBI GI	g2352925
BLAST score	450

E value	1.0e-44
Match length	103
% identity	83
NCBI Description	(AF012864) plastidic 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 2 [Petroselinum crispum]

Seq. No.	388912
Contig ID	13697_1.R1084
5'-most EST	g4715816
Method	BLASTX
NCBI GI	g5903099
BLAST score	738
E value	6.0e-78
Match length	266
% identity	51
NCBI Description	(AC008017) Unknown protein [Arabidopsis thaliana]

Seq. No.	388913
Contig ID	13698_1.R1084
5'-most EST	LIB3432-002-P1-K1-E2
Method	BLASTX
NCBI GI	g418507
BLAST score	222
E value	8.0e-18
Match length	112
% identity	40
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical protein f161 - Escherichia coli >gi_305032 (L19201) ORF_f161 [Escherichia coli] >gi_1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	388914
Contig ID	13704_1.R1084
5'-most EST	LIB3475-006-P1-K1-F6
Method	BLASTX
NCBI GI	g1335862
BLAST score	150
E value	3.0e-09
Match length	36
% identity	78
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	388915
Contig ID	13726_1.R1084
5'-most EST	uC-osroM202004d05b1
Method	BLASTX
NCBI GI	g3882215
BLAST score	182
E value	6.0e-13
Match length	197
% identity	18
NCBI Description	(AB018290) KIAA0747 protein [Homo sapiens]

Seq. No.	388916

Contig ID	13726_2.R1084
5'-most EST	uC-osroM202019g12b1
Method	BLASTX
NCBI GI	g5701984
BLAST score	192
E value	3.0e-14
Match length	206
% identity	25
NCBI Description	(AL109734) putative C2 domain family protein [Schizosaccharomyces pombe]

Seq. No.	388917
Contig ID	13728_1.R1084
5'-most EST	uC-osflcyp160g05a1
Method	BLASTX
NCBI GI	g2739382
BLAST score	288
E value	1.0e-25
Match length	166
% identity	42
NCBI Description	(AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No.	388918
Contig ID	13729_1.R1084
5'-most EST	LIB3432-002-P1-K1-H12
Method	BLASTX
NCBI GI	g4585884
BLAST score	293
E value	2.0e-26
Match length	144
% identity	46
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	388919
Contig ID	13733_1.R1084
5'-most EST	LIB3432-002-P1-K1-H4
Method	BLASTX
NCBI GI	g3549670
BLAST score	636
E value	3.0e-66
Match length	177
% identity	71
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	388920
Contig ID	13738_1.R1084
5'-most EST	g2442876
Method	BLASTX
NCBI GI	g2982245
BLAST score	382
E value	2.0e-36
Match length	131
% identity	60
NCBI Description	(AF051205) hypothetical protein [Picea mariana]

Seq. No.	388921

Contig ID	13742_1.R1084
5'-most EST	uC-osrocyp014g11b1

Seq. No.	388922
Contig ID	13745_1.R1084
5'-most EST	LIB3432-003-P1-K1-A6
Method	BLASTX
NCBI GI	g1170029
BLAST score	549
E value	2.0e-56
Match length	114
% identity	94
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_100581_pir__A35789 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - barley >gi_506383 (M31545) glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]

Seq. No.	388923
Contig ID	13758_1.R1084
5'-most EST	LIB3432-003-P1-K1-B9
Method	BLASTX
NCBI GI	g586858
BLAST score	255
E value	8.0e-22
Match length	115
% identity	45
NCBI Description	HYPOTHETICAL 21.4 KD PROTEIN IN DACA-SERS INTERGENIC REGION >gi_2127020_pir__S66042 hypothetical protein - Bacillus subtilis >gi_467402_dbj_BAA05248_ (D26185) unknown [Bacillus subtilis] >gi_2632279_emb_CAB11788_ (Z99104) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	388924
Contig ID	13768_1.R1084
5'-most EST	LIB3432-003-P1-K1-C9
Method	BLASTN
NCBI GI	g6015437
BLAST score	38
E value	1.0e-11
Match length	51
% identity	67
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	388925
Contig ID	13773_1.R1084
5'-most EST	uC-osflcyp161d08b1
Method	BLASTX
NCBI GI	g2244839
BLAST score	234
E value	4.0e-19
Match length	100
% identity	40
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388926
Contig ID	13782_1.R1084

5'-most EST	LIB3432-003-P1-K1-E11
Method	BLASTX
NCBI GI	g5669650
BLAST score	500
E value	3.0e-50
Match length	226
% identity	46
NCBI Description	(AF096260) ER66 protein [Lycopersicon esculentum]

Seq. No.	388927
Contig ID	13785_1.R1084
5'-most EST	g2798872
Method	BLASTN
NCBI GI	g619119
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Calothrix D253 genomic DNA (clone AG5R)

Seq. No.	388928
Contig ID	13796_1.R1084
5'-most EST	g4714666
Method	BLASTX
NCBI GI	g4093155
BLAST score	428
E value	2.0e-41
Match length	162
% identity	54
NCBI Description	(AF088281) phytochrome-associated protein 1 [Arabidopsis thaliana]

Seq. No.	388929
Contig ID	13796_2.R1084
5'-most EST	g4715467
Method	BLASTX
NCBI GI	g4093155
BLAST score	308
E value	5.0e-30
Match length	155
% identity	50
NCBI Description	(AF088281) phytochrome-associated protein 1 [Arabidopsis thaliana]

Seq. No.	388930
Contig ID	13801_1.R1084
5'-most EST	g701569

Seq. No.	388931
Contig ID	13803_1.R1084
5'-most EST	LIB3432-003-P1-K1-F9

Seq. No.	388932
Contig ID	13805_1.R1084
5'-most EST	g4879544

Seq. No.	388933

Contig ID	13807_1.R1084
5'-most EST	LIB3434-008-P1-K1-F11
Method	BLASTX
NCBI GI	g5042409
BLAST score	494
E value	6.0e-50
Match length	127
% identity	72
NCBI Description	(AC006193) Putative membrane related protein [Arabidopsis thaliana]

Seq. No.	388934
Contig ID	13820_1.R1084
5'-most EST	uC-osf1m202108e01b1
Method	BLASTX
NCBI GI	g5263320
BLAST score	599
E value	4.0e-62
Match length	131
% identity	89
NCBI Description	(AC007727) Similar to gb_M87339 replication factor C, 37-kDa subunit from Homo sapiens and is a member of PF_00004 ATPases associated with various cellular activities. [Arabidopsis thaliana]

Seq. No.	388935
Contig ID	13831_1.R1084
5'-most EST	g428111

Seq. No.	388936
Contig ID	13833_1.R1084
5'-most EST	g4715415

Seq. No.	388937
Contig ID	13835_1.R1084
5'-most EST	LIB3432-004-P1-K1-B12
Method	BLASTX
NCBI GI	g1653767
BLAST score	680
E value	2.0e-71
Match length	215
% identity	59
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	388938
Contig ID	13842_1.R1084
5'-most EST	LIB3432-004-P1-K1-C11
Method	BLASTX
NCBI GI	g133872
BLAST score	565
E value	5.0e-58
Match length	146
% identity	81
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_

(X66135) ribosomal protein S1 [Spinacia oleracea]
>gi_170143 (M82923) chloroplast ribosomal protein S1
[Spinacia oleracea]

Seq. No.	388939
Contig ID	13843_1.R1084
5'-most EST	LIB3432-004-P1-K1-C12
Method	BLASTX
NCBI GI	g5777631
BLAST score	187
E value	8.0e-14
Match length	43
% identity	84
NCBI Description	(AJ245900) CAA303719.1 protein [Oryza sativa]

Seq. No.	388940
Contig ID	13850_1.R1084
5'-most EST	LIB3432-004-P1-K1-D11
Method	BLASTX
NCBI GI	g3080440
BLAST score	188
E value	6.0e-14
Match length	96
% identity	42
NCBI Description	(AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388941
Contig ID	13854_1.R1084
5'-most EST	LIB3432-004-P1-K1-D7

Seq. No.	388942
Contig ID	13856_1.R1084
5'-most EST	g2797434

Seq. No.	388943
Contig ID	13861_1.R1084
5'-most EST	g426060
Method	BLASTX
NCBI GI	g1871194
BLAST score	438
E value	1.0e-42
Match length	208
% identity	48
NCBI Description	(U90439) DNA binding protein isolog [Arabidopsis thaliana] >gi_2335092 (AC002339) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	388944
Contig ID	13862_1.R1084
5'-most EST	g699944
Method	BLASTX
NCBI GI	g4835766
BLAST score	417
E value	1.0e-40
Match length	132
% identity	63
NCBI Description	(AC007202) Contains similarity to gb_AB017693 transfactor

(WERBP-1) from Nicotiana tabacum. ESTs gb_H39299, gb_T41875, gb_H38232 and gb_N38325 come from this gene. [Arabidopsis thaliana]

Seq. No.	388945
Contig ID	13869_1.R1084
5'-most EST	uC-osroM202032b04a1
Method	BLASTX
NCBI GI	g5902707
BLAST score	311
E value	2.0e-28
Match length	92
% identity	65
NCBI Description	ZEAXANTHIN EPOXIDASE PRECURSOR >gi_2129941_pir__S69548 zeaxanthin epoxidase precursor - curled-leaved tobacco >gi_1370274_emb_CAA65048_ (X95732) zeaxanthin epoxidase [Nicotiana plumbaginifolia]

Seq. No.	388946
Contig ID	13884_1.R1084
5'-most EST	LIB3432-004-P1-K1-H4
Method	BLASTX
NCBI GI	g133028
BLAST score	485
E value	8.0e-52
Match length	147
% identity	66
NCBI Description	50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9) >gi_71257_pir__R5MUL9 ribosomal protein L9 precursor, chloroplast - Arabidopsis thaliana >gi_16499_emb_CAA77480_ (Z11129) plastid ribosomal protein CL9 [Arabidopsis thaliana] >gi_16501_emb_CAA77594_ (Z11509) Chloroplast ribosomal protein CL9 [Arabidopsis thaliana]

Seq. No.	388947
Contig ID	13899_1.R1084
5'-most EST	uC-osflM202095d09b1
Method	BLASTX
NCBI GI	g4455351
BLAST score	610
E value	5.0e-63
Match length	166
% identity	68
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	388948
Contig ID	13904_1.R1084
5'-most EST	uC-osflcyp062g07a1
Method	BLASTN
NCBI GI	g5042437
BLAST score	476
E value	0.0e+00
Match length	585
% identity	83
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	388949

Contig ID	13905_1.R1084
5'-most EST	g5455328
Method	BLASTX
NCBI GI	g170031
BLAST score	788
E value	1.0e-105
Match length	277
% identity	68
NCBI Description	(M10594) nodulin 35 [Glycine max]

Seq. No.	388950
Contig ID	13912_1.R1084
5'-most EST	g5803503

Seq. No.	388951
Contig ID	13915_1.R1084
5'-most EST	LIB3433-040-P1-K1-C5
Method	BLASTX
NCBI GI	g3249064
BLAST score	555
E value	1.0e-56
Match length	163
% identity	67
NCBI Description	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4 contig gb_Z97344. [Arabidopsis thaliana]

Seq. No.	388952
Contig ID	13921_1.R1084
5'-most EST	LIB3432-041-P1-K1-E10
Method	BLASTX
NCBI GI	g3913182
BLAST score	361
E value	1.0e-65
Match length	240
% identity	60
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) (BROWN-MIDRIB 1 PROTEIN) >gi_2239258_emb_CAA74070_ (Y13733) cinnamyl alcohol dehydrogenase [Zea mays]

Seq. No.	388953
Contig ID	13943_1.R1084
5'-most EST	LIB3432-025-P1-K1-F12

Seq. No.	388954
Contig ID	13944_1.R1084
5'-most EST	LIB3432-025-P1-K1-F2
Method	BLASTX
NCBI GI	g2130091
BLAST score	1092
E value	1.0e-119
Match length	219
% identity	93
NCBI Description	aspartate aminotransferase - proso millet >gi_633095_dbj_BAA08106_ (D45076) plastidic aspartate aminotransferase [Panicum miliaceum]

Seq. No.	388955
Contig ID	13954_1.R1084
5'-most EST	LIB3434-045-P1-K1-A7
Method	BLASTX
NCBI GI	g5777631
BLAST score	701
E value	6.0e-74
Match length	207
% identity	68
NCBI Description	(AJ245900) CAA303719.1 protein [Oryza sativa]

Seq. No.	388956
Contig ID	13958_1.R1084
5'-most EST	uC-osflcyp154f04b1
Method	BLASTX
NCBI GI	g3183094
BLAST score	958
E value	1.0e-104
Match length	215
% identity	85
NCBI Description	ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE) (ORNITHINE TRANSCARBAMYLASE) >gi_971168 (U13684) ornithine carbamoyltransferase [Pisum sativum]

Seq. No.	388957
Contig ID	13969_1.R1084
5'-most EST	LIB3434-029-P1-K1-G1
Method	BLASTX
NCBI GI	g4539452
BLAST score	1390
E value	1.0e-154
Match length	367
% identity	70
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	388958
Contig ID	13972_1.R1084
5'-most EST	LIB3432-026-P1-K1-A11

Seq. No.	388959
Contig ID	13985_1.R1084
5'-most EST	LIB3433-016-Q6-K6-E1
Method	BLASTX
NCBI GI	g2459445
BLAST score	379
E value	4.0e-36
Match length	213
% identity	32
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	388960
Contig ID	14008_1.R1084
5'-most EST	LIB3434-060-P1-K1-G9

Seq. No.	388961

Contig ID	14018_1.R1084
5'-most EST	LIB3432-026-P1-K1-E2
Method	BLASTX
NCBI GI	g4538897
BLAST score	595
E value	1.0e-61
Match length	203
% identity	55
NCBI Description	(AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No.	388962
Contig ID	14027_1.R1084
5'-most EST	LIB3432-026-P1-K1-F10
Method	BLASTX
NCBI GI	g2795806
BLAST score	369
E value	3.0e-35
Match length	107
% identity	64
NCBI Description	(AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	388963
Contig ID	14032_1.R1084
5'-most EST	LIB3479-009-Q6-K1-D3

Seq. No.	388964
Contig ID	14034_1.R1084
5'-most EST	g4879613
Method	BLASTX
NCBI GI	g2275219
BLAST score	590
E value	8.0e-75
Match length	280
% identity	44
NCBI Description	(AC002337) unknown protein [Arabidopsis thaliana]

Seq. No.	388965
Contig ID	14048_1.R1084
5'-most EST	g1632200

Seq. No.	388966
Contig ID	14052_1.R1084
5'-most EST	LIB3432-026-P1-K1-H3
Method	BLASTX
NCBI GI	g5902363
BLAST score	737
E value	3.0e-78
Match length	165
% identity	83
NCBI Description	(AC009322) Putative coatomer protein complex, subunit beta 2 (beta prime) [Arabidopsis thaliana]

Seq. No.	388967
Contig ID	14054_1.R1084
5'-most EST	LIB3432-026-P1-K1-H5
Method	BLASTX
NCBI GI	g4733959

BLAST score	225
E value	5.0e-18
Match length	75
% identity	61
NCBI Description	(AC007294) putative glucose inhibited division protein A [Arabidopsis thaliana]

Seq. No.	388968
Contig ID	14058_1.R1084
5'-most EST	LIB3474-004-P1-K1-E4

Seq. No.	388969
Contig ID	14077_1.R1084
5'-most EST	uC-osrocyp015a11b1
Method	BLASTX
NCBI GI	g5903045
BLAST score	750
E value	2.0e-79
Match length	180
% identity	79
NCBI Description	(AC008016) Similar to gb_AF108945 signal peptidase 18 kDa subunit from Homo sapiens. ESTs gb_H76629, gb_H76949 and gb_H76216 come from this gene. [Arabidopsis thaliana]

Seq. No.	388970
Contig ID	14081_1.R1084
5'-most EST	g2427998
Method	BLASTX
NCBI GI	g3540204
BLAST score	203
E value	1.0e-15
Match length	111
% identity	51
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	388971
Contig ID	14089_1.R1084
5'-most EST	LIB3432-027-P1-K1-C5
Method	BLASTX
NCBI GI	g6056385
BLAST score	376
E value	6.0e-36
Match length	127
% identity	56
NCBI Description	(AC009894) Unknown protein [Arabidopsis thaliana]

Seq. No.	388972
Contig ID	14090_1.R1084
5'-most EST	g286605
Method	BLASTX
NCBI GI	g5903104
BLAST score	151
E value	3.0e-09
Match length	92
% identity	36
NCBI Description	(AC008017) Highly similar to non intermediate filament IFA binding protein [Arabidopsis thaliana]

Seq. No.	388973
Contig ID	14096_1.R1084
5'-most EST	g3760887
Method	BLASTX
NCBI GI	g1723440
BLAST score	177
E value	6.0e-14
Match length	164
% identity	34
NCBI Description	HYPOTHETICAL 35.9 KD PROTEIN C56F8.08 IN CHROMOSOME I >gi_1204230_emb_CAA93579_ (Z69728) unknown [Schizosaccharomyces pombe]

Seq. No.	388974
Contig ID	14101_1.R1084
5'-most EST	LIB3432-027-P1-K1-D5
Method	BLASTX
NCBI GI	g3608412
BLAST score	346
E value	2.0e-32
Match length	157
% identity	50
NCBI Description	(AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No.	388975
Contig ID	14109_1.R1084
5'-most EST	LIB3432-027-P1-K1-E2
Method	BLASTN
NCBI GI	g2773153
BLAST score	61
E value	2.0e-25
Match length	211
% identity	87
NCBI Description	Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds

Seq. No.	388976
Contig ID	14113_1.R1084
5'-most EST	g5003847
Method	BLASTX
NCBI GI	g2506275
BLAST score	1052
E value	1.0e-115
Match length	233
% identity	93
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR

Seq. No.	388977
Contig ID	14113_2.R1084
5'-most EST	uC-osroM202016a05a1
Method	BLASTX
NCBI GI	g2493646
BLAST score	869
E value	2.0e-93
Match length	187

% identity	96
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi_309559 (L21008) chaperonin 60 [Zea mays] >gi_309561 (L21006) mitochondrial chaperonin 60 [Zea mays]

Seq. No.	388978
Contig ID	14116_1.R1084
5'-most EST	LIB3432-027-P1-K1-E9
Method	BLASTX
NCBI GI	g1143511
BLAST score	433
E value	1.0e-55
Match length	123
% identity	92
NCBI Description	(Z47076) Ser/Thr protein phosphatase homologous to PPX [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein phosphatase [Malus domestica]

Seq. No.	388979
Contig ID	14118_1.R1084
5'-most EST	uC-osflm202108g04b1

Seq. No.	388980
Contig ID	14127_1.R1084
5'-most EST	LIB3432-027-P1-K1-F8

Seq. No.	388981
Contig ID	14129_1.R1084
5'-most EST	g4716572

Seq. No.	388982
Contig ID	14148_1.R1084
5'-most EST	g3768533
Method	BLASTX
NCBI GI	g1769901
BLAST score	214
E value	2.0e-21
Match length	107
% identity	55
NCBI Description	(X95737) proline transporter 1 [Arabidopsis thaliana] >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]

Seq. No.	388983
Contig ID	14154_1.R1084
5'-most EST	LIB3432-028-P1-K1-A8
Method	BLASTX
NCBI GI	g4200165
BLAST score	977
E value	1.0e-106
Match length	217
% identity	79
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	388984
Contig ID	14157_1.R1084
5'-most EST	LIB3432-028-P1-K1-A5

Method	BLASTX
NCBI GI	g6041814
BLAST score	151
E value	1.0e-09
Match length	36
% identity	69
NCBI Description	(AC009918) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388985
Contig ID	14159_1.R1084
5'-most EST	uC-osf1cyp172g04b1
Method	BLASTX
NCBI GI	g4103320
BLAST score	306
E value	2.0e-27
Match length	138
% identity	43
NCBI Description	(AF022231) unknown protein [Homo sapiens]

Seq. No.	388986
Contig ID	14166_1.R1084
5'-most EST	LIB3432-028-P1-K1-B4

Seq. No.	388987
Contig ID	14170_1.R1084
5'-most EST	LIB3432-028-P1-K1-B9
Method	BLASTX
NCBI GI	g4337175
BLAST score	318
E value	1.0e-28
Match length	129
% identity	48
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	388988
Contig ID	14172_1.R1084
5'-most EST	uC-osrocyp017c02b1

Seq. No.	388989
Contig ID	14176_1.R1084
5'-most EST	g2275812
Method	BLASTX
NCBI GI	g4454467
BLAST score	418
E value	2.0e-52
Match length	285
% identity	44
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	388990
Contig ID	14178_1.R1084
5'-most EST	LIB3599-001-P1-K6-F12
Method	BLASTX
NCBI GI	g2129929

BLAST score	369
E value	5.0e-35
Match length	76
% identity	91
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 - tomato >gi_1049068 (U28403) RNA polymerase II subunit 2 [Solanum lycopersicum]

Seq. No.	388991
Contig ID	14183_1.R1084
5'-most EST	LIB3432-028-P1-K1-D11

Seq. No.	388992
Contig ID	14187_1.R1084
5'-most EST	uC-osroM202029h11b1
Method	BLASTX
NCBI GI	g5107819
BLAST score	991
E value	1.0e-107
Match length	384
% identity	53
NCBI Description	(AF149413) contains similarity to arabinosidase [Arabidopsis thaliana]

Seq. No.	388993
Contig ID	14190_1.R1084
5'-most EST	g701974
Method	BLASTX
NCBI GI	g4455258
BLAST score	244
E value	1.0e-20
Match length	92
% identity	48
NCBI Description	(AL035523) acid phosphatase-like protein [Arabidopsis thaliana]

Seq. No.	388994
Contig ID	14190_2.R1084
5'-most EST	LIB3432-028-P1-K1-D9
Method	BLASTX
NCBI GI	g3341443
BLAST score	164
E value	1.0e-15
Match length	87
% identity	49
NCBI Description	(AJ223074) acid phosphatase [Glycine max]

Seq. No.	388995
Contig ID	14207_2.R1084
5'-most EST	g3107391
Method	BLASTX
NCBI GI	g4469019
BLAST score	191
E value	3.0e-14
Match length	85
% identity	51
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	388996
Contig ID	14213_1.R1084
5'-most EST	uC-osflcyp027d12b1
Method	BLASTX
NCBI GI	g3176690
BLAST score	785
E value	9.0e-84
Match length	182
% identity	86
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	388997
Contig ID	14216_1.R1084
5'-most EST	uC-osroM202031e07b1
Method	BLASTX
NCBI GI	g3241943
BLAST score	677
E value	5.0e-93
Match length	207
% identity	77
NCBI Description	(AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388998
Contig ID	14223_1.R1084
5'-most EST	LIB3432-028-P1-K1-G6
Method	BLASTX
NCBI GI	g2618688
BLAST score	526
E value	2.0e-53
Match length	149
% identity	66
NCBI Description	(AC002510) putative esterase D [Arabidopsis thaliana]

Seq. No.	388999
Contig ID	14235_1.R1084
5'-most EST	uC-osflM202020d08b1
Method	BLASTX
NCBI GI	g2129855
BLAST score	1196
E value	1.0e-176
Match length	360
% identity	82
NCBI Description	mitogen-activated protein kinase MMK2 (EC 2.7.1.-) - alfalfa

Seq. No.	389000
Contig ID	14239_1.R1084
5'-most EST	LIB3477-003-P1-K1-D2

Seq. No.	389001
Contig ID	14244_1.R1084
5'-most EST	LIB3432-029-P1-K1-A6
Method	BLASTX
NCBI GI	g2148018

BLAST score	299
E value	1.0e-38
Match length	207
% identity	38
NCBI Description	ribonuclease II precursor, wound-induced - Zinnia elegans >gi_642958 (U19924) wounding-induced ribonuclease gene [Zinnia elegans]

Seq. No.	389002
Contig ID	14250_1.R1084
5'-most EST	LIB3432-029-P1-K1-B11
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	4.0e-10
Match length	35
% identity	42
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389003
Contig ID	14254_1.R1084
5'-most EST	g5038791
Method	BLASTX
NCBI GI	g4218535
BLAST score	820
E value	1.0e-87
Match length	223
% identity	70
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	389004
Contig ID	14262_1.R1084
5'-most EST	LIB3432-029-P1-K1-C12
Method	BLASTX
NCBI GI	g6056209
BLAST score	214
E value	7.0e-17
Match length	47
% identity	85
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	389005
Contig ID	14275_1.R1084
5'-most EST	uC-osroM202013e04b1
Method	BLASTX
NCBI GI	g3851005
BLAST score	1161
E value	1.0e-128
Match length	245
% identity	91
NCBI Description	(AF069911) pyruvate dehydrogenase E1 alpha subunit [Zea mays]

Seq. No.	389006
Contig ID	14279_2.R1084
5'-most EST	g2275825

Seq. No.	389007
Contig ID	14280_1.R1084
5'-most EST	uC-osflM202016b09b1
Method	BLASTX
NCBI GI	g136640
BLAST score	796
E value	7.0e-85
Match length	152
% identity	96
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720) ubiquitin carrier protein [Triticum aestivum]

Seq. No.	389008
Contig ID	14286_1.R1084
5'-most EST	LIB3433-014-Q6-K1-G1
Method	BLASTN
NCBI GI	g5803242
BLAST score	305
E value	1.0e-171
Match length	481
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	389009
Contig ID	14293_1.R1084
5'-most EST	uC-osflcyp074c10b1

Seq. No.	389010
Contig ID	14297_1.R1084
5'-most EST	g3760551
Method	BLASTN
NCBI GI	g2618602
BLAST score	45
E value	1.0e-15
Match length	85
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence

Seq. No.	389011
Contig ID	14298_1.R1084
5'-most EST	g5003514
Method	BLASTX
NCBI GI	g4455210
BLAST score	1349
E value	1.0e-149
Match length	388
% identity	68
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	389012
Contig ID	14312_1.R1084
5'-most EST	g700362
Method	BLASTX
NCBI GI	g2914700

BLAST score	337
E value	3.0e-31
Match length	117
% identity	56
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	389013
Contig ID	14325_1.R1084
5'-most EST	LIB3432-030-P1-K1-A4

Seq. No.	389014
Contig ID	14336_1.R1084
5'-most EST	LIB3434-051-P1-K1-G3
Method	BLASTX
NCBI GI	g4490316
BLAST score	438
E value	1.0e-42
Match length	277
% identity	40
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	389015
Contig ID	14342_1.R1084
5'-most EST	LIB3432-030-P1-K1-C1
Method	BLASTX
NCBI GI	g5731754
BLAST score	329
E value	2.0e-30
Match length	111
% identity	58
NCBI Description	(AL109819) putative protein [Arabidopsis thaliana]

Seq. No.	389016
Contig ID	14351_1.R1084
5'-most EST	LIB3434-054-P1-K1-D1

Seq. No.	389017
Contig ID	14353_1.R1084
5'-most EST	LIB3432-030-P1-K1-D1

Seq. No.	389018
Contig ID	14355_1.R1084
5'-most EST	LIB3432-030-P1-K1-D11

Seq. No.	389019
Contig ID	14356_2.R1084
5'-most EST	g4714668
Method	BLASTX
NCBI GI	g5080776
BLAST score	375
E value	5.0e-69
Match length	221
% identity	64
NCBI Description	(AC007576) Similar to protein kinases [Arabidopsis thaliana]

Seq. No.	389020
Contig ID	14363_1.R1084
5'-most EST	uC-osflcyp174h01a1

Seq. No.	389021
Contig ID	14368_1.R1084
5'-most EST	LIB3432-030-P1-K1-E5
Method	BLASTX
NCBI GI	g5051773
BLAST score	214
E value	9.0e-17
Match length	161
% identity	32
NCBI Description	(AL078637) putative protein [Arabidopsis thaliana]

Seq. No.	389022
Contig ID	14372_1.R1084
5'-most EST	LIB3432-030-P1-K1-E9
Method	BLASTX
NCBI GI	g3603401
BLAST score	390
E value	5.0e-71
Match length	233
% identity	59
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	389023
Contig ID	14384_1.R1084
5'-most EST	g5607466
Method	BLASTX
NCBI GI	g132005
BLAST score	1120
E value	1.0e-123
Match length	218
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (RUBISCO LARGE SUBUNIT) >gi_68145_pir__RKRZL ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain precursor - rice chloroplast >gi_11992_emb_CAA34004_ (X15901) rbcL; RuBisCO large subunit [Oryza sativa] >gi_344017_dbj_BAA00147_ (D00207) ribulose 1,5-bisphosphate carboxylase large subunit [Oryza sativa] >gi_226613_prf__1603356AK ribulose bisphosphate carboxylase oxygenase L [Oryza sativa]

Seq. No.	389024
Contig ID	14385_1.R1084
5'-most EST	g5003249
Method	BLASTX
NCBI GI	g2648032
BLAST score	722
E value	1.0e-76
Match length	159
% identity	77
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	389025

Contig ID	14386_1.R1084
5'-most EST	LIB3432-030-P1-K1-G5

Seq. No.	389026
Contig ID	14410_1.R1084
5'-most EST	LIB3432-031-P1-K1-B1
Method	BLASTX
NCBI GI	g5262218
BLAST score	184
E value	1.0e-13
Match length	77
% identity	48
NCBI Description	(AL080254) calcium-binding protein-like [Arabidopsis thaliana]

Seq. No.	389027
Contig ID	14411_1.R1084
5'-most EST	g3768611
Method	BLASTX
NCBI GI	g1737492
BLAST score	2321
E value	0.0e+00
Match length	627
% identity	69
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	389028
Contig ID	14419_1.R1084
5'-most EST	uC-osflcyp162e01a1

Seq. No.	389029
Contig ID	14419_2.R1084
5'-most EST	LIB3432-031-P1-K1-B7

Seq. No.	389030
Contig ID	14425_1.R1084
5'-most EST	uC-osroM202001b03b1
Method	BLASTX
NCBI GI	g1352830
BLAST score	2148
E value	0.0e+00
Match length	428
% identity	97
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_1049253 (U36436) vacuolar ATPase 69 kDa subunit [Zea mays]

Seq. No.	389031
Contig ID	14426_1.R1084
5'-most EST	LIB3434-005-P1-K1-G5

Seq. No.	389032
Contig ID	14428_1.R1084
5'-most EST	LIB3432-031-P1-K1-C5
Method	BLASTN
NCBI GI	g6015437
BLAST score	36

E value	2.0e-10
Match length	36
% identity	59
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389033
Contig ID	14434_1.R1084
5'-most EST	g2442333

Seq. No.	389034
Contig ID	14435_1.R1084
5'-most EST	LIB3432-031-P1-K1-D12

Seq. No.	389035
Contig ID	14437_1.R1084
5'-most EST	g4879948
Method	BLASTX
NCBI GI	g4469024
BLAST score	200
E value	2.0e-28
Match length	107
% identity	60
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	389036
Contig ID	14447_1.R1084
5'-most EST	LIB3432-031-P1-K1-E4
Method	BLASTX
NCBI GI	g4680498
BLAST score	402
E value	5.0e-39
Match length	87
% identity	54
NCBI Description	(AF119222) TIA-1 related protein [Oryza sativa]

Seq. No.	389037
Contig ID	14479_1.R1084
5'-most EST	LIB3432-031-P1-K1-H2
Method	BLASTX
NCBI GI	g3025205
BLAST score	241
E value	7.0e-20
Match length	161
% identity	36
NCBI Description	HYPOTHETICAL 65.1 KD PROTEIN SLR1919 >gi_1652223_dbj_BAA17147_ (D90903) ABC1-like [Synechocystis sp.]

Seq. No.	389038
Contig ID	14485_1.R1084
5'-most EST	LIB3477-005-P1-K1-C8
Method	BLASTX
NCBI GI	g5929932
BLAST score	1130
E value	1.0e-124
Match length	270
% identity	80

NCBI Description	(AF178952) voltage-dependent anion channel protein 2 [Zea mays]

Seq. No.	389039
Contig ID	14499_1.R1084
5'-most EST	uC-osflM202048f08b1
Method	BLASTX
NCBI GI	g2088647
BLAST score	777
E value	5.0e-86
Match length	272
% identity	58
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No.	389040
Contig ID	14500_1.R1084
5'-most EST	LIB3432-037-P1-K1-B3
Method	BLASTX
NCBI GI	g4586109
BLAST score	272
E value	9.0e-24
Match length	93
% identity	51
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	389041
Contig ID	14513_1.R1084
5'-most EST	g4716575
Method	BLASTX
NCBI GI	g4567095
BLAST score	351
E value	8.0e-33
Match length	91
% identity	66
NCBI Description	(AF129516) fertilization-independent endosperm protein [Arabidopsis thaliana]

Seq. No.	389042
Contig ID	14525_1.R1084
5'-most EST	g3758964
Method	BLASTX
NCBI GI	g5042420
BLAST score	329
E value	2.0e-31
Match length	154
% identity	51
NCBI Description	(AC006193) Unknown protein [Arabidopsis thaliana]

Seq. No.	389043
Contig ID	14531_1.R1084
5'-most EST	uC-osflm202106h04b1
Method	BLASTX
NCBI GI	g5803272
BLAST score	493
E value	9.0e-53

Match length	153
% identity	75
NCBI Description	(AP000399) ESTs AU055950(S20175),C73125(E2952), AU055951(S20175) correspond to a region of the predicted gene; similar to acyl-ACP thioesterase (U92878) [Oryza sativa]

Seq. No.	389044
Contig ID	14533_1.R1084
5'-most EST	LIB3432-037-P1-K1-E7
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	3.0e-10
Match length	47
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389045
Contig ID	14538_1.R1084
5'-most EST	g4714242
Method	BLASTX
NCBI GI	g4587615
BLAST score	1026
E value	1.0e-128
Match length	348
% identity	64
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	389046
Contig ID	14542_1.R1084
5'-most EST	uC-osrocyp028h02b1
Method	BLASTX
NCBI GI	g1657621
BLAST score	494
E value	6.0e-90
Match length	241
% identity	64
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]

Seq. No.	389047
Contig ID	14557_1.R1084
5'-most EST	uC-osflcyp027g03b1
Method	BLASTX
NCBI GI	g4432864
BLAST score	654
E value	2.0e-68
Match length	202
% identity	59
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389048

Contig ID	14569_1.R1084
5'-most EST	uC-osflcyp157d03b1
Method	BLASTX
NCBI GI	g3182915
BLAST score	481
E value	3.0e-59
Match length	177
% identity	63
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1842150_dbj_BAA19225_ (AB001051) ADP-ribosylation factor [Dugesia japonica]

Seq. No.	389049
Contig ID	14570_1.R1084
5'-most EST	LIB3477-002-P1-K1-C4
Method	BLASTX
NCBI GI	g3122572
BLAST score	1048
E value	1.0e-114
Match length	296
% identity	68
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	389050
Contig ID	14578_1.R1084
5'-most EST	LIB3599-001-P1-K6-C2
Method	BLASTX
NCBI GI	g2465151
BLAST score	237
E value	2.0e-19
Match length	118
% identity	47
NCBI Description	(Z99753) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	389051
Contig ID	14578_2.R1084
5'-most EST	g3444996

Seq. No.	389052
Contig ID	14584_1.R1084
5'-most EST	LIB3432-039-P1-K1-B7
Method	BLASTX
NCBI GI	g3914191
BLAST score	245
E value	2.0e-20
Match length	108
% identity	45
NCBI Description	UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT) >gi_1931579 (U76557) O-GlcNAc transferase, p110 subunit [Rattus norvegicus]

Seq. No. 389053

Contig ID	14588_1.R1084
5'-most EST	LIB3432-039-P1-K1-C10

Seq. No.	389054
Contig ID	14590_1.R1084
5'-most EST	LIB3432-039-P1-K1-C2
Method	BLASTX
NCBI GI	g3123161
BLAST score	181
E value	1.0e-12
Match length	167
% identity	32
NCBI Description	HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F35G12.4 IN CHROMOSOME III >gi_3876723_emb_CAA86335.1_ (Z46242) similar to beta-transducin; cDNA EST EMBL:Z14703 comes from this gene; cDNA EST EMBL:D67532 comes from this gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST EMBL:D64515 comes from this gene; cDNA EST EMBL:D6

Seq. No.	389055
Contig ID	14600_1.R1084
5'-most EST	g5038835
Method	BLASTX
NCBI GI	g1438883
BLAST score	162
E value	6.0e-11
Match length	60
% identity	48
NCBI Description	(U43840) GmCK3p [Glycine max]

Seq. No.	389056
Contig ID	14603_1.R1084
5'-most EST	g700468
Method	BLASTX
NCBI GI	g4033424
BLAST score	1051
E value	1.0e-115
Match length	213
% identity	96
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No.	389057
Contig ID	14604_1.R1084
5'-most EST	uC-osf1M202068b05b1
Method	BLASTX
NCBI GI	g3763916
BLAST score	694
E value	1.0e-145
Match length	487
% identity	55
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	389058

Contig ID	14616_1.R1084
5'-most EST	LIB3434-044-P1-K1-F8
Seq. No.	389059
Contig ID	14622_1.R1084
5'-most EST	LIB3475-008-P1-K1-H1
Seq. No.	389060
Contig ID	14628_2.R1084
5'-most EST	g2311335
Method	BLASTX
NCBI GI	g131755
BLAST score	225
E value	2.0e-20
Match length	97
% identity	61
NCBI Description	PPLZ12 PROTEIN >gi_81843_pir__S14688 hypothetical protein pPLZ12 - large-leaved lupine >gi_19501_emb_CAA36070_ (X51768) pPLZ12 gene product (AA 1-184) [Lupinus polyphyllus]
Seq. No.	389061
Contig ID	14636_1.R1084
5'-most EST	g5003512
Method	BLASTX
NCBI GI	g4680707
BLAST score	360
E value	1.0e-33
Match length	173
% identity	44
NCBI Description	(AF132968) CGI-34 protein [Homo sapiens]
Seq. No.	389062
Contig ID	14649_1.R1084
5'-most EST	g2311411
Method	BLASTX
NCBI GI	g1825645
BLAST score	158
E value	9.0e-22
Match length	69
% identity	77
NCBI Description	(U88173) weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [Caenorhabditis elegans]
Seq. No.	389063
Contig ID	14649_2.R1084
5'-most EST	LIB3434-034-P1-K1-D5
Method	BLASTX
NCBI GI	g1825645
BLAST score	304
E value	2.0e-27
Match length	72
% identity	76
NCBI Description	(U88173) weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [Caenorhabditis elegans]
Seq. No.	389064

Contig ID	14649_3.R1084
5'-most EST	LIB3475-008-P1-K1-F2
Method	BLASTX
NCBI GI	g1825645
BLAST score	304
E value	2.0e-27
Match length	72
% identity	76
NCBI Description	(U88173) weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [Caenorhabditis elegans]

Seq. No.	389065
Contig ID	14661_1.R1084
5'-most EST	LIB3432-040-P1-K1-B12

Seq. No.	389066
Contig ID	14669_1.R1084
5'-most EST	LIB3432-040-P1-K1-B9
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	7.0e-10
Match length	35
% identity	42
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389067
Contig ID	14682_1.R1084
5'-most EST	g699716
Method	BLASTX
NCBI GI	g2980798
BLAST score	736
E value	8.0e-78
Match length	263
% identity	54
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	389068
Contig ID	14684_1.R1084
5'-most EST	LIB3432-040-P1-K1-D8

Seq. No.	389069
Contig ID	14696_1.R1084
5'-most EST	uC-osroM202029g04a1

Seq. No.	389070
Contig ID	14700_1.R1084
5'-most EST	g426306
Method	BLASTX
NCBI GI	g5734755
BLAST score	370
E value	1.0e-38
Match length	236
% identity	42
NCBI Description	(AC007651) Unknown protein [Arabidopsis thaliana]

Seq. No. 389071

Contig ID	14705_1.R1084
5'-most EST	g701559
Method	BLASTX
NCBI GI	g1706958
BLAST score	878
E value	1.0e-142
Match length	299
% identity	77
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	389072
Contig ID	14713_1.R1084
5'-most EST	LIB3432-040-P1-K1-H10

Seq. No.	389073
Contig ID	14715_1.R1084
5'-most EST	g426809
Method	BLASTX
NCBI GI	g3142290
BLAST score	571
E value	1.0e-58
Match length	188
% identity	65
NCBI Description	(AC002411) Contains similarity to gb_Z69902 from C. elegans. [Arabidopsis thaliana]

Seq. No.	389074
Contig ID	14719_1.R1084
5'-most EST	LIB3432-041-P1-K1-A1

Seq. No.	389075
Contig ID	14729_1.R1084
5'-most EST	LIB3432-041-P1-K1-A8
Method	BLASTX
NCBI GI	g2225877
BLAST score	301
E value	4.0e-27
Match length	121
% identity	50
NCBI Description	(AB002406) TIP49 [Rattus norvegicus] >gi_4106528 (AF100694) Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_ (AB001581) DNA helicase p50 [Rattus norvegicus]

Seq. No.	389076
Contig ID	14747_1.R1084
5'-most EST	LIB3432-041-P1-K1-C2
Method	BLASTX
NCBI GI	g4680206
BLAST score	308
E value	6.0e-28
Match length	69
% identity	90
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	389077
Contig ID	14753_1.R1084
5'-most EST	uC-osflcyp024h06b1

Method	BLASTX
NCBI GI	g3080427
BLAST score	748
E value	1.0e-79
Match length	182
% identity	75
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	389078
Contig ID	14763_1.R1084
5'-most EST	g428273

Seq. No.	389079
Contig ID	14770_1.R1084
5'-most EST	LIB3433-006-Q6-K6-A6
Method	BLASTX
NCBI GI	g4510377
BLAST score	660
E value	5.0e-69
Match length	162
% identity	78
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	389080
Contig ID	14771_1.R1084
5'-most EST	LIB3432-041-P1-K1-E5

Seq. No.	389081
Contig ID	14778_1.R1084
5'-most EST	uC-osflcyp152f03b1
Method	BLASTX
NCBI GI	g2827666
BLAST score	385
E value	9.0e-37
Match length	198
% identity	59
NCBI Description	(AL021637) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389082
Contig ID	14781_1.R1084
5'-most EST	LIB3479-003-Q6-K2-B6

Seq. No.	389083
Contig ID	14783_1.R1084
5'-most EST	uC-osrocyp016a07b1
Method	BLASTX
NCBI GI	g100907
BLAST score	582
E value	7.0e-60
Match length	140
% identity	75
NCBI Description	pathogenesis-related protein 1 - maize >gi_228409_prf__1803521A pathogenesis-related protein 1 [Zea mays]

Seq. No.	389084
Contig ID	14784_1.R1084

5'-most EST	LIB3432-041-P1-K1-F6
Method	BLASTX
NCBI GI	g5830787
BLAST score	214
E value	8.0e-17
Match length	124
% identity	26
NCBI Description	(AL117188) ankyrin repeat-containing protein 2 [Arabidopsis thaliana]

Seq. No.	389085
Contig ID	14788_1.R1084
5'-most EST	uC-osf1cyp017c02b1

Seq. No.	389086
Contig ID	14796_1.R1084
5'-most EST	LIB3474-007-P1-K1-G8
Method	BLASTX
NCBI GI	g5616313
BLAST score	289
E value	7.0e-26
Match length	69
% identity	31
NCBI Description	(AF160977) zinc finger protein [Pisum sativum]

Seq. No.	389087
Contig ID	14801_1.R1084
5'-most EST	LIB3432-041-P1-K1-H11
Method	BLASTX
NCBI GI	g3860272
BLAST score	358
E value	5.0e-34
Match length	76
% identity	92
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	389088
Contig ID	14884_1.R1084
5'-most EST	LIB3433-007-Q6-K1-A2
Method	BLASTX
NCBI GI	g1173187
BLAST score	662
E value	3.0e-69
Match length	135
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	389089
Contig ID	14887_1.R1084
5'-most EST	g2443096
Method	BLASTX
NCBI GI	g3264767

BLAST score	187
E value	8.0e-14
Match length	68
% identity	50
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	389090
Contig ID	14887_2.R1084
5'-most EST	g2800671

Seq. No.	389091
Contig ID	14890_1.R1084
5'-most EST	LIB3433-007-Q6-K1-A8
Method	BLASTX
NCBI GI	g3702342
BLAST score	168
E value	1.0e-11
Match length	99
% identity	42
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389092
Contig ID	14892_1.R1084
5'-most EST	g4879601
Method	BLASTX
NCBI GI	g3881976
BLAST score	937
E value	1.0e-101
Match length	255
% identity	69
NCBI Description	(AJ012409) hypothetical protein [Homo sapiens]

Seq. No.	389093
Contig ID	14894_1.R1084
5'-most EST	g5667389

Seq. No.	389094
Contig ID	14898_1.R1084
5'-most EST	LIB3433-011-Q6-K1-F6
Method	BLASTX
NCBI GI	g1848225
BLAST score	293
E value	4.0e-26
Match length	62
% identity	79
NCBI Description	(U88090) nonspecific lipid transfer protein [Hordeum vulgare]

Seq. No.	389095
Contig ID	14900_1.R1084
5'-most EST	g2442466

Seq. No.	389096
Contig ID	14902_1.R1084
5'-most EST	LIB3433-007-Q6-K1-C1
Method	BLASTN
NCBI GI	g2407286

BLAST score	118
E value	2.0e-59
Match length	224
% identity	88
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	389097
Contig ID	14903_1.R1084
5'-most EST	LIB3433-007-Q6-K1-E1
Method	BLASTX
NCBI GI	g5262202
BLAST score	314
E value	2.0e-28
Match length	188
% identity	33
NCBI Description	(AL080252) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	389098
Contig ID	14908_1.R1084
5'-most EST	LIB3433-057-P1-K1-H3
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	3.0e-10
Match length	36
% identity	59
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389099
Contig ID	14908_2.R1084
5'-most EST	uC-osflcyp086g05b1
Method	BLASTX
NCBI GI	g5230423
BLAST score	1322
E value	1.0e-146
Match length	300
% identity	80
NCBI Description	(AF091713) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	389100
Contig ID	14908_3.R1084
5'-most EST	LIB3475-007-P1-K1-B6
Method	BLASTX
NCBI GI	g4886756
BLAST score	445
E value	1.0e-52
Match length	125
% identity	82
NCBI Description	(AF088917) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	389101
Contig ID	14908_4.R1084
5'-most EST	g3767927
Method	BLASTX

NCBI GI	g1706958
BLAST score	671
E value	1.0e-70
Match length	162
% identity	80
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	389102
Contig ID	14908_5.R1084
5'-most EST	LIB3433-020-P1-K1-G12
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	46
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	389103
Contig ID	14909_1.R1084
5'-most EST	g427958
Method	BLASTX
NCBI GI	g6056419
BLAST score	295
E value	3.0e-26
Match length	110
% identity	55
NCBI Description	(AC009525) 60S ribosomal protein L22 [Arabidopsis thaliana]

Seq. No.	389104
Contig ID	14909_2.R1084
5'-most EST	uC-osrocyp021e02b1
Method	BLASTX
NCBI GI	g6056419
BLAST score	254
E value	2.0e-21
Match length	110
% identity	51
NCBI Description	(AC009525) 60S ribosomal protein L22 [Arabidopsis thaliana]

Seq. No.	389105
Contig ID	14911_1.R1084
5'-most EST	g2311289
Method	BLASTX
NCBI GI	g2342735
BLAST score	431
E value	3.0e-42
Match length	125
% identity	71
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	389106
Contig ID	14911_2.R1084
5'-most EST	LIB3433-024-P1-K1-D6
Method	BLASTX

NCBI GI	g2342735
BLAST score	299
E value	5.0e-41
Match length	113
% identity	75
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	389107
Contig ID	14912_1.R1084
5'-most EST	LIB3433-007-Q6-K1-D10

Seq. No.	389108
Contig ID	14913_1.R1084
5'-most EST	LIB3433-008-Q6-K1-H8
Method	BLASTX
NCBI GI	g2407287
BLAST score	188
E value	1.0e-13
Match length	59
% identity	64
NCBI Description	(AF017366) metallothionein-like protein [Oryza sativa]

Seq. No.	389109
Contig ID	14913_2.R1084
5'-most EST	LIB3434-004-P1-K1-D1
Method	BLASTX
NCBI GI	g2647938
BLAST score	187
E value	1.0e-13
Match length	60
% identity	60
NCBI Description	(D50641) plant metallothionein-like protein [Hordeum vulgare]

Seq. No.	389110
Contig ID	14913_3.R1084
5'-most EST	LIB3433-060-P1-K1-F1
Method	BLASTN
NCBI GI	g2647937
BLAST score	42
E value	5.0e-14
Match length	66
% identity	91
NCBI Description	Hordeum vulgare DNA for plant metallothionein-like protein, complete cds

Seq. No.	389111
Contig ID	14913_4.R1084
5'-most EST	LIB3434-053-P1-K1-G2
Method	BLASTX
NCBI GI	g2647938
BLAST score	187
E value	8.0e-14
Match length	60
% identity	60
NCBI Description	(D50641) plant metallothionein-like protein [Hordeum vulgare]

Seq. No.	389112
Contig ID	14913_5.R1084
5'-most EST	LIB3433-006-Q6-K6-G10
Method	BLASTX
NCBI GI	g2407287
BLAST score	190
E value	5.0e-14
Match length	60
% identity	67
NCBI Description	(AF017366) metallothionein-like protein [Oryza sativa]

Seq. No.	389113
Contig ID	14913_6.R1084
5'-most EST	LIB3434-059-P1-K1-F10
Method	BLASTX
NCBI GI	g2647938
BLAST score	177
E value	1.0e-12
Match length	60
% identity	58
NCBI Description	(D50641) plant metallothionein-like protein [Hordeum vulgare]

Seq. No.	389114
Contig ID	14913_7.R1084
5'-most EST	LIB3433-054-P1-K1-F2

Seq. No.	389115
Contig ID	14916_1.R1084
5'-most EST	uC-osflcyp112c01b1
Method	BLASTX
NCBI GI	g4510381
BLAST score	452
E value	1.0e-44
Match length	161
% identity	59
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	389116
Contig ID	14924_1.R1084
5'-most EST	LIB3433-007-Q6-K1-E11

Seq. No.	389117
Contig ID	14931_1.R1084
5'-most EST	LIB3434-013-P1-K1-A1

Seq. No.	389118
Contig ID	14933_1.R1084
5'-most EST	uC-osflcyp121f08b1
Method	BLASTX
NCBI GI	g4769004
BLAST score	513
E value	9.0e-52
Match length	89
% identity	98
NCBI Description	(AF140598) ring-box protein 1 [Homo sapiens]

>gi_4769006_gb_AAD29716.1_AF140599_1 (AF140599) ring-box protein 1 [Mus musculus]
>gi_4809216_gb_AAD30146.1_AF142059_1 (AF142059) RING finger protein [Homo sapiens]

Seq. No.	389119
Contig ID	14933_2.R1084
5'-most EST	g5004079
Method	BLASTX
NCBI GI	g4769004
BLAST score	505
E value	6.0e-51
Match length	88
% identity	97
NCBI Description	(AF140598) ring-box protein 1 [Homo sapiens] >gi_4769006_gb_AAD29716.1_AF140599_1 (AF140599) ring-box protein 1 [Mus musculus] >gi_4809216_gb_AAD30146.1_AF142059_1 (AF142059) RING finger protein [Homo sapiens]

Seq. No.	389120
Contig ID	14936_1.R1084
5'-most EST	LIB3433-007-Q6-K1-F4

Seq. No.	389121
Contig ID	14937_1.R1084
5'-most EST	LIB3433-007-Q6-K1-F5
Method	BLASTX
NCBI GI	g3522961
BLAST score	690
E value	2.0e-89
Match length	181
% identity	93
NCBI Description	(AC004411) putative pto kinase [Arabidopsis thaliana]

Seq. No.	389122
Contig ID	14937_2.R1084
5'-most EST	uC-osflM202052g08b1
Method	BLASTX
NCBI GI	g3668069
BLAST score	1068
E value	1.0e-117
Match length	266
% identity	77
NCBI Description	(U28007) Pto kinase interactor 1 [Lycopersicon esculentum]

Seq. No.	389123
Contig ID	14944_1.R1084
5'-most EST	uC-osroM202006f04b1
Method	BLASTX
NCBI GI	g5882745
BLAST score	669
E value	2.0e-70
Match length	174
% identity	69
NCBI Description	(AC008263) F25A4.24 [Arabidopsis thaliana]

Seq. No.	389124
Contig ID	14947_1.R1084
5'-most EST	LIB3433-008-Q6-K1-E12
Method	BLASTX
NCBI GI	g1351208
BLAST score	623
E value	5.0e-80
Match length	211
% identity	67
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_1046266 (U25632) CCT-2 [Caenorhabditis elegans]

Seq. No.	389125
Contig ID	14950_1.R1084
5'-most EST	LIB3433-007-Q6-K1-G7
Method	BLASTX
NCBI GI	g2244973
BLAST score	169
E value	1.0e-11
Match length	59
% identity	53
NCBI Description	(Z97340) transcription factor like protein [Arabidopsis thaliana]

Seq. No.	389126
Contig ID	14954_1.R1084
5'-most EST	LIB3433-039-P1-K1-A5
Method	BLASTX
NCBI GI	g4760700
BLAST score	355
E value	3.0e-33
Match length	184
% identity	46
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]

Seq. No.	389127
Contig ID	14954_2.R1084
5'-most EST	LIB3433-017-Q6-K1-C11
Method	BLASTX
NCBI GI	g4760700
BLAST score	352
E value	5.0e-33
Match length	194
% identity	45
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]

Seq. No.	389128
Contig ID	14955_1.R1084
5'-most EST	LIB3434-010-P1-K1-H4
Method	BLASTX
NCBI GI	g2370461
BLAST score	201
E value	2.0e-32
Match length	140
% identity	58
NCBI Description	(Y14675) putative glycoprotein [Sorghum bicolor]

Seq. No.	389129
Contig ID	14962_1.R1084
5'-most EST	LIB3434-039-P1-K1-B12
Method	BLASTX
NCBI GI	g3861402
BLAST score	172
E value	5.0e-12
Match length	53
% identity	62
NCBI Description	(AJ235273) 50S RIBOSOMAL PROTEIN L33 (rpmG) [Rickettsia prowazekii]

Seq. No.	389130
Contig ID	14963_1.R1084
5'-most EST	LIB3433-008-Q6-K1-A1
Method	BLASTX
NCBI GI	g4586027
BLAST score	546
E value	1.0e-55
Match length	128
% identity	84
NCBI Description	(AC007109) putative ribosomal protein L14 [Arabidopsis thaliana]

Seq. No.	389131
Contig ID	14964_1.R1084
5'-most EST	uC-osrocyp015h01b1
Method	BLASTN
NCBI GI	g4959460
BLAST score	34
E value	2.0e-09
Match length	35
% identity	59
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	389132
Contig ID	14968_1.R1084
5'-most EST	g426874
Method	BLASTX
NCBI GI	g3935169
BLAST score	291
E value	5.0e-26
Match length	68
% identity	84
NCBI Description	(AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No.	389133
Contig ID	14968_2.R1084
5'-most EST	g2798774
Method	BLASTX
NCBI GI	g3935169
BLAST score	293
E value	3.0e-26
Match length	68
% identity	84
NCBI Description	(AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No. 389134
Contig ID 14969_1.R1084
5'-most EST LIB3433-008-Q6-K1-A4

Seq. No. 389135
Contig ID 14972_1.R1084
5'-most EST LIB3433-008-Q6-K1-A7

Seq. No. 389136
Contig ID 14976_1.R1084
5'-most EST g4716079

Seq. No. 389137
Contig ID 14979_1.R1084
5'-most EST LIB3433-008-Q6-K1-B2
Method BLASTX
NCBI GI g121528
BLAST score 680
E value 3.0e-71
Match length 139
% identity 96
NCBI Description GOS9 PROTEIN >gi_100683_pir__S19115 GOS9 protein - rice >gi_20242_emb_CAA36189_ (X51909) GOS9 [Oryza sativa]

Seq. No. 389138
Contig ID 14988_1.R1084
5'-most EST LIB3474-002-P1-K1-A11
Method BLASTX
NCBI GI g82263
BLAST score 909
E value 4.0e-98
Match length 190
% identity 91
NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato

Seq. No. 389139
Contig ID 14991_1.R1084
5'-most EST uC-osflcyp011d12b1

Seq. No. 389140
Contig ID 15003_1.R1084
5'-most EST LIB3433-008-Q6-K1-D4

Seq. No. 389141
Contig ID 15004_1.R1084
5'-most EST LIB3433-008-Q6-K1-D5

Seq. No. 389142
Contig ID 15005_1.R1084
5'-most EST LIB3433-008-Q6-K1-D6

Seq. No. 389143
Contig ID 15009_1.R1084
5'-most EST LIB3474-004-P1-K1-F8
Method BLASTX
NCBI GI g3668089

BLAST score	1190
E value	1.0e-131
Match length	391
% identity	64
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	389144
Contig ID	15013_2.R1084
5'-most EST	LIB3434-045-P1-K1-G9
Method	BLASTX
NCBI GI	g2459429
BLAST score	131
E value	7.0e-09
Match length	98
% identity	35
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	389145
Contig ID	15016_1.R1084
5'-most EST	uC-osflcyp174d04b1
Method	BLASTX
NCBI GI	g4559339
BLAST score	522
E value	1.0e-52
Match length	108
% identity	91
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	389146
Contig ID	15019_1.R1084
5'-most EST	LIB3433-008-Q6-K1-F11

Seq. No.	389147
Contig ID	15025_1.R1084
5'-most EST	LIB3434-065-P1-K1-F8
Method	BLASTX
NCBI GI	g4220481
BLAST score	379
E value	7.0e-36
Match length	173
% identity	47
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	389148
Contig ID	15027_1.R1084
5'-most EST	g287091
Method	BLASTX
NCBI GI	g4539408
BLAST score	476
E value	1.0e-47
Match length	132
% identity	74
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	389149
Contig ID	15034_1.R1084

5'-most EST	uC-osflcyp117c12a1
Method	BLASTX
NCBI GI	g3915254
BLAST score	216
E value	4.0e-17
Match length	87
% identity	56
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT)

Seq. No.	389150
Contig ID	15039_1.R1084
5'-most EST	g3763744
Method	BLASTX
NCBI GI	g551288
BLAST score	744
E value	5.0e-79
Match length	158
% identity	91
NCBI Description	(Z33611) phosphoglycerate mutase [Zea mays]

Seq. No.	389151
Contig ID	15042_1.R1084
5'-most EST	g3763380
Method	BLASTX
NCBI GI	g6094014
BLAST score	548
E value	5.0e-56
Match length	114
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_3608479 (AF088912) ribosomal protein L15 [Petunia x hybrida]

Seq. No.	389152
Contig ID	15042_2.R1084
5'-most EST	LIB3479-003-Q6-K1-A3
Method	BLASTX
NCBI GI	g6094014
BLAST score	629
E value	2.0e-65
Match length	166
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_3608479 (AF088912) ribosomal protein L15 [Petunia x hybrida]

Seq. No.	389153
Contig ID	15042_3.R1084
5'-most EST	LIB3433-059-P1-K1-C3
Method	BLASTX
NCBI GI	g6094014
BLAST score	787
E value	6.0e-84
Match length	188
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_3608479 (AF088912) ribosomal protein L15 [Petunia x hybrida]

Seq. No.	389154
Contig ID	15042_4.R1084
5'-most EST	g5004066
Method	BLASTX
NCBI GI	g3122673
BLAST score	216
E value	8.0e-30
Match length	116
% identity	60
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447.1_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	389155
Contig ID	15044_1.R1084
5'-most EST	LIB3433-008-Q6-K1-H7

Seq. No.	389156
Contig ID	15046_1.R1084
5'-most EST	g5851105
Method	BLASTN
NCBI GI	g6006355
BLAST score	628
E value	0.0e+00
Match length	657
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	389157
Contig ID	15047_1.R1084
5'-most EST	g3763774

Seq. No.	389158
Contig ID	15050_1.R1084
5'-most EST	LIB3434-037-P1-K1-D10

Seq. No.	389159
Contig ID	15051_1.R1084
5'-most EST	uC-osroM202029a06a1
Method	BLASTX
NCBI GI	g2244797
BLAST score	362
E value	6.0e-34
Match length	187
% identity	45
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389160
Contig ID	15057_1.R1084
5'-most EST	LIB3434-005-P1-K1-D9
Method	BLASTX
NCBI GI	g5912424
BLAST score	598
E value	1.0e-61
Match length	151
% identity	79
NCBI Description	(AJ242970) BTF3b-like factor [Arabidopsis thaliana]

Seq. No.	389161
Contig ID	15058_1.R1084
5'-most EST	LIB3433-009-Q6-K1-A9

Seq. No.	389162
Contig ID	15060_1.R1084
5'-most EST	LIB3434-058-P1-K1-C11
Method	BLASTX
NCBI GI	g2735841
BLAST score	954
E value	1.0e-103
Match length	245
% identity	80
NCBI Description	(AF010283) No definition line found [Sorghum bicolor]

Seq. No.	389163
Contig ID	15064_1.R1084
5'-most EST	LIB3433-022-P1-K1-E8
Method	BLASTX
NCBI GI	g1402918
BLAST score	619
E value	3.0e-64
Match length	185
% identity	64
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]

Seq. No.	389164
Contig ID	15064_2.R1084
5'-most EST	LIB3475-004-P1-K2-G9
Method	BLASTX
NCBI GI	g1402918
BLAST score	784
E value	1.0e-83
Match length	201
% identity	76
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]

Seq. No.	389165
Contig ID	15066_1.R1084
5'-most EST	g3762390
Method	BLASTX
NCBI GI	g2864615
BLAST score	314
E value	2.0e-28
Match length	153
% identity	48
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	389166
Contig ID	15068_1.R1084
5'-most EST	g428423
Method	BLASTX
NCBI GI	g4584539

BLAST score	349
E value	1.0e-60
Match length	215
% identity	42
NCBI Description	(AL049608) extensin-like protein [Arabidopsis thaliana]

Seq. No.	389167
Contig ID	15071_1.R1084
5'-most EST	g428532

Seq. No.	389168
Contig ID	15073_1.R1084
5'-most EST	g571923
Method	BLASTX
NCBI GI	g5734716
BLAST score	272
E value	6.0e-24
Match length	98
% identity	52
NCBI Description	(AC008075) Simialr to gb_AF049928 PGP224 protein from Petunia x hybrida. [Arabidopsis thaliana]

Seq. No.	389169
Contig ID	15074_1.R1084
5'-most EST	uC-osflcyp171d09b1
Method	BLASTX
NCBI GI	g4960150
BLAST score	469
E value	1.0e-46
Match length	102
% identity	89
NCBI Description	(AF153277) DNA-directed RNA polymerase IIa [Nicotiana tabacum] >gi_4960152_gb_AAD34614.1_AF153278_1 (AF153278) DNA-directed RNA polymerase IIb [Nicotiana tabacum]

Seq. No.	389170
Contig ID	15081_1.R1084
5'-most EST	g5003921
Method	BLASTX
NCBI GI	g3450842
BLAST score	662
E value	8.0e-91
Match length	373
% identity	52
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	389171
Contig ID	15088_1.R1084
5'-most EST	uC-osflcyp155g03b1
Method	BLASTX
NCBI GI	g2196878
BLAST score	1203
E value	1.0e-138
Match length	301
% identity	76
NCBI Description	(Y08292) NADH glutamate dehydrogenase [Nicotiana

plumbaginifolia]

Seq. No.	389172
Contig ID	15093_1.R1084
5'-most EST	g2799468

Seq. No.	389173
Contig ID	15097_1.R1084
5'-most EST	g2427362
Method	BLASTX
NCBI GI	g3548801
BLAST score	316
E value	2.0e-42
Match length	191
% identity	45
NCBI Description	(AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	389174
Contig ID	15098_1.R1084
5'-most EST	LIB3434-017-P1-K1-F2
Method	BLASTX
NCBI GI	g4406814
BLAST score	384
E value	9.0e-37
Match length	115
% identity	63
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	389175
Contig ID	15100_1.R1084
5'-most EST	g2801255

Seq. No.	389176
Contig ID	15110_1.R1084
5'-most EST	uC-osflcyp074e02b1

Seq. No.	389177
Contig ID	15111_1.R1084
5'-most EST	uC-osflcyp079c11a1

Seq. No.	389178
Contig ID	15112_1.R1084
5'-most EST	g569592
Method	BLASTX
NCBI GI	g5453379
BLAST score	299
E value	2.0e-50
Match length	140
% identity	75
NCBI Description	(AF155124) bacterial-induced peroxidase precursor [Gossypium hirsutum]

Seq. No.	389179
Contig ID	15115_1.R1084

5'-most EST	LIB3433-009-Q6-K1-H6
Method	BLASTX
NCBI GI	g4056506
BLAST score	294
E value	2.0e-26
Match length	106
% identity	54
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	389180
Contig ID	15119_1.R1084
5'-most EST	LIB3433-011-Q6-K1-A10

Seq. No.	389181
Contig ID	15120_1.R1084
5'-most EST	LIB3433-011-Q6-K1-A6
Method	BLASTX
NCBI GI	g4507311
BLAST score	220
E value	2.0e-17
Match length	103
% identity	42
NCBI Description	suppressor of Ty (S.cerevisiae) 4 homolog 1 >gi_3122873_sp_Q16550_SPT4_HUMAN TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1 >gi_1209779 (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] >gi_1401053 (U38818) SUPT4H [Homo sapiens] >gi_1401055 (U38817) SUPT4H [Homo sapiens] >gi_1401066 (U43154) Supt4h [Mus musculus] >gi_3779194 (U96809) chromatin structural protein homolog [Mus musculus]

Seq. No.	389182
Contig ID	15121_1.R1084
5'-most EST	LIB3433-019-P1-K1-B6
Method	BLASTX
NCBI GI	g1076732
BLAST score	572
E value	9.0e-59
Match length	144
% identity	74
NCBI Description	type-1 pathogenesis-related protein - barley >gi_732807_emb_CAA88618_ (Z48728) type-1 pathogenesis-related protein [Hordeum vulgare]

Seq. No.	389183
Contig ID	15128_1.R1084
5'-most EST	g3761236

Seq. No.	389184
Contig ID	15129_1.R1084
5'-most EST	LIB3433-011-Q6-K1-B10

Seq. No.	389185
Contig ID	15133_1.R1084
5'-most EST	g2311481

Seq. No.	389186
Contig ID	15138_1.R1084
5'-most EST	uC-osflcyp027b09b1
Method	BLASTX
NCBI GI	g3183568
BLAST score	608
E value	1.0e-62
Match length	325
% identity	41
NCBI Description	HYPOTHETICAL 45.1 KD PROTEIN IN CDD-MGLC INTERGENIC REGION

Seq. No.	389187
Contig ID	15140_1.R1084
5'-most EST	g4715876
Method	BLASTX
NCBI GI	g421989
BLAST score	487
E value	1.0e-66
Match length	201
% identity	68
NCBI Description	serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx [Hordeum vulgare] >gi_444778_prf__1908213A protein Zx [Hordeum vulgare]

Seq. No.	389188
Contig ID	15141_1.R1084
5'-most EST	LIB3434-023-P1-K1-C5
Method	BLASTX
NCBI GI	g4490306
BLAST score	348
E value	9.0e-33
Match length	156
% identity	49
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	389189
Contig ID	15143_1.R1084
5'-most EST	uC-osflcyp033c04b1
Method	BLASTX
NCBI GI	g137476
BLAST score	579
E value	8.0e-60
Match length	135
% identity	59
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_82334_pir__A40814 H+-transporting ATPase (EC 3.6.1.35) proteolipid chain, vacuolar - oat >gi_166549 (M73232) H+-ATPase [Avena sativa]

Seq. No.	389190
Contig ID	15145_1.R1084
5'-most EST	LIB3433-011-Q6-K1-C5

Seq. No.	389191
Contig ID	15147_1.R1084
5'-most EST	LIB3433-011-Q6-K1-C7
Method	BLASTX

NCBI GI	g4056568
BLAST score	354
E value	2.0e-33
Match length	92
% identity	70
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	389192
Contig ID	15151_1.R1084
5'-most EST	g5005118
Method	BLASTX
NCBI GI	g1841355
BLAST score	585
E value	3.0e-60
Match length	108
% identity	100
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa]

Seq. No.	389193
Contig ID	15153_1.R1084
5'-most EST	LIB3433-011-Q6-K1-D12
Method	BLASTX
NCBI GI	g4759068
BLAST score	452
E value	1.0e-44
Match length	158
% identity	50
NCBI Description	SCO (cytochrome oxidase deficient, yeast) homolog 1 >gi_3599966 (AF026852) h-sco1 [Homo sapiens]

Seq. No.	389194
Contig ID	15155_1.R1084
5'-most EST	LIB3433-011-Q6-K1-D3

Seq. No.	389195
Contig ID	15158_1.R1084
5'-most EST	LIB3433-011-Q6-K1-D7
Method	BLASTX
NCBI GI	g4519671
BLAST score	478
E value	7.0e-48
Match length	156
% identity	62
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No.	389196
Contig ID	15159_1.R1084
5'-most EST	uC-osrocyp021f12b1

Seq. No.	389197
Contig ID	15161_1.R1084
5'-most EST	LIB3433-011-Q6-K1-E10

Seq. No.	389198
Contig ID	15163_1.R1084
5'-most EST	LIB3474-004-P1-K1-C2

Method	BLASTX
NCBI GI	g6094335
BLAST score	758
E value	1.0e-80
Match length	202
% identity	66
NCBI Description	SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE) (SPDSY) >gi_3242659_dbj_BAA29033_ (AB015599) spermidine synthase [Coffea arabica]

Seq. No.	389199
Contig ID	15164_1.R1084
5'-most EST	LIB3433-059-P1-K1-E9
Method	BLASTX
NCBI GI	g4826730
BLAST score	547
E value	4.0e-56
Match length	140
% identity	75
NCBI Description	FK506 binding protein 12-rapamycin associated protein 1 >gi_1169735_sp_P42345_FRAP_HUMAN FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN) >gi_2135120_pir__S45340 FKBP-rapamycin-associated protein (FRAP) - human >gi_508482 (L34075) FKBP-rapamycin associated protein [Homo sapiens]

Seq. No.	389200
Contig ID	15166_1.R1084
5'-most EST	g3768100
Method	BLASTX
NCBI GI	g3193324
BLAST score	730
E value	1.0e-98
Match length	250
% identity	64
NCBI Description	(AF069299) contains similarity to WD domains, G-beta repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84) [Arabidopsis thaliana]

Seq. No.	389201
Contig ID	15167_1.R1084
5'-most EST	g286957
Method	BLASTN
NCBI GI	g416320
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Yeast centromere vector pRS415 with LEU2 marker, complete sequence

Seq. No.	389202
Contig ID	15168_1.R1084
5'-most EST	LIB3475-009-P1-K1-F9

Seq. No.	389203
Contig ID	15169_1.R1084

5'-most EST	LIB3434-005-P1-K1-H11
Seq. No.	389204
Contig ID	15172_1.R1084
5'-most EST	uC-osflcyp141f07b1
Seq. No.	389205
Contig ID	15172_2.R1084
5'-most EST	g2427806
Seq. No.	389206
Contig ID	15172_3.R1084
5'-most EST	uC-osflM202095b03b1
Seq. No.	389207
Contig ID	15174_1.R1084
5'-most EST	LIB3433-057-P1-K1-G3
Method	BLASTX
NCBI GI	g1323742
BLAST score	294
E value	5.0e-26
Match length	151
% identity	46
NCBI Description	(U32427) unknown [Triticum aestivum]
Seq. No.	389208
Contig ID	15176_1.R1084
5'-most EST	uC-osflM202062d05b1
Method	BLASTX
NCBI GI	g100099
BLAST score	649
E value	5.0e-70
Match length	209
% identity	67
NCBI Description	DNA-binding protein VBP1 - fava bean >gi_1372966 (M81827) CREB-like protein [Vicia faba]
Seq. No.	389209
Contig ID	15180_1.R1084
5'-most EST	g2442977
Method	BLASTX
NCBI GI	g3023721
BLAST score	175
E value	4.0e-12
Match length	75
% identity	55
NCBI Description	FLOWERING TIME CONTROL PROTEIN FCA >gi_2204095_emb_CAB05391_ (Z82992) FCA gamma [Arabidopsis thaliana]
Seq. No.	389210
Contig ID	15186_1.R1084
5'-most EST	g2311444
Seq. No.	389211
Contig ID	15188_1.R1084
5'-most EST	LIB3433-011-Q6-K1-G3

Seq. No.	389212
Contig ID	15192_1.R1084
5'-most EST	g5005346
Method	BLASTN
NCBI GI	g4220645
BLAST score	83
E value	2.0e-38
Match length	303
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence

Seq. No.	389213
Contig ID	15193_1.R1084
5'-most EST	uC-osrocyp012c08b1
Method	BLASTX
NCBI GI	g1421730
BLAST score	990
E value	1.0e-107
Match length	313
% identity	59
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	389214
Contig ID	15195_1.R1084
5'-most EST	LIB3433-011-Q6-K1-H11
Method	BLASTX
NCBI GI	g3169883
BLAST score	718
E value	6.0e-76
Match length	208
% identity	65
NCBI Description	(AF033194) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] >gi_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum]

Seq. No.	389215
Contig ID	15201_1.R1084
5'-most EST	g3768880

Seq. No.	389216
Contig ID	15201_2.R1084
5'-most EST	g286295
Method	BLASTX
NCBI GI	g3695408
BLAST score	133
E value	6.0e-09
Match length	49
% identity	69
NCBI Description	(AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi_4538956_emb_CAB39780.1_ (AL049488) probable wound-induced protein [Arabidopsis thaliana]

Seq. No.	389217

Contig ID	15201_3.R1084
5'-most EST	g286506

Seq. No.	389218
Contig ID	15201_4.R1084
5'-most EST	LIB3433-011-Q6-K1-H6
Method	BLASTX
NCBI GI	g3695408
BLAST score	172
E value	3.0e-12
Match length	87
% identity	45
NCBI Description	(AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi_4538956_emb_CAB39780.1_ (AL049488) probable wound-induced protein [Arabidopsis thaliana]

Seq. No.	389219
Contig ID	15203_1.R1084
5'-most EST	g3767487
Method	BLASTX
NCBI GI	g4490738
BLAST score	435
E value	3.0e-45
Match length	140
% identity	66
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	389220
Contig ID	15205_1.R1084
5'-most EST	LIB3433-012-Q6-K1-A12
Method	BLASTX
NCBI GI	g1684851
BLAST score	175
E value	3.0e-12
Match length	98
% identity	42
NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No.	389221
Contig ID	15215_1.R1084
5'-most EST	LIB3433-012-Q6-K1-B6
Method	BLASTX
NCBI GI	g3193303
BLAST score	258
E value	4.0e-22
Match length	101
% identity	52
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No.	389222
Contig ID	15216_1.R1084
5'-most EST	LIB3433-012-Q6-K1-B7

Seq. No.	389223
Contig ID	15223_1.R1084
5'-most EST	LIB3433-012-Q6-K1-C3

Seq. No.	389224
Contig ID	15224_1.R1084
5'-most EST	LIB3433-012-Q6-K1-C4

Seq. No.	389225
Contig ID	15225_1.R1084
5'-most EST	g2800793
Method	BLASTN
NCBI GI	g762924
BLAST score	59
E value	7.0e-24
Match length	66
% identity	99
NCBI Description	D.melanogaster mRNA for elastin-like protein

Seq. No.	389226
Contig ID	15231_1.R1084
5'-most EST	g2428266

Seq. No.	389227
Contig ID	15232_1.R1084
5'-most EST	g4716419

Seq. No.	389228
Contig ID	15241_1.R1084
5'-most EST	LIB3433-012-Q6-K1-E2
Method	BLASTX
NCBI GI	g1872521
BLAST score	293
E value	3.0e-34
Match length	115
% identity	43
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_5262161_emb_CAB45804.1_ (AL080253) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	389229
Contig ID	15242_1.R1084
5'-most EST	LIB3433-037-P1-K1-E3
Method	BLASTX
NCBI GI	g5257275
BLAST score	437
E value	7.0e-43
Match length	120
% identity	73
NCBI Description	(AP000364) ESTs AU030740(E60171),AU030739(E60171) correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase. (U27116) [Oryza sativa]

Seq. No.	389230
Contig ID	15242_2.R1084

5'-most EST	g3766629
Method	BLASTX
NCBI GI	g5257275
BLAST score	822
E value	1.0e-87
Match length	205
% identity	84
NCBI Description	(AP000364) ESTs AU030740(E60171),AU030739(E60171) correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase. (U27116) [Oryza sativa]

Seq. No.	389231
Contig ID	15245_1.R1084
5'-most EST	LIB3434-007-P1-K1-A7
Method	BLASTX
NCBI GI	g100226
BLAST score	391
E value	1.0e-37
Match length	164
% identity	50
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	389232
Contig ID	15252_1.R1084
5'-most EST	g2427423

Seq. No.	389233
Contig ID	15259_1.R1084
5'-most EST	LIB3433-012-Q6-K1-H4

Seq. No.	389234
Contig ID	15261_1.R1084
5'-most EST	LIB3434-044-P1-K1-F11
Method	BLASTX
NCBI GI	g1888551
BLAST score	321
E value	2.0e-29
Match length	136
% identity	46
NCBI Description	(U89895) pathogenesis-related protein class 1 [Oryza sativa]

Seq. No.	389235
Contig ID	15265_1.R1084
5'-most EST	LIB3433-035-P1-K1-H6
Method	BLASTX
NCBI GI	g3281846
BLAST score	377
E value	1.0e-35
Match length	266
% identity	39
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	389236
Contig ID	15266_1.R1084
5'-most EST	uC-osf1M202047b09b1
Method	BLASTX
NCBI GI	g3023788
BLAST score	254
E value	2.0e-21
Match length	118
% identity	40
NCBI Description	DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi_2160684 (U72662) dihydroneopterin aldolase [Methylobacterium extorquens]

Seq. No.	389237
Contig ID	15269_1.R1084
5'-most EST	LIB3475-010-P1-K1-C5
Method	BLASTX
NCBI GI	g2695937
BLAST score	406
E value	2.0e-39
Match length	104
% identity	72
NCBI Description	(AJ222782) subtilisin-like protease [Hordeum vulgare]

Seq. No.	389238
Contig ID	15273_1.R1084
5'-most EST	g4714645

Seq. No.	389239
Contig ID	15274_1.R1084
5'-most EST	LIB3434-025-P1-K1-H5
Method	BLASTX
NCBI GI	g5901954
BLAST score	169
E value	1.0e-11
Match length	103
% identity	39
NCBI Description	FGFR1 oncogene partner >gi_4454263_emb_CAA77020_ (Y18046) FGFR1 oncogene partner (FOP) [Homo sapiens]

Seq. No.	389240
Contig ID	15283_1.R1084
5'-most EST	g431809
Method	BLASTX
NCBI GI	g1653395
BLAST score	245
E value	1.0e-20
Match length	90
% identity	51
NCBI Description	(D90913) PET112 [Synechocystis sp.]

Seq. No.	389241
Contig ID	15285_1.R1084
5'-most EST	g2428216
Method	BLASTX
NCBI GI	g5668780
BLAST score	809
E value	3.0e-86

Match length	250
% identity	64
NCBI Description	(AC007894) Strong similarity to gb_AF092432 protein phosphatase type 2C from Lotus japonicus. EST gb_T76026 comes from this gene. [Arabidopsis thaliana]

Seq. No.	389242
Contig ID	15286_1.R1084
5'-most EST	LIB3433-022-P1-K1-H6
Method	BLASTX
NCBI GI	g3941480
BLAST score	268
E value	6.0e-23
Match length	173
% identity	38
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	389243
Contig ID	15289_1.R1084
5'-most EST	uC-osrocyp037a09b1
Method	BLASTX
NCBI GI	g3023817
BLAST score	512
E value	7.0e-52
Match length	107
% identity	89
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	389244
Contig ID	15290_1.R1084
5'-most EST	LIB3433-013-Q6-K1-B2

Seq. No.	389245
Contig ID	15291_1.R1084
5'-most EST	g569535
Method	BLASTX
NCBI GI	g4966343
BLAST score	453
E value	1.0e-93
Match length	337
% identity	52
NCBI Description	(AC006341) Is a member of PF_00481 Protein phosphatase 2C family. [Arabidopsis thaliana]

Seq. No.	389246
Contig ID	15293_1.R1084
5'-most EST	LIB3433-057-P1-K1-A4

Seq. No.	389247
Contig ID	15294_1.R1084
5'-most EST	LIB3433-013-Q6-K1-B6

Seq. No.	389248
Contig ID	15296_1.R1084

5'-most EST	g5455320
Method	BLASTX
NCBI GI	g3023947
BLAST score	238
E value	8.0e-21
Match length	117
% identity	52
NCBI Description	PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi_2665840 (AF035815) putative histone deacetylase RPD3 [Zea mays]

Seq. No.	389249
Contig ID	15298_1.R1084
5'-most EST	g700190
Method	BLASTX
NCBI GI	g2244797
BLAST score	322
E value	2.0e-29
Match length	184
% identity	42
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389250
Contig ID	15302_1.R1084
5'-most EST	g5005424

Seq. No.	389251
Contig ID	15305_1.R1084
5'-most EST	LIB3433-013-Q6-K1-C7

Seq. No.	389252
Contig ID	15310_1.R1084
5'-most EST	g3762235
Method	BLASTX
NCBI GI	g127579
BLAST score	198
E value	4.0e-15
Match length	74
% identity	65
NCBI Description	MYB-RELATED PROTEIN HV1 >gi_82423_pir__S04896 transforming protein (myb) homolog (clone Hv1) - barley >gi_2130044_pir__S61506 Myb1 protein - barley >gi_19051_emb_CAA50222_ (X70877) MybHv1 [Hordeum vulgare] >gi_19053_emb_CAA50224_ (X70879) MybHv1 [Hordeum vulgare] >gi_227030_prf__1613412A myb-related gene Hv1 [Hordeum vulgare var. distichum]

Seq. No.	389253
Contig ID	15310_2.R1084
5'-most EST	g3769181
Method	BLASTN
NCBI GI	g19050
BLAST score	51
E value	1.0e-19
Match length	131
% identity	77
NCBI Description	H.vulgare myb1 mRNA

Seq. No.	389254
Contig ID	15322_1.R1084
5'-most EST	LIB3433-015-Q6-K7-E3
Method	BLASTX
NCBI GI	g4512685
BLAST score	304
E value	3.0e-27
Match length	180
% identity	41
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389255
Contig ID	15322_2.R1084
5'-most EST	g3762945
Method	BLASTX
NCBI GI	g4512685
BLAST score	363
E value	3.0e-34
Match length	176
% identity	43
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389256
Contig ID	15325_1.R1084
5'-most EST	uC-osflM202053c09b1

Seq. No.	389257
Contig ID	15325_2.R1084
5'-most EST	uC-osflcyp002c01b1

Seq. No.	389258
Contig ID	15327_1.R1084
5'-most EST	LIB3474-004-P1-K1-A3

Seq. No.	389259
Contig ID	15328_1.R1084
5'-most EST	LIB3434-013-P1-K1-G9
Method	BLASTX
NCBI GI	g3747044
BLAST score	257
E value	9.0e-22
Match length	112
% identity	52
NCBI Description	(AF093537) blue copper protein [Zea mays]

Seq. No.	389260
Contig ID	15334_1.R1084
5'-most EST	g700956
Method	BLASTX
NCBI GI	g4981053
BLAST score	701
E value	1.0e-73
Match length	266

% identity	53
NCBI Description	(AE001729) tryptophan synthase, beta subunit [Thermotoga maritima]

Seq. No.	389261
Contig ID	15337_1.R1084
5'-most EST	g2310397
Method	BLASTX
NCBI GI	g2826786
BLAST score	381
E value	5.0e-41
Match length	194
% identity	53
NCBI Description	(Y10905) RAPB protein [Oryza sativa]

Seq. No.	389262
Contig ID	15342_1.R1084
5'-most EST	g428567
Method	BLASTX
NCBI GI	g4490706
BLAST score	578
E value	1.0e-59
Match length	180
% identity	61
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	389263
Contig ID	15349_1.R1084
5'-most EST	g3462563
Method	BLASTX
NCBI GI	g629783
BLAST score	387
E value	4.0e-43
Match length	166
% identity	53
NCBI Description	ES43 protein - barley >gi_1345528_emb_CAA54682_ (X77575) ES43 [Hordeum vulgare]

Seq. No.	389264
Contig ID	15354_1.R1084
5'-most EST	uC-osflcyp155d02b1
Method	BLASTX
NCBI GI	g2865177
BLAST score	469
E value	1.0e-46
Match length	170
% identity	54
NCBI Description	(AB010946) AtRer1B [Arabidopsis thaliana]

Seq. No.	389265
Contig ID	15354_2.R1084
5'-most EST	g2798222
Method	BLASTX
NCBI GI	g2865175
BLAST score	419
E value	1.0e-40
Match length	87

% identity	85
NCBI Description	(AB010945) AtRer1A [Arabidopsis thaliana] >gi_4914434_emb_CAB43637.1_ (AL050351) AtRer1A [Arabidopsis thaliana]

Seq. No.	389266
Contig ID	15355_1.R1084
5'-most EST	g3763265
Method	BLASTX
NCBI GI	g4586433
BLAST score	206
E value	7.0e-16
Match length	52
% identity	71
NCBI Description	(AB016798) ribosomal protein L29/cell surface heparin binding protein HIP [Sus scrofa] >gi_4586439_dbj_BAA76404.1_ (AB017196) ribosomal protein L29/heparin/heparan sulfate interacting protein [Sus scrofa]

Seq. No.	389267
Contig ID	15355_2.R1084
5'-most EST	g5004671
Method	BLASTX
NCBI GI	g1350707
BLAST score	206
E value	4.0e-16
Match length	52
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L29 >gi_539923_pir__JC2012 ribosomal protein 17K - mouse >gi_404766 (L08651) ribosomal protein [Mus musculus]

Seq. No.	389268
Contig ID	15358_1.R1084
5'-most EST	LIB3433-014-Q6-K1-A6

Seq. No.	389269
Contig ID	15361_1.R1084
5'-most EST	g427222

Seq. No.	389270
Contig ID	15361_2.R1084
5'-most EST	LIB3433-034-P1-K1-F8

Seq. No.	389271
Contig ID	15371_1.R1084
5'-most EST	uC-osrocyp005c09b1
Method	BLASTX
NCBI GI	g2924772
BLAST score	604
E value	3.0e-62
Match length	139
% identity	80
NCBI Description	(AC002334) unknown protein [Arabidopsis thaliana]

Seq. No.	389272

Contig ID	15376_1.R1084
5'-most EST	g3761934
Method	BLASTX
NCBI GI	g231503
BLAST score	1033
E value	0.0e+00
Match length	377
% identity	97
NCBI Description	ACTIN 97 >gi_100417_pir__S20098 actin - potato >gi_21544_emb_CAA39280_ (X55751) actin [Solanum tuberosum]

Seq. No.	389273
Contig ID	15377_1.R1084
5'-most EST	LIB3433-014-Q6-K1-D10
Method	BLASTX
NCBI GI	g4314401
BLAST score	436
E value	4.0e-43
Match length	124
% identity	65
NCBI Description	(AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	389274
Contig ID	15381_1.R1084
5'-most EST	LIB3433-014-Q6-K1-D3
Method	BLASTX
NCBI GI	g4455274
BLAST score	493
E value	1.0e-106
Match length	260
% identity	78
NCBI Description	(AL035527) spliceosome associated protein-like [Arabidopsis thaliana]

Seq. No.	389275
Contig ID	15383_1.R1084
5'-most EST	LIB3434-052-P1-K1-E8
Method	BLASTX
NCBI GI	g2130099
BLAST score	285
E value	2.0e-25
Match length	76
% identity	72
NCBI Description	acetyl-CoA carboxylase (EC 6.4.1.2) - wheat >gi_514306 (U10187) acetyl-CoA carboxylase [Triticum aestivum]

Seq. No.	389276
Contig ID	15384_1.R1084
5'-most EST	g569330
Method	BLASTX
NCBI GI	g1150406
BLAST score	199
E value	4.0e-17
Match length	181
% identity	45
NCBI Description	(Z46868) exo-1,3-beta-glucanase/1,3-beta-D-glucan

glucanohydrolase [Pichia angusta]

Seq. No.	389277
Contig ID	15385_1.R1084
5'-most EST	LIB3433-014-Q6-K1-D7

Seq. No.	389278
Contig ID	15386_1.R1084
5'-most EST	LIB3434-039-P1-K1-E4

Seq. No.	389279
Contig ID	15386_2.R1084
5'-most EST	LIB3433-014-Q6-K1-D8

Seq. No.	389280
Contig ID	15387_1.R1084
5'-most EST	g3759092

Seq. No.	389281
Contig ID	15388_1.R1084
5'-most EST	uC-osflm202101e04b1
Method	BLASTX
NCBI GI	g2832628
BLAST score	388
E value	2.0e-40
Match length	140
% identity	64
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	389282
Contig ID	15398_1.R1084
5'-most EST	LIB3433-061-P1-K1-A12
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	5.0e-11
Match length	37
% identity	60
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389283
Contig ID	15399_1.R1084
5'-most EST	g5003093
Method	BLASTX
NCBI GI	g4490316
BLAST score	427
E value	7.0e-58
Match length	237
% identity	50
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	389284
Contig ID	15400_1.R1084
5'-most EST	uC-osflcyp120b03b1
Method	BLASTX
NCBI GI	g4336436
BLAST score	474

E value 2.0e-47
Match length 156
% identity 60
NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No. 389285
Contig ID 15402_1.R1084
5'-most EST LIB3434-058-P1-K1-H4
Method BLASTX
NCBI GI g2832632
BLAST score 505
E value 8.0e-51
Match length 165
% identity 67
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No. 389286
Contig ID 15405_1.R1084
5'-most EST LIB3433-014-Q6-K1-F9

Seq. No. 389287
Contig ID 15407_1.R1084
5'-most EST uC-osflm202107f04b1
Method BLASTX
NCBI GI g2335108
BLAST score 490
E value 2.0e-51
Match length 162
% identity 60
NCBI Description (AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No. 389288
Contig ID 15408_1.R1084
5'-most EST LIB3433-014-Q6-K1-G11
Method BLASTX
NCBI GI g4835765
BLAST score 528
E value 8.0e-54
Match length 155
% identity 69
NCBI Description (AC007202) Is a member of the PF_00171 aldehyde dehydrogenase family. ESTs gb_T21534, gb_N65241 and gb_AA395614 come from this gene. [Arabidopsis thaliana]

Seq. No. 389289
Contig ID 15409_1.R1084
5'-most EST g4714853
Method BLASTX
NCBI GI g2827536
BLAST score 285
E value 8.0e-25
Match length 153
% identity 37
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 389290
Contig ID 15412_1.R1084

5'-most EST	LIB3433-029-P1-K1-A10
Seq. No.	389291
Contig ID	15414_1.R1084
5'-most EST	LIB3433-014-Q6-K1-G7
Method	BLASTX
NCBI GI	g478809
BLAST score	554
E value	2.0e-56
Match length	242
% identity	42
NCBI Description	protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449) protein kinase [Glycine max] >gi_444789_prf__1908223A protein kinase [Glycine max]
Seq. No.	389292
Contig ID	15418_1.R1084
5'-most EST	LIB3434-025-P1-K1-E2
Method	BLASTX
NCBI GI	g728880
BLAST score	533
E value	5.0e-54
Match length	147
% identity	69
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]
Seq. No.	389293
Contig ID	15423_1.R1084
5'-most EST	uC-osflm202106f11b1
Seq. No.	389294
Contig ID	15425_1.R1084
5'-most EST	LIB3433-014-Q6-K1-H9
Seq. No.	389295
Contig ID	15426_1.R1084
5'-most EST	g4969181
Method	BLASTX
NCBI GI	g4160292
BLAST score	387
E value	3.0e-37
Match length	121
% identity	60
NCBI Description	(Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]
Seq. No.	389296
Contig ID	15428_1.R1084
5'-most EST	g2310159
Method	BLASTX
NCBI GI	g4127348
BLAST score	410
E value	7.0e-40
Match length	154
% identity	52

NCBI Description (AJ010449) glutathione transferase [Alopecurus myosuroides]

Seq. No. 389297
Contig ID 15431_1.R1084
5'-most EST uC-osflcyp139c09b1

Seq. No. 389298
Contig ID 15432_1.R1084
5'-most EST g3762102
Method BLASTX
NCBI GI g5541697
BLAST score 227
E value 3.0e-18
Match length 96
% identity 50
NCBI Description (AL096860) putative protein [Arabidopsis thaliana]

Seq. No. 389299
Contig ID 15435_1.R1084
5'-most EST LIB3433-020-P1-K1-A8
Method BLASTX
NCBI GI g6006892
BLAST score 166
E value 2.0e-11
Match length 46
% identity 63
NCBI Description (AC008153) unknown protein [Arabidopsis thaliana]

Seq. No. 389300
Contig ID 15439_1.R1084
5'-most EST g3768381
Method BLASTX
NCBI GI g2262105
BLAST score 430
E value 4.0e-57
Match length 214
% identity 52
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 389301
Contig ID 15443_1.R1084
5'-most EST LIB3433-020-P1-K1-B6
Method BLASTX
NCBI GI g3047096
BLAST score 146
E value 6.0e-21
Match length 182
% identity 38
NCBI Description (AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]

Seq. No. 389302
Contig ID 15444_1.R1084
5'-most EST LIB3474-001-P1-K1-G3
Method BLASTX
NCBI GI g3075391
BLAST score 248

E value	7.0e-29
Match length	220
% identity	44
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	389303
Contig ID	15447_1.R1084
5'-most EST	LIB3433-020-P1-K1-C1

Seq. No.	389304
Contig ID	15461_1.R1084
5'-most EST	uC-osf1cyp131b10a1

Seq. No.	389305
Contig ID	15464_1.R1084
5'-most EST	LIB3474-011-P1-K1-E5

Seq. No.	389306
Contig ID	15465_1.R1084
5'-most EST	LIB3433-020-P1-K1-D7
Method	BLASTX
NCBI GI	g3935170
BLAST score	738
E value	3.0e-78
Match length	227
% identity	61
NCBI Description	(AC004557) F17L21.13 [Arabidopsis thaliana]

Seq. No.	389307
Contig ID	15474_1.R1084
5'-most EST	LIB3433-020-P1-K1-E5
Method	BLASTX
NCBI GI	g2244898
BLAST score	567
E value	3.0e-60
Match length	170
% identity	66
NCBI Description	(Z97338) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	389308
Contig ID	15476_1.R1084
5'-most EST	g6012902
Method	BLASTX
NCBI GI	g169363
BLAST score	285
E value	6.0e-25
Match length	62
% identity	77
NCBI Description	(M75856) PVPR3 [Phaseolus vulgaris]

Seq. No.	389309
Contig ID	15476_2.R1084
5'-most EST	g5607544

Seq. No.	389310
Contig ID	15476_3.R1084
5'-most EST	LIB3434-032-P1-K1-D3

Method	BLASTX
NCBI GI	g169363
BLAST score	285
E value	5.0e-25
Match length	63
% identity	79
NCBI Description	(M75856) PVPR3 [Phaseolus vulgaris]

Seq. No.	389311
Contig ID	15476_4.R1084
5'-most EST	LIB3479-001-Q6-K2-D12

Seq. No.	389312
Contig ID	15477_1.R1084
5'-most EST	uC-osrocyp037d05b1
Method	BLASTX
NCBI GI	g3237304
BLAST score	518
E value	3.0e-52
Match length	194
% identity	54
NCBI Description	(U91561) pyridoxine 5'-phosphate oxidase [Rattus norvegicus]

Seq. No.	389313
Contig ID	15478_1.R1084
5'-most EST	LIB3433-020-P1-K1-E9

Seq. No.	389314
Contig ID	15489_1.R1084
5'-most EST	uC-osf1cyp140c12b1
Method	BLASTX
NCBI GI	g1362051
BLAST score	945
E value	1.0e-102
Match length	205
% identity	86
NCBI Description	protein kinase 3 - soybean >gi_310582 (L19361) protein kinase 3 [Glycine max]

Seq. No.	389315
Contig ID	15491_1.R1084
5'-most EST	LIB3433-020-P1-K1-G10
Method	BLASTX
NCBI GI	g4678941
BLAST score	362
E value	1.0e-34
Match length	139
% identity	58
NCBI Description	(AL049711) gamma response I protein [Arabidopsis thaliana]

Seq. No.	389316
Contig ID	15492_1.R1084
5'-most EST	LIB3433-020-P1-K1-G11
Method	BLASTX
NCBI GI	g4587514
BLAST score	923

E value	1.0e-100
Match length	227
% identity	78
NCBI Description	(AC007060) Similar to WO8E3.3 gi_3880615 putative GTP-binding protein from C. elegans cosmid gb_Z92773. EST gb_AA597331 comes from this gene. [Arabidopsis thaliana]

Seq. No.	389317
Contig ID	15494_1.R1084
5'-most EST	g2431310
Method	BLASTX
NCBI GI	g4895197
BLAST score	154
E value	9.0e-10
Match length	48
% identity	58
NCBI Description	(AC007661) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389318
Contig ID	15498_1.R1084
5'-most EST	LIB3433-020-P1-K1-G6
Method	BLASTX
NCBI GI	g1888357
BLAST score	325
E value	7.0e-34
Match length	148
% identity	55
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	389319
Contig ID	15510_1.R1084
5'-most EST	LIB3433-020-P1-K1-H9
Method	BLASTX
NCBI GI	g2246380
BLAST score	352
E value	3.0e-33
Match length	97
% identity	67
NCBI Description	(Z86095) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	389320
Contig ID	15517_1.R1084
5'-most EST	LIB3433-027-P1-K1-A4
Method	BLASTX
NCBI GI	g4760700
BLAST score	263
E value	2.0e-22
Match length	138
% identity	41
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]

Seq. No.	389321
Contig ID	15521_1.R1084
5'-most EST	g2427736

Method	BLASTX
NCBI GI	g2288982
BLAST score	592
E value	5.0e-61
Match length	169
% identity	69
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389322
Contig ID	15527_1.R1084
5'-most EST	uC-osroM202001e03a1

Seq. No.	389323
Contig ID	15529_1.R1084
5'-most EST	LIB3433-027-P1-K1-B5

Seq. No.	389324
Contig ID	15531_1.R1084
5'-most EST	LIB3474-012-P1-K1-D2
Method	BLASTX
NCBI GI	g5679841
BLAST score	548
E value	6.0e-56
Match length	217
% identity	52
NCBI Description	(AJ243961) contains eukaryotic protein kinase domain PF_00069 [Oryza sativa]

Seq. No.	389325
Contig ID	15533_1.R1084
5'-most EST	g699784
Method	BLASTX
NCBI GI	g4006882
BLAST score	741
E value	2.0e-78
Match length	216
% identity	62
NCBI Description	(Z99707) UDP-glucuronyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	389326
Contig ID	15536_1.R1084
5'-most EST	uC-osrocyp027b02a1

Seq. No.	389327
Contig ID	15538_1.R1084
5'-most EST	LIB3475-007-P1-K1-H8

Seq. No.	389328
Contig ID	15539_1.R1084
5'-most EST	g428808
Method	BLASTX
NCBI GI	g1706958
BLAST score	915
E value	1.0e-98
Match length	219
% identity	74

NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	389329
Contig ID	15542_1.R1084
5'-most EST	uC-osrocyp034h10a1
Method	BLASTX
NCBI GI	g5441874
BLAST score	422
E value	2.0e-41
Match length	79
% identity	100
NCBI Description	(AP000366) Similar to maize transposon MuDR mudrA-like protein. (AC002340) [Oryza sativa]

Seq. No.	389330
Contig ID	15543_1.R1084
5'-most EST	g427792

Seq. No.	389331
Contig ID	15545_1.R1084
5'-most EST	g3762758
Method	BLASTX
NCBI GI	g6093429
BLAST score	356
E value	9.0e-34
Match length	109
% identity	61
NCBI Description	PUTATIVE METHYLTRANSFERASE >gi_2911587_emb_CAA11944_ (AJ224442) methyltransferase [Homo sapiens]

Seq. No.	389332
Contig ID	15546_1.R1084
5'-most EST	LIB3475-007-P1-K1-H11
Method	BLASTX
NCBI GI	g3941480
BLAST score	325
E value	2.0e-29
Match length	106
% identity	77
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	389333
Contig ID	15547_1.R1084
5'-most EST	LIB3433-027-P1-K1-D10

Seq. No.	389334
Contig ID	15551_1.R1084
5'-most EST	g3766865

Seq. No.	389335
Contig ID	15552_1.R1084
5'-most EST	uC-osflcyp027d07b1
Method	BLASTX
NCBI GI	g3915085
BLAST score	601
E value	2.0e-62

Match length	152
% identity	79
NCBI Description	TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi_1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis thaliana] >gi_1946370 (U93215) cinnamate-4-hydroxylase [Arabidopsis thaliana]

Seq. No.	389336
Contig ID	15556_1.R1084
5'-most EST	LIB3434-043-P1-K1-F3

Seq. No.	389337
Contig ID	15559_1.R1084
5'-most EST	uC-osflcyp174e05b1
Method	BLASTX
NCBI GI	g3297816
BLAST score	533
E value	4.0e-54
Match length	162
% identity	65
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	389338
Contig ID	15565_1.R1084
5'-most EST	LIB3433-027-P1-K1-E6

Seq. No.	389339
Contig ID	15567_1.R1084
5'-most EST	g4880928
Method	BLASTX
NCBI GI	g1352613
BLAST score	532
E value	8.0e-54
Match length	121
% identity	91
NCBI Description	OCS-ELEMENT BINDING FACTOR 1 (OCSBF-1) >gi_444047_emb_CAA44607_ (X62745) ocs-binding factor 1 [Zea mays]

Seq. No.	389340
Contig ID	15570_1.R1084
5'-most EST	g5038892

Seq. No.	389341
Contig ID	15580_1.R1084
5'-most EST	uC-osroM202019f06b1
Method	BLASTX
NCBI GI	g6016877
BLAST score	307
E value	1.0e-27
Match length	77
% identity	75
NCBI Description	(AP000570) ESTs AU077642(E30706),AU077641(E30706) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	389342
Contig ID	15580_2.R1084
5'-most EST	g5900709
Method	BLASTX
NCBI GI	g6016877
BLAST score	253
E value	2.0e-21
Match length	65
% identity	77
NCBI Description	(AP000570) ESTs AU077642(E30706),AU077641(E30706) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	389343
Contig ID	15580_3.R1084
5'-most EST	uC-osflcyp171d04b1
Method	BLASTX
NCBI GI	g6016877
BLAST score	222
E value	9.0e-18
Match length	48
% identity	79
NCBI Description	(AP000570) ESTs AU077642(E30706),AU077641(E30706) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	389344
Contig ID	15586_1.R1084
5'-most EST	g3766791

Seq. No.	389345
Contig ID	15588_1.R1084
5'-most EST	uC-osroM202011b05b1

Seq. No.	389346
Contig ID	15588_2.R1084
5'-most EST	g3761521
Method	BLASTN
NCBI GI	g58063
BLAST score	83
E value	2.0e-38
Match length	117
% identity	95
NCBI Description	pBluescript II SK(+) vector DNA, phagemid excised from lambda ZAPII

Seq. No.	389347
Contig ID	15591_1.R1084
5'-most EST	g6062525
Method	BLASTN
NCBI GI	g5257255
BLAST score	42
E value	2.0e-14
Match length	254
% identity	57
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	389348
Contig ID	15592_1.R1084
5'-most EST	LIB3433-027-P1-K1-H3
Method	BLASTX
NCBI GI	g3747050
BLAST score	479
E value	7.0e-48
Match length	113
% identity	85
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]

Seq. No.	389349
Contig ID	15592_2.R1084
5'-most EST	g6012813
Method	BLASTX
NCBI GI	g2618687
BLAST score	191
E value	2.0e-14
Match length	59
% identity	35
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389350
Contig ID	15594_1.R1084
5'-most EST	LIB3434-049-P1-K1-C9
Method	BLASTX
NCBI GI	g1352660
BLAST score	212
E value	2.0e-16
Match length	137
% identity	33
NCBI Description	COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR >gi_924850 (U26264) CHOp24 [Cricetulus griseus]

Seq. No.	389351
Contig ID	15595_1.R1084
5'-most EST	LIB3433-060-P1-K1-D11
Method	BLASTX
NCBI GI	g1420887
BLAST score	144
E value	1.0e-08
Match length	47
% identity	51
NCBI Description	(U34334) non-specific lipid transfer-like protein [Phaseolus vulgaris]

Seq. No.	389352
Contig ID	15597_1.R1084
5'-most EST	LIB3434-060-P1-K1-G12
Method	BLASTX
NCBI GI	g2708624
BLAST score	1071
E value	1.0e-117
Match length	216
% identity	87
NCBI Description	(AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	389353
Contig ID	15600_1.R1084
5'-most EST	LIB3433-028-P1-K1-A3
Method	BLASTX
NCBI GI	g4467147
BLAST score	790
E value	2.0e-84
Match length	227
% identity	68
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	389354
Contig ID	15603_1.R1084
5'-most EST	LIB3433-050-P1-K1-B7
Method	BLASTX
NCBI GI	g6016877
BLAST score	232
E value	7.0e-19
Match length	53
% identity	81
NCBI Description	(AP000570) ESTs AU077642(E30706),AU077641(E30706) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	389355
Contig ID	15608_1.R1084
5'-most EST	uC-osrocyp015f10b1
Method	BLASTN
NCBI GI	g6006355
BLAST score	38
E value	3.0e-11
Match length	139
% identity	87
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	389356
Contig ID	15611_1.R1084
5'-most EST	uC-osflcyp157g12b1

Seq. No.	389357
Contig ID	15614_1.R1084
5'-most EST	g702264
Method	BLASTX
NCBI GI	g2827544
BLAST score	631
E value	1.0e-65
Match length	164
% identity	75
NCBI Description	(AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No.	389358
Contig ID	15617_1.R1084
5'-most EST	g3767429

Seq. No.	389359
Contig ID	15624_1.R1084

5'-most EST	g2442267
Method	BLASTX
NCBI GI	g1169369
BLAST score	208
E value	5.0e-16
Match length	73
% identity	52
NCBI Description	DNAJ PROTEIN >gi_541427_pir__S41758 heat shock protein dnaJ - Clostridium acetobutylicum >gi_433079_emb_CAA48792_ (X69050) DnaJ [Clostridium acetobutylicum]

Seq. No.	389360
Contig ID	15625_1.R1084
5'-most EST	LIB3433-028-P1-K1-C5
Method	BLASTX
NCBI GI	g2129628
BLAST score	254
E value	2.0e-21
Match length	95
% identity	55
NCBI Description	ketoconazole resistent protein - Arabidopsis thaliana >gi_928938_emb_CAA61433_ (X89036) ketoconazole resistent protein [Arabidopsis thaliana]

Seq. No.	389361
Contig ID	15630_1.R1084
5'-most EST	g3766718
Method	BLASTX
NCBI GI	g4432860
BLAST score	310
E value	9.0e-28
Match length	138
% identity	10
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	389362
Contig ID	15633_1.R1084
5'-most EST	uC-osroM202014e07b1
Method	BLASTX
NCBI GI	g1542941
BLAST score	1463
E value	1.0e-163
Match length	379
% identity	76
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	389363
Contig ID	15634_1.R1084
5'-most EST	LIB3433-028-P1-K1-D2

Seq. No.	389364
Contig ID	15637_1.R1084
5'-most EST	LIB3433-028-P1-K1-D5

Seq. No.	389365
Contig ID	15643_1.R1084

5'-most EST	LIB3433-028-P1-K1-E10
Method	BLASTX
NCBI GI	g2194125
BLAST score	793
E value	1.0e-84
Match length	176
% identity	82
NCBI Description	(AC002062) ESTs gb_R30459,gb_N38441 come from this gene. [Arabidopsis thaliana]

Seq. No.	389366
Contig ID	15646_1.R1084
5'-most EST	LIB3477-007-P1-K1-D1
Method	BLASTX
NCBI GI	g3850587
BLAST score	592
E value	2.0e-67
Match length	216
% identity	69
NCBI Description	(AC005278) Strong similarity to gi_2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No.	389367
Contig ID	15647_1.R1084
5'-most EST	g4714816
Method	BLASTX
NCBI GI	g1076821
BLAST score	412
E value	3.0e-47
Match length	114
% identity	85
NCBI Description	probable 1-acyl-glycerol-3-phosphate acyltransferase - maize >gi_575960_emb_CAA82638_ (Z29518) 1-acyl-glycerol-3-phosphate acyltransferase (putative) [Zea mays]

Seq. No.	389368
Contig ID	15650_1.R1084
5'-most EST	LIB3433-028-P1-K1-E7
Method	BLASTX
NCBI GI	g4038471
BLAST score	256
E value	5.0e-22
Match length	47
% identity	98
NCBI Description	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No.	389369
Contig ID	15651_1.R1084
5'-most EST	g2799767
Method	BLASTX
NCBI GI	g116054
BLAST score	391
E value	4.0e-72
Match length	182
% identity	55

NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) >gi_280393_pir__A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean >gi_169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]

Seq. No.	389370
Contig ID	15652_1.R1084
5'-most EST	LIB3433-028-P1-K1-E9
Method	BLASTX
NCBI GI	g2765140
BLAST score	628
E value	2.0e-65
Match length	151
% identity	76
NCBI Description	(Y11931) 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase [Nicotiana rustica]

Seq. No.	389371
Contig ID	15653_1.R1084
5'-most EST	LIB3433-028-P1-K1-F1
Method	BLASTX
NCBI GI	g462234
BLAST score	408
E value	1.0e-39
Match length	111
% identity	77
NCBI Description	HISTONE H2A >gi_419741_pir__S30155 histone H2A - Norway spruce >gi_297871_emb_CAA48030_ (X67819) histone H2A [Picea abies]

Seq. No.	389372
Contig ID	15658_1.R1084
5'-most EST	LIB3434-051-P1-K1-A12
Method	BLASTX
NCBI GI	g5103810
BLAST score	290
E value	7.0e-26
Match length	59
% identity	80
NCBI Description	(AC007591) Similar to gb_X79273 cytochrome c reductase hinge protein subunit from Solanum tuberosum. ESTs gb_T45282 and gb_T21596 come from this gene. [Arabidopsis thaliana]

Seq. No.	389373
Contig ID	15660_1.R1084
5'-most EST	LIB3433-028-P1-K1-F5
Method	BLASTX
NCBI GI	g4835752
BLAST score	593
E value	2.0e-61
Match length	146
% identity	75
NCBI Description	(AC007202) Is a member of the PF_00069 Eukaryotic protein kinase family. ESTs gb_T46484, gb_AF066875 and gb_N96237 come from this gene. [Arabidopsis thaliana]

Seq. No.	389374
Contig ID	15664_1.R1084
5'-most EST	g568152
Method	BLASTX
NCBI GI	g4680212
BLAST score	157
E value	5.0e-10
Match length	40
% identity	78
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	389375
Contig ID	15665_1.R1084
5'-most EST	g3768676
Method	BLASTN
NCBI GI	g2766447
BLAST score	46
E value	2.0e-16
Match length	138
% identity	86
NCBI Description	Sorghum bicolor cytochrome P450 CYP98A1 (CYP98A1) mRNA, complete cds

Seq. No.	389376
Contig ID	15665_2.R1084
5'-most EST	uC-osflcyp175f06b1
Method	BLASTX
NCBI GI	g5915857
BLAST score	1442
E value	0.0e+00
Match length	372
% identity	89
NCBI Description	CYTOCHROME P450 98A1 >gi_2766448 (AF029856) cytochrome P450 CYP98A1 [Sorghum bicolor]

Seq. No.	389377
Contig ID	15671_1.R1084
5'-most EST	g3762247
Method	BLASTX
NCBI GI	g1203832
BLAST score	368
E value	5.0e-35
Match length	75
% identity	87
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No.	389378
Contig ID	15674_1.R1084
5'-most EST	g702001
Method	BLASTX
NCBI GI	g4850400
BLAST score	686
E value	1.0e-109
Match length	209
% identity	84

NCBI Description	(AC007357) Similar to gb_M86917 oxysterol-binding protein from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	389379
Contig ID	15675_1.R1084
5'-most EST	uC-osflm202102f09b1

Seq. No.	389380
Contig ID	15676_1.R1084
5'-most EST	LIB3433-028-P1-K1-H1
Method	BLASTX
NCBI GI	g77794
BLAST score	158
E value	3.0e-10
Match length	83
% identity	36
NCBI Description	alpha-amylase (EC 3.2.1.1) precursor - Pseudomonas sp

Seq. No.	389381
Contig ID	15679_1.R1084
5'-most EST	uC-osflcyp061h07b1
Method	BLASTX
NCBI GI	g6091734
BLAST score	172
E value	4.0e-12
Match length	66
% identity	45
NCBI Description	(AC010797) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389382
Contig ID	15679_2.R1084
5'-most EST	LIB3433-028-P1-K1-H2
Method	BLASTX
NCBI GI	g6091733
BLAST score	146
E value	4.0e-14
Match length	65
% identity	63
NCBI Description	(AC010797) unknown protein [Arabidopsis thaliana]

Seq. No.	389383
Contig ID	15680_1.R1084
5'-most EST	g3767609
Method	BLASTX
NCBI GI	g1172553
BLAST score	500
E value	3.0e-50
Match length	126
% identity	80
NCBI Description	OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_456672_emb_CAA54788_ (X77733) voltage dependent anion channel (VDAC) [Triticum aestivum]

Seq. No.	389384
Contig ID	15680_2.R1084
5'-most EST	g699630

Method	BLASTX
NCBI GI	g1172553
BLAST score	1004
E value	1.0e-109
Match length	242
% identity	83
NCBI Description	OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_456672_emb_CAA54788_ (X77733) voltage dependent anion channel (VDAC) [Triticum aestivum]

Seq. No.	389385
Contig ID	15686_1.R1084
5'-most EST	uC-osf1M202068g11b1
Method	BLASTX
NCBI GI	g3202026
BLAST score	1231
E value	1.0e-135
Match length	264
% identity	85
NCBI Description	(AF069316) stromal L-ascorbate peroxidase precursor [Mesembryanthemum crystallinum]

Seq. No.	389386
Contig ID	15693_1.R1084
5'-most EST	LIB3434-056-P1-K1-C7
Method	BLASTX
NCBI GI	g6009521
BLAST score	654
E value	6.0e-68
Match length	471
% identity	25
NCBI Description	(AB021491) p100 co-activator [Mus musculus]

Seq. No.	389387
Contig ID	15704_1.R1084
5'-most EST	LIB3433-029-P1-K1-B7
Method	BLASTX
NCBI GI	g2827529
BLAST score	291
E value	3.0e-26
Match length	109
% identity	49
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]

Seq. No.	389388
Contig ID	15707_1.R1084
5'-most EST	LIB3433-029-P1-K1-C1
Method	BLASTX
NCBI GI	g2995953
BLAST score	247
E value	6.0e-21
Match length	79
% identity	61
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No. 389389

Contig ID	15715_1.R1084
5'-most EST	LIB3433-029-P1-K1-C7
Method	BLASTX
NCBI GI	g3152572
BLAST score	405
E value	3.0e-39
Match length	201
% identity	45
NCBI Description	(AC002986) Contains homology to DNAJ heatshock protein gb_U32803 from Haemophilus influenzae. [Arabidopsis thaliana]

Seq. No.	389390
Contig ID	15720_1.R1084
5'-most EST	LIB3433-029-P1-K1-D12
Method	BLASTX
NCBI GI	g3549667
BLAST score	514
E value	4.0e-52
Match length	163
% identity	61
NCBI Description	(AL031394) Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	389391
Contig ID	15723_1.R1084
5'-most EST	uC-osroM202024b08a1

Seq. No.	389392
Contig ID	15724_1.R1084
5'-most EST	g3762214
Method	BLASTX
NCBI GI	g4580389
BLAST score	395
E value	3.0e-38
Match length	100
% identity	73
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	389393
Contig ID	15733_1.R1084
5'-most EST	LIB3433-029-P1-K1-E5
Method	BLASTX
NCBI GI	g3193330
BLAST score	408
E value	1.0e-39
Match length	124
% identity	65
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	389394
Contig ID	15734_1.R1084
5'-most EST	g2442270
Method	BLASTX
NCBI GI	g2467274
BLAST score	222

E value	2.0e-25
Match length	122
% identity	56
NCBI Description	(Z99759) rna binding protein [Schizosaccharomyces pombe]

Seq. No.	389395
Contig ID	15736_1.R1084
5'-most EST	LIB3433-029-P1-K1-F1
Method	BLASTN
NCBI GI	g6015437
BLAST score	38
E value	7.0e-12
Match length	39
% identity	61
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389396
Contig ID	15737_1.R1084
5'-most EST	g426999

Seq. No.	389397
Contig ID	15738_1.R1084
5'-most EST	LIB3433-029-P1-K1-F11

Seq. No.	389398
Contig ID	15747_1.R1084
5'-most EST	g428248
Method	BLASTX
NCBI GI	g4314378
BLAST score	561
E value	8.0e-71
Match length	352
% identity	44
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana] >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative lipase [Arabidopsis thaliana]

Seq. No.	389399
Contig ID	15749_1.R1084
5'-most EST	LIB3433-029-P1-K1-G12

Seq. No.	389400
Contig ID	15750_1.R1084
5'-most EST	g571991
Method	BLASTX
NCBI GI	g2739381
BLAST score	698
E value	1.0e-107
Match length	328
% identity	58
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	389401
Contig ID	15756_1.R1084
5'-most EST	LIB3433-029-P1-K1-G8

Seq. No.	389402

Contig ID	15757_1.R1084
5'-most EST	LIB3433-029-P1-K1-G9

Seq. No.	389403
Contig ID	15759_1.R1084
5'-most EST	g2311797

Seq. No.	389404
Contig ID	15761_1.R1084
5'-most EST	uC-osroM202011c06b1

Seq. No.	389405
Contig ID	15763_1.R1084
5'-most EST	uC-osflcyp157h03b1
Method	BLASTX
NCBI GI	g6016737
BLAST score	169
E value	3.0e-11
Match length	215
% identity	28
NCBI Description	(AC009325) hypothetical protein [Arabidopsis thaliana] >gi_6091741_gb_AAF03453.1_AC010797_29 (AC010797) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389406
Contig ID	15766_1.R1084
5'-most EST	LIB3433-029-P1-K1-H8
Method	BLASTX
NCBI GI	g3169175
BLAST score	185
E value	2.0e-36
Match length	148
% identity	52
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	389407
Contig ID	15767_1.R1084
5'-most EST	LIB3433-029-P1-K1-H9
Method	BLASTX
NCBI GI	g2829918
BLAST score	121
E value	1.0e-11
Match length	43
% identity	69
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	389408
Contig ID	15773_1.R1084
5'-most EST	g2801152
Method	BLASTX
NCBI GI	g294845
BLAST score	972
E value	1.0e-105
Match length	247
% identity	74

NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	389409
Contig ID	15774_1.R1084
5'-most EST	LIB3433-030-P1-K1-A5
Method	BLASTX
NCBI GI	g4678293
BLAST score	276
E value	4.0e-24
Match length	121
% identity	26
NCBI Description	(AL049655) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389410
Contig ID	15782_1.R1084
5'-most EST	g2800741
Method	BLASTX
NCBI GI	g6094554
BLAST score	382
E value	1.0e-36
Match length	138
% identity	62
NCBI Description	(AC010676) putative protein kinase [Arabidopsis thaliana]

Seq. No.	389411
Contig ID	15782_2.R1084
5'-most EST	LIB3433-030-P1-K1-B3
Method	BLASTX
NCBI GI	g6094554
BLAST score	1001
E value	1.0e-109
Match length	260
% identity	76
NCBI Description	(AC010676) putative protein kinase [Arabidopsis thaliana]

Seq. No.	389412
Contig ID	15785_1.R1084
5'-most EST	LIB3433-030-P1-K1-B6
Method	BLASTX
NCBI GI	g1174853
BLAST score	707
E value	4.0e-75
Match length	152
% identity	88
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42) >gi_481811_pir__S39483 ubiquitin-conjugating enzyme UBC2-1 - Arabidopsis thaliana >gi_22658_emb_CAA48378_ (X68306) ubiquitin-conjugating enzyme [Arabidopsis thaliana]

Seq. No.	389413
Contig ID	15786_1.R1084
5'-most EST	LIB3434-007-P1-K1-C8
Method	BLASTX
NCBI GI	g4417280
BLAST score	627

E value 6.0e-65
Match length 228
% identity 56
NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No. 389414
Contig ID 15786_2.R1084
5'-most EST g2797020
Method BLASTN
NCBI GI g4158227
BLAST score 48
E value 1.0e-17
Match length 52
% identity 98
NCBI Description Oryctolagus cuniculus mRNA for epithelial sodium channel, gamma subunit

Seq. No. 389415
Contig ID 15786_3.R1084
5'-most EST LIB3433-024-P1-K1-F6
Method BLASTX
NCBI GI g4417280
BLAST score 288
E value 1.0e-25
Match length 89
% identity 60
NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No. 389416
Contig ID 15790_1.R1084
5'-most EST g2796913
Method BLASTX
NCBI GI g4455359
BLAST score 428
E value 9.0e-42
Match length 206
% identity 47
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 389417
Contig ID 15793_1.R1084
5'-most EST g5039002
Method BLASTX
NCBI GI g2493318
BLAST score 178
E value 2.0e-20
Match length 95
% identity 59
NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No. 389418
Contig ID 15795_1.R1084
5'-most EST LIB3433-030-P1-K1-C4

Seq. No. 389419

Contig ID	15799_1.R1084
5'-most EST	g5771185
Method	BLASTN
NCBI GI	g5803242
BLAST score	396
E value	0.0e+00
Match length	723
% identity	92
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	389420
Contig ID	15801_1.R1084
5'-most EST	LIB3433-030-P1-K1-D1
Method	BLASTX
NCBI GI	g2252851
BLAST score	205
E value	1.0e-15
Match length	139
% identity	37
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	389421
Contig ID	15803_1.R1084
5'-most EST	LIB3433-030-P1-K1-D11
Method	BLASTX
NCBI GI	g3004558
BLAST score	272
E value	1.0e-42
Match length	179
% identity	54
NCBI Description	(AC003673) peroxidase ATP22a [Arabidopsis thaliana]

Seq. No.	389422
Contig ID	15806_1.R1084
5'-most EST	g2312795
Method	BLASTX
NCBI GI	g4585963
BLAST score	149
E value	5.0e-09
Match length	150
% identity	27
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	389423
Contig ID	15808_1.R1084
5'-most EST	LIB3433-042-P1-K1-C2
Method	BLASTX
NCBI GI	g135794
BLAST score	323
E value	2.0e-29
Match length	123
% identity	48
NCBI Description	LEAF-SPECIFIC THIONIN PRECURSOR (CLONES PKG1348, PKG1940, PKG2872 AND DG3) >gi_167102 (M19046) precursor thionin [Hordeum vulgare] >gi_167104 (M19047) precursor thionin [Hordeum vulgare] >gi_167106 (M19048) precursor thionin [Hordeum vulgare]

Seq. No.	389424
Contig ID	15809_1.R1084
5'-most EST	g569532

Seq. No.	389425
Contig ID	15810_1.R1084
5'-most EST	LIB3433-059-P1-K1-A2

Seq. No.	389426
Contig ID	15818_1.R1084
5'-most EST	g1854143
Method	BLASTX
NCBI GI	g4572671
BLAST score	774
E value	2.0e-82
Match length	229
% identity	66
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	389427
Contig ID	15819_1.R1084
5'-most EST	LIB3433-030-P1-K1-E5

Seq. No.	389428
Contig ID	15822_1.R1084
5'-most EST	g427164
Method	BLASTX
NCBI GI	g3759184
BLAST score	389
E value	2.0e-64
Match length	265
% identity	59
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	389429
Contig ID	15824_1.R1084
5'-most EST	LIB3433-030-P1-K1-F1
Method	BLASTX
NCBI GI	g4432841
BLAST score	215
E value	7.0e-17
Match length	121
% identity	44
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389430
Contig ID	15825_1.R1084
5'-most EST	LIB3433-030-P1-K1-F11

Seq. No.	389431
Contig ID	15827_1.R1084
5'-most EST	LIB3433-030-P1-K1-F2
Method	BLASTX
NCBI GI	g4455206
BLAST score	305

E value	1.0e-27
Match length	181
% identity	44
NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No.	389432
Contig ID	15837_1.R1084
5'-most EST	uC-osflcyp170a09a1
Method	BLASTX
NCBI GI	g1620982
BLAST score	205
E value	5.0e-16
Match length	58
% identity	76
NCBI Description	(Y08860) 40S ribosomal protein S5 [Nicotiana plumbaginifolia]

Seq. No.	389433
Contig ID	15845_1.R1084
5'-most EST	g1632318

Seq. No.	389434
Contig ID	15854_1.R1084
5'-most EST	LIB3433-031-P1-K1-A1
Method	BLASTX
NCBI GI	g1781226
BLAST score	148
E value	4.0e-09
Match length	100
% identity	33
NCBI Description	(Z83867) fadB4 [Mycobacterium tuberculosis]

Seq. No.	389435
Contig ID	15855_1.R1084
5'-most EST	LIB3433-031-P1-K1-A10

Seq. No.	389436
Contig ID	15861_1.R1084
5'-most EST	LIB3433-031-P1-K1-A5
Method	BLASTX
NCBI GI	g3738309
BLAST score	689
E value	2.0e-72
Match length	216
% identity	65
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	389437
Contig ID	15862_1.R1084
5'-most EST	uC-osrocyp026h05a1
Method	BLASTX
NCBI GI	g6056376
BLAST score	351
E value	5.0e-33
Match length	117
% identity	56

NCBI Description	(AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	389438
Contig ID	15865_1.R1084
5'-most EST	uC-osflcyp169b04b1
Method	BLASTX
NCBI GI	g4680199
BLAST score	237
E value	2.0e-21
Match length	159
% identity	38
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	389439
Contig ID	15870_1.R1084
5'-most EST	g3106894
Method	BLASTX
NCBI GI	g3288883
BLAST score	171
E value	1.0e-11
Match length	226
% identity	29
NCBI Description	(AB015431) SAR DNA binding protein [Oryza sativa]

Seq. No.	389440
Contig ID	15870_2.R1084
5'-most EST	LIB3433-031-P1-K1-B3
Method	BLASTN
NCBI GI	g287403
BLAST score	134
E value	8.0e-69
Match length	166
% identity	95
NCBI Description	Rice gene for starch branching enzyme

Seq. No.	389441
Contig ID	15871_1.R1084
5'-most EST	LIB3433-053-P1-K1-D10
Method	BLASTX
NCBI GI	g5281051
BLAST score	772
E value	1.0e-148
Match length	347
% identity	28
NCBI Description	(AL080318) stress-induced protein sti1-like protein [Arabidopsis thaliana]

Seq. No.	389442
Contig ID	15873_1.R1084
5'-most EST	g572126
Method	BLASTX
NCBI GI	g3128168
BLAST score	948
E value	1.0e-116
Match length	318
% identity	62

NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	389443
Contig ID	15873_2.R1084
5'-most EST	uC-osroM202019a10a1
Method	BLASTX
NCBI GI	g3128168
BLAST score	541
E value	4.0e-55
Match length	134
% identity	68
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	389444
Contig ID	15876_1.R1084
5'-most EST	LIB3433-031-P1-K1-B9
Method	BLASTX
NCBI GI	g6016691
BLAST score	455
E value	3.0e-45
Match length	176
% identity	47
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	389445
Contig ID	15879_1.R1084
5'-most EST	g571726
Method	BLASTX
NCBI GI	g3687235
BLAST score	283
E value	3.0e-49
Match length	150
% identity	73
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	389446
Contig ID	15881_1.R1084
5'-most EST	LIB3475-007-P1-K1-H3
Method	BLASTX
NCBI GI	g1703108
BLAST score	1859
E value	0.0e+00
Match length	373
% identity	94
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	389447
Contig ID	15883_1.R1084
5'-most EST	LIB3433-031-P1-K1-C4

Seq. No.	389448
Contig ID	15885_1.R1084
5'-most EST	uC-osrocyp010g11b1

Seq. No.	389449
Contig ID	15886_1.R1084
5'-most EST	uC-osflcyp126f11b1

Seq. No.	389450
Contig ID	15890_1.R1084
5'-most EST	uC-osroM202035h03b1
Method	BLASTX
NCBI GI	g2492834
BLAST score	130
E value	6.0e-10
Match length	99
% identity	40
NCBI Description	PUTATIVE AMIDASE >gi_1224069 (U49269) amidase [Moraxella catarrhalis]

Seq. No.	389451
Contig ID	15891_1.R1084
5'-most EST	LIB3433-031-P1-K1-D4
Method	BLASTX
NCBI GI	g2947063
BLAST score	372
E value	1.0e-35
Match length	133
% identity	56
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	389452
Contig ID	15893_1.R1084
5'-most EST	uC-osflcyp011a10b1
Method	BLASTX
NCBI GI	g4680499
BLAST score	247
E value	3.0e-34
Match length	149
% identity	68
NCBI Description	(AF119222) hypothetical protein [Oryza sativa]

Seq. No.	389453
Contig ID	15902_1.R1084
5'-most EST	g4716354

Seq. No.	389454
Contig ID	15905_1.R1084
5'-most EST	g2310104
Method	BLASTX
NCBI GI	g3170570
BLAST score	166
E value	3.0e-11
Match length	137
% identity	33
NCBI Description	(AF058302) FrnE [Streptomyces roseofulvus]

Seq. No.	389455
Contig ID	15912_1.R1084
5'-most EST	g5607456
Method	BLASTN
NCBI GI	g1184321
BLAST score	34
E value	3.0e-09
Match length	37
% identity	97
NCBI Description	Cloning vector pCRSCRIPT SK[+], complete sequence

Seq. No.	389456
Contig ID	15912_2.R1084
5'-most EST	LIB3477-008-P1-K1-F12

Seq. No.	389457
Contig ID	15914_1.R1084
5'-most EST	LIB3433-031-P1-K1-F7
Method	BLASTX
NCBI GI	g5123553
BLAST score	555
E value	8.0e-57
Match length	125
% identity	83
NCBI Description	(AL079344) putative protein [Arabidopsis thaliana]

Seq. No.	389458
Contig ID	15915_1.R1084
5'-most EST	LIB3433-031-P1-K1-F8
Method	BLASTX
NCBI GI	g128405
BLAST score	278
E value	1.0e-24
Match length	92
% identity	60
NCBI Description	NODULIN 21 (N-21) >gi_99942_pir__S08632 nodulin-21 - soybean >gi_18694_emb_CAA34506_ (X16488) nodulin-21 (AA 1-201) [Glycine max]

Seq. No.	389459
Contig ID	15916_1.R1084
5'-most EST	LIB3475-008-P1-K1-H12
Method	BLASTX
NCBI GI	g5734713
BLAST score	200
E value	5.0e-24
Match length	129
% identity	51
NCBI Description	(AC008075) Is a member of PF_01169 Uncharacterized (transmembrane domain) protein family. [Arabidopsis thaliana]

Seq. No.	389460
Contig ID	15917_1.R1084
5'-most EST	LIB3433-031-P1-K1-G12
Method	BLASTX

NCBI GI	g1172754
BLAST score	629
E value	9.0e-66
Match length	136
% identity	88
NCBI Description	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PRECURSOR (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) >gi_541885_pir__JQ2256 phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) precursor - Arabidopsis thaliana >gi_289188 (L12457) 5'-phosphoribosyl-5-aminoimidazole synthetase [Arabidopsis thaliana]

Seq. No.	389461
Contig ID	15919_1.R1084
5'-most EST	g3763806

Seq. No.	389462
Contig ID	15929_1.R1084
5'-most EST	uC-osflcyp152g05b1
Method	BLASTN
NCBI GI	g6002775
BLAST score	587
E value	0.0e+00
Match length	606
% identity	99
NCBI Description	Oryza sativa hypothetical protein, fertilin alpha subunit, membrane protein homolog, and Myb-related protein genes, complete cds; and unknown gene

Seq. No.	389463
Contig ID	15930_1.R1084
5'-most EST	uC-osroM202031h05b1

Seq. No.	389464
Contig ID	15932_1.R1084
5'-most EST	LIB3434-056-P1-K1-H5

Seq. No.	389465
Contig ID	15934_1.R1084
5'-most EST	uC-osflM202031h08a1

Seq. No.	389466
Contig ID	15939_1.R1084
5'-most EST	LIB3433-032-P1-K1-A12
Method	BLASTX
NCBI GI	g4263818
BLAST score	208
E value	1.0e-16
Match length	99
% identity	43
NCBI Description	(AC006067) unknown protein [Arabidopsis thaliana]

Seq. No.	389467
Contig ID	15941_1.R1084
5'-most EST	uC-osroM202037e01b1
Method	BLASTX

NCBI GI	g5441879
BLAST score	524
E value	3.0e-53
Match length	123
% identity	83
NCBI Description	(AP000367) ESTs AU070372(S13446),AU075541(S0353) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana BAC genomic sequence. (AC002292) [Oryza sativa]

Seq. No.	389468
Contig ID	15946_1.R1084
5'-most EST	uC-osroM202004h02b1
Method	BLASTX
NCBI GI	g2078350
BLAST score	1637
E value	0.0e+00
Match length	380
% identity	83
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	389469
Contig ID	15946_2.R1084
5'-most EST	uC-osflcyp085c02b1
Method	BLASTX
NCBI GI	g2078350
BLAST score	637
E value	1.0e-66
Match length	137
% identity	91
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	389470
Contig ID	15951_1.R1084
5'-most EST	g286682
Method	BLASTX
NCBI GI	g4835245
BLAST score	344
E value	5.0e-32
Match length	120
% identity	56
NCBI Description	(AL049862) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	389471
Contig ID	15954_1.R1084
5'-most EST	g3766569
Method	BLASTX
NCBI GI	g3738283
BLAST score	319
E value	4.0e-29
Match length	60
% identity	90
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	389472
Contig ID	15955_1.R1084
5'-most EST	uC-osflcyp157d04b1

Method	BLASTX
NCBI GI	g2642165
BLAST score	546
E value	1.0e-55
Match length	260
% identity	44
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389473
Contig ID	15957_1.R1084
5'-most EST	g2427777
Method	BLASTX
NCBI GI	g2708532
BLAST score	1013
E value	1.0e-110
Match length	285
% identity	65
NCBI Description	(AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No.	389474
Contig ID	15960_1.R1084
5'-most EST	uC-osflcyp017b10b1
Method	BLASTX
NCBI GI	g4314370
BLAST score	744
E value	4.0e-79
Match length	183
% identity	75
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389475
Contig ID	15961_1.R1084
5'-most EST	g4881142
Method	BLASTX
NCBI GI	g2244975
BLAST score	827
E value	1.0e-88
Match length	205
% identity	77
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389476
Contig ID	15973_1.R1084
5'-most EST	uC-osrocyp027e05b1
Method	BLASTX
NCBI GI	g2827139
BLAST score	1339
E value	1.0e-148
Match length	281
% identity	85
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568.1_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	389477
Contig ID	15974_1.R1084

5'-most EST	uC-osroM202031e05b1
Seq. No.	389478
Contig ID	15977_1.R1084
5'-most EST	LIB3433-051-P1-K1-C12
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	7.0e-10
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	389479
Contig ID	15982_1.R1084
5'-most EST	LIB3434-025-P1-K1-D6
Method	BLASTX
NCBI GI	g5051780
BLAST score	453
E value	8.0e-66
Match length	180
% identity	68
NCBI Description	(AL078637) putative protein [Arabidopsis thaliana]
Seq. No.	389480
Contig ID	15984_1.R1084
5'-most EST	LIB3433-032-P1-K1-E11
Method	BLASTX
NCBI GI	g2462834
BLAST score	214
E value	5.0e-17
Match length	95
% identity	45
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.	389481
Contig ID	15986_1.R1084
5'-most EST	uC-osflm202111b07b1
Method	BLASTX
NCBI GI	g1947015
BLAST score	509
E value	2.0e-51
Match length	185
% identity	52
NCBI Description	(AF000263) Similar to phenylalanyl-tRNA synthetase; coded for by C. elegans cDNA yk174a7.3; coded for by C. elegans cDNA yk174a7.5; coded for by C. elegans cDNA CEESP75F; coded for by C. elegans cDNA CEESV94F; coded for by C. elegans cDNA CE
Seq. No.	389482
Contig ID	15990_1.R1084
5'-most EST	uC-osflM202040c01b1
Seq. No.	389483
Contig ID	16001_1.R1084
5'-most EST	LIB3433-032-P1-K1-G3

Seq. No.	389484
Contig ID	16007_1.R1084
5'-most EST	LIB3433-032-P1-K1-H11
Method	BLASTX
NCBI GI	g2760844
BLAST score	463
E value	4.0e-46
Match length	135
% identity	62
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389485
Contig ID	16011_1.R1084
5'-most EST	LIB3433-032-P1-K1-H7
Method	BLASTX
NCBI GI	g229737
BLAST score	441
E value	2.0e-43
Match length	110
% identity	75
NCBI Description	Cytochrome c

Seq. No.	389486
Contig ID	16015_1.R1084
5'-most EST	LIB3433-033-P1-K1-A11

Seq. No.	389487
Contig ID	16016_1.R1084
5'-most EST	LIB3434-046-P1-K1-D8
Method	BLASTX
NCBI GI	g5803253
BLAST score	250
E value	8.0e-21
Match length	208
% identity	26
NCBI Description	(AP000399) ESTs AU068856(C50756),AU077979(C61370) correspond to a region of the predicted gene; similar to serine protease (AF097709) [Oryza sativa]

Seq. No.	389488
Contig ID	16017_1.R1084
5'-most EST	LIB3475-010-P1-K1-F2

Seq. No.	389489
Contig ID	16018_1.R1084
5'-most EST	g2275898
Method	BLASTN
NCBI GI	g1808687
BLAST score	87
E value	1.0e-40
Match length	236
% identity	89
NCBI Description	S.stapfianus pSD.13 mRNA

Seq. No.	389490
Contig ID	16019_1.R1084

5'-most EST	LIB3434-055-P1-K1-B9
Method	BLASTX
NCBI GI	g1360090
BLAST score	322
E value	7.0e-56
Match length	203
% identity	58
NCBI Description	(X95576) C1C-Nt1 [Nicotiana tabacum]

Seq. No.	389491
Contig ID	16021_1.R1084
5'-most EST	LIB3433-033-P1-K1-A7

Seq. No.	389492
Contig ID	16026_1.R1084
5'-most EST	g3763305

Seq. No.	389493
Contig ID	16027_1.R1084
5'-most EST	uC-osroM202034b07b1
Method	BLASTX
NCBI GI	g3757527
BLAST score	501
E value	2.0e-50
Match length	105
% identity	83
NCBI Description	(AC005167) putative ribosomal protein L27 [Arabidopsis thaliana]

Seq. No.	389494
Contig ID	16033_1.R1084
5'-most EST	LIB3433-033-P1-K1-B7

Seq. No.	389495
Contig ID	16038_1.R1084
5'-most EST	LIB3433-033-P1-K1-C11

Seq. No.	389496
Contig ID	16043_1.R1084
5'-most EST	g5002757
Method	BLASTX
NCBI GI	g1890573
BLAST score	1154
E value	1.0e-126
Match length	264
% identity	79
NCBI Description	(X93173) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]

Seq. No.	389497
Contig ID	16044_1.R1084
5'-most EST	g2798446
Method	BLASTX
NCBI GI	g5596484
BLAST score	1047
E value	1.0e-151
Match length	444

% identity	65
NCBI Description	(AL096882) beta-adaptin-like protein [Arabidopsis thaliana]

Seq. No.	389498
Contig ID	16044_2.R1084
5'-most EST	uC-osrocyp009b07b1
Method	BLASTX
NCBI GI	g5596484
BLAST score	1170
E value	1.0e-131
Match length	255
% identity	93
NCBI Description	(AL096882) beta-adaptin-like protein [Arabidopsis thaliana]

Seq. No.	389499
Contig ID	16049_1.R1084
5'-most EST	g3766844
Method	BLASTX
NCBI GI	g4490317
BLAST score	176
E value	3.0e-16
Match length	102
% identity	49
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	389500
Contig ID	16053_1.R1084
5'-most EST	g571772

Seq. No.	389501
Contig ID	16055_1.R1084
5'-most EST	LIB3433-033-P1-K1-D8

Seq. No.	389502
Contig ID	16057_1.R1084
5'-most EST	LIB3433-033-P1-K1-E1
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	46
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389503
Contig ID	16061_1.R1084
5'-most EST	LIB3433-033-P1-K1-E2
Method	BLASTX
NCBI GI	g4115377
BLAST score	754
E value	3.0e-80
Match length	187
% identity	76
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	389504
Contig ID	16065_1.R1084

5'-most EST	uC-osroM202033g06a1
Seq. No.	389505
Contig ID	16071_1.R1084
5'-most EST	LIB3433-033-P1-K1-F12
Method	BLASTX
NCBI GI	g2506825
BLAST score	1091
E value	1.0e-119
Match length	259
% identity	77
NCBI Description	LIPOXYGENASE 1 >gi_532572 (L35931) lipoxygenase 1 [Hordeum vulgare] >gi_1094924_prf__2107185A lipoxygenase [Hordeum vulgare]
Seq. No.	389506
Contig ID	16072_1.R1084
5'-most EST	LIB3433-033-P1-K1-F2
Seq. No.	389507
Contig ID	16075_1.R1084
5'-most EST	uC-osf1cyp085d02b1
Seq. No.	389508
Contig ID	16076_1.R1084
5'-most EST	LIB3433-033-P1-K1-F8
Seq. No.	389509
Contig ID	16077_1.R1084
5'-most EST	uC-osroM202014a03b1
Seq. No.	389510
Contig ID	16082_1.R1084
5'-most EST	uC-osroM202007a06b1
Seq. No.	389511
Contig ID	16082_2.R1084
5'-most EST	g426385
Seq. No.	389512
Contig ID	16082_4.R1084
5'-most EST	g287158
Seq. No.	389513
Contig ID	16083_1.R1084
5'-most EST	LIB3433-033-P1-K1-G3
Seq. No.	389514
Contig ID	16089_1.R1084
5'-most EST	g4881016
Method	BLASTX
NCBI GI	g4454464
BLAST score	644
E value	3.0e-67
Match length	152
% identity	78
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	389515
Contig ID	16092_1.R1084
5'-most EST	LIB3433-033-P1-K1-H12
Method	BLASTX
NCBI GI	g4836904
BLAST score	808
E value	2.0e-86
Match length	193
% identity	78
NCBI Description	(AC007369) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	389516
Contig ID	16094_1.R1084
5'-most EST	g2428244

Seq. No.	389517
Contig ID	16097_1.R1084
5'-most EST	LIB3433-033-P1-K1-H6

Seq. No.	389518
Contig ID	16101_1.R1084
5'-most EST	g2431119
Method	BLASTX
NCBI GI	g3386565
BLAST score	786
E value	1.0e-101
Match length	223
% identity	79
NCBI Description	(AF079588) 1-aminocyclopropane-1-carboxylate oxidase [Sorghum bicolor]

Seq. No.	389519
Contig ID	16106_1.R1084
5'-most EST	LIB3433-034-P1-K1-A5

Seq. No.	389520
Contig ID	16112_1.R1084
5'-most EST	LIB3433-034-P1-K1-B11
Method	BLASTX
NCBI GI	g1708794
BLAST score	289
E value	8.0e-26
Match length	107
% identity	51
NCBI Description	GTP-BINDING PROTEIN LEPA >gi_1122398_emb_CAA62842_ (X91655) lepA [Bacillus subtilis] >gi_1303804_dbj_BAA12460_ (D84432) YqeQ [Bacillus subtilis] >gi_2634997_emb_CAB14493_ (Z99117) GTP-binding protein [Bacillus subtilis]

Seq. No.	389521
Contig ID	16122_1.R1084
5'-most EST	LIB3433-023-P1-K1-B2
Method	BLASTX
NCBI GI	g4468798
BLAST score	568

E value 2.0e-66
Match length 231
% identity 57
NCBI Description (AJ010440) GST7 protein [Zea mays]

Seq. No. 389522
Contig ID 16123_1.R1084
5'-most EST LIB3433-025-P1-K1-D1
Method BLASTX
NCBI GI g2708749
BLAST score 213
E value 8.0e-17
Match length 95
% identity 51
NCBI Description (AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No. 389523
Contig ID 16124_1.R1084
5'-most EST LIB3433-034-P1-K1-C11

Seq. No. 389524
Contig ID 16127_1.R1084
5'-most EST uC-osflcyp155c02b1

Seq. No. 389525
Contig ID 16132_1.R1084
5'-most EST LIB3433-026-P1-K1-A11
Method BLASTX
NCBI GI g4204265
BLAST score 772
E value 8.0e-82
Match length 193
% identity 74
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 389526
Contig ID 16132_2.R1084
5'-most EST g4715063
Method BLASTX
NCBI GI g4204265
BLAST score 162
E value 6.0e-17
Match length 156
% identity 39
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 389527
Contig ID 16133_1.R1084
5'-most EST LIB3433-034-P1-K1-C9
Method BLASTX
NCBI GI g4454484
BLAST score 390
E value 1.0e-37
Match length 136
% identity 56
NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No.	389528
Contig ID	16142_1.R1084
5'-most EST	g4714352
Method	BLASTX
NCBI GI	g4678332
BLAST score	451
E value	5.0e-63
Match length	236
% identity	50
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	389529
Contig ID	16143_1.R1084
5'-most EST	LIB3433-034-P1-K1-D7
Method	BLASTX
NCBI GI	g4490325
BLAST score	201
E value	3.0e-15
Match length	67
% identity	60
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389530
Contig ID	16145_1.R1084
5'-most EST	LIB3433-034-P1-K1-D9
Method	BLASTX
NCBI GI	g3763940
BLAST score	343
E value	1.0e-35
Match length	132
% identity	62
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389531
Contig ID	16146_1.R1084
5'-most EST	uC-osroM202032c11b1

Seq. No.	389532
Contig ID	16148_1.R1084
5'-most EST	g1631545
Method	BLASTX
NCBI GI	g2505940
BLAST score	481
E value	1.0e-114
Match length	303
% identity	71
NCBI Description	(Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]

Seq. No.	389533
Contig ID	16148_2.R1084
5'-most EST	g5667465
Method	BLASTX
NCBI GI	g2505940
BLAST score	419

E value	4.0e-41
Match length	121
% identity	73
NCBI Description	(Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]

Seq. No.	389534
Contig ID	16152_1.R1084
5'-most EST	LIB3433-034-P1-K1-E4

Seq. No.	389535
Contig ID	16155_1.R1084
5'-most EST	LIB3433-034-P1-K1-E7
Method	BLASTX
NCBI GI	g4154279
BLAST score	284
E value	3.0e-40
Match length	124
% identity	67
NCBI Description	(AF082346) C13 endopeptidase NP1 precursor [Hordeum vulgare]

Seq. No.	389536
Contig ID	16160_1.R1084
5'-most EST	LIB3433-034-P1-K1-F2

Seq. No.	389537
Contig ID	16161_1.R1084
5'-most EST	LIB3433-034-P1-K1-F3

Seq. No.	389538
Contig ID	16163_1.R1084
5'-most EST	g701003

Seq. No.	389539
Contig ID	16164_1.R1084
5'-most EST	LIB3433-034-P1-K1-F6
Method	BLASTX
NCBI GI	g2117615
BLAST score	165
E value	5.0e-11
Match length	30
% identity	93
NCBI Description	catalase - Campylobacter jejuni >gi_2120538_pir__S71937 catalase - Campylobacter jejuni >gi_984737_emb_CAA59444_ (X85130) catalase [Campylobacter jejuni]

Seq. No.	389540
Contig ID	16165_1.R1084
5'-most EST	LIB3433-034-P1-K1-F7
Method	BLASTX
NCBI GI	g2118425
BLAST score	243
E value	2.0e-20
Match length	60
% identity	80
NCBI Description	subtilisin/chymotrypsin inhibitor - maize >gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea

mays] >gi_475922_emb_CAA49593_ (X69972) proteinase inhibitor [Zea mays] >gi_559538_emb_CAA57677_ (X82187) substilin /chymotrypsin-like inhibitor [Zea mays]

Seq. No.	389541
Contig ID	16165_2.R1084
5'-most EST	LIB3433-018-Q6-K6-E3
Method	BLASTX
NCBI GI	g2118425
BLAST score	192
E value	2.0e-14
Match length	62
% identity	69
NCBI Description	subtilisin/chymotrypsin inhibitor - maize >gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea mays] >gi_475922_emb_CAA49593_ (X69972) proteinase inhibitor [Zea mays] >gi_559538_emb_CAA57677_ (X82187) substilin /chymotrypsin-like inhibitor [Zea mays]

Seq. No.	389542
Contig ID	16167_1.R1084
5'-most EST	LIB3433-058-P1-K1-B10
Method	BLASTX
NCBI GI	g4322346
BLAST score	200
E value	2.0e-27
Match length	180
% identity	44
NCBI Description	(AF081825) sodium-dependent high-affinity dicarboxylate transporter [Rattus norvegicus] >gi_4837725_gb_AAD30657.1_AF080451_1 (AF080451) sodium-dependent dicarboxylate transporter SDCT2 [Rattus norvegicus]

Seq. No.	389543
Contig ID	16169_1.R1084
5'-most EST	LIB3433-034-P1-K1-G10
Method	BLASTX
NCBI GI	g3913426
BLAST score	263
E value	4.0e-35
Match length	152
% identity	61
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532048_emb_CAA69074_ (Y07766) S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No.	389544
Contig ID	16175_1.R1084
5'-most EST	g428955
Method	BLASTX
NCBI GI	g6056209
BLAST score	383
E value	1.0e-36
Match length	84
% identity	83
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	389545
Contig ID	16179_2.R1084
5'-most EST	LIB3433-034-P1-K1-H3

Seq. No.	389546
Contig ID	16180_1.R1084
5'-most EST	LIB3433-034-P1-K1-H5

Seq. No.	389547
Contig ID	16190_1.R1084
5'-most EST	g2428163

Seq. No.	389548
Contig ID	16201_1.R1084
5'-most EST	LIB3433-035-P1-K1-B5
Method	BLASTX
NCBI GI	g2982455
BLAST score	525
E value	3.0e-62
Match length	160
% identity	76
NCBI Description	(AL022223) putative uracil phosphoribosyl transferase [Arabidopsis thaliana]

Seq. No.	389549
Contig ID	16203_1.R1084
5'-most EST	LIB3433-035-P1-K1-B8

Seq. No.	389550
Contig ID	16208_1.R1084
5'-most EST	LIB3433-035-P1-K1-C12
Method	BLASTN
NCBI GI	g4733953
BLAST score	38
E value	1.0e-11
Match length	94
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	389551
Contig ID	16210_1.R1084
5'-most EST	LIB3433-035-P1-K1-C3

Seq. No.	389552
Contig ID	16211_1.R1084
5'-most EST	LIB3477-009-P1-K1-A10
Method	BLASTX
NCBI GI	g5091607
BLAST score	253
E value	1.0e-21
Match length	50
% identity	94
NCBI Description	(AC007858) Contains similarity to gb_CAB16841 trichohyalin like protein from Arabidopsis thaliana. [Oryza sativa]

Seq. No.	389553
Contig ID	16215_1.R1084
5'-most EST	LIB3433-035-P1-K1-C8
Method	BLASTX
NCBI GI	g1097876
BLAST score	149
E value	2.0e-09
Match length	105
% identity	39
NCBI Description	peroxidase:ISOTYPE=RPN [Oryza sativa]

Seq. No.	389554
Contig ID	16225_1.R1084
5'-most EST	LIB3433-035-P1-K1-D7
Method	BLASTX
NCBI GI	g5689035
BLAST score	776
E value	1.0e-82
Match length	225
% identity	64
NCBI Description	(AB022053) prolyl oligopeptidase [Mus musculus]

Seq. No.	389555
Contig ID	16227_1.R1084
5'-most EST	LIB3479-012-Q6-K1-G6

Seq. No.	389556
Contig ID	16229_1.R1084
5'-most EST	LIB3433-035-P1-K1-E11

Seq. No.	389557
Contig ID	16232_1.R1084
5'-most EST	LIB3433-035-P1-K1-E3
Method	BLASTX
NCBI GI	g4455323
BLAST score	429
E value	2.0e-57
Match length	208
% identity	55
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	389558
Contig ID	16238_1.R1084
5'-most EST	g4716675
Method	BLASTX
NCBI GI	g2702279
BLAST score	220
E value	1.0e-17
Match length	98
% identity	49
NCBI Description	(AC003033) putative phosphate transporter [Arabidopsis thaliana] >gi_2780345_dbj_BAA24280_ (AB000093) inorganic phosphate transporter [Arabidopsis thaliana] >gi_2914691 (AC003974) putative phosphate transporter [Arabidopsis thaliana]

Seq. No.	389559
Contig ID	16240_1.R1084
5'-most EST	LIB3433-035-P1-K1-F2

Seq. No.	389560
Contig ID	16251_1.R1084
5'-most EST	LIB3433-035-P1-K1-G12
Method	BLASTX
NCBI GI	g2583128
BLAST score	207
E value	6.0e-16
Match length	85
% identity	47
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389561
Contig ID	16253_1.R1084
5'-most EST	uC-osroM202013h04b1
Method	BLASTX
NCBI GI	g99733
BLAST score	659
E value	5.0e-69
Match length	230
% identity	62
NCBI Description	hypothetical protein H1flk - Arabidopsis thaliana (fragment) >gi_16482_emb_CAA44318_ (X62461) H1flk [Arabidopsis thaliana]

Seq. No.	389562
Contig ID	16254_1.R1084
5'-most EST	uC-osroM202011g09b1

Seq. No.	389563
Contig ID	16260_1.R1084
5'-most EST	LIB3477-002-P1-K1-H3
Method	BLASTX
NCBI GI	g3063701
BLAST score	472
E value	4.0e-47
Match length	142
% identity	70
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	389564
Contig ID	16261_1.R1084
5'-most EST	uC-osrocyp004e04a1

Seq. No.	389565
Contig ID	16263_1.R1084
5'-most EST	LIB3433-035-P1-K1-H3
Method	BLASTX
NCBI GI	g2132388
BLAST score	261
E value	3.0e-22
Match length	158
% identity	42
NCBI Description	PHO85 protein - yeast (Saccharomyces cerevisiae)

>gi_1163103 (U43503) Lph16p [Saccharomyces cerevisiae]

Seq. No.	389566
Contig ID	16265_1.R1084
5'-most EST	LIB3433-035-P1-K1-H5
Method	BLASTX
NCBI GI	g5729706
BLAST score	171
E value	5.0e-12
Match length	82
% identity	35
NCBI Description	(AC007927) unknown protein [Arabidopsis thaliana]

Seq. No.	389567
Contig ID	16267_1.R1084
5'-most EST	uC-osflcyp034h05b1

Seq. No.	389568
Contig ID	16268_1.R1084
5'-most EST	g2317404
Method	BLASTX
NCBI GI	g5091508
BLAST score	530
E value	3.0e-89
Match length	202
% identity	83
NCBI Description	(AB023482) ESTs C22458(C62866),C22459(C62866) correspond to a region of the predicted gene.; Similar to genomic sequence of Arabidopsis thaliana BAC F8A5, complete sequence.(AC002292) [Oryza sativa]

Seq. No.	389569
Contig ID	16273_1.R1084
5'-most EST	g2800609
Method	BLASTX
NCBI GI	g121695
BLAST score	294
E value	3.0e-26
Match length	112
% identity	56
NCBI Description	GLUTATHIONE S-TRANSFERASE I (GST-I) (GST-29) (GST CLASS-PHI) >gi_22315_emb_CAA29928_ (X06754) GST I (AA 1-214) [Zea mays]

Seq. No.	389570
Contig ID	16273_2.R1084
5'-most EST	g2312063
Method	BLASTX
NCBI GI	g1170092
BLAST score	637
E value	2.0e-66
Match length	206
% identity	60
NCBI Description	GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (GST CLASS PHI) >gi_1076807_pir__S52037 glutathione transferase (EC 2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione S-transferase IV [Zea mays] >gi_695789_emb_CAA56047_

	(X79515) glutathione transferase [Zea mays] >gi_1094866_prf__2106424A glutathione S-transferase:ISOTYPE=IV [Zea mays]
Seq. No.	389571
Contig ID	16283_1.R1084
5'-most EST	g428245
Method	BLASTX
NCBI GI	g2129473
BLAST score	334
E value	1.0e-30
Match length	149
% identity	48
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.	389572
Contig ID	16290_1.R1084
5'-most EST	LIB3433-036-P1-K1-B8
Seq. No.	389573
Contig ID	16294_1.R1084
5'-most EST	LIB3433-036-P1-K1-C2
Method	BLASTX
NCBI GI	g1389835
BLAST score	329
E value	7.0e-37
Match length	201
% identity	48
NCBI Description	(U59284) Linum usitatissimum peroxidase (FLXPER3) mRNA, complete cds. [Linum usitatissimum]
Seq. No.	389574
Contig ID	16295_1.R1084
5'-most EST	uC-osflcyp144a09b1
Method	BLASTX
NCBI GI	g4586253
BLAST score	637
E value	4.0e-66
Match length	227
% identity	61
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]
Seq. No.	389575
Contig ID	16299_1.R1084
5'-most EST	g702854
Method	BLASTX
NCBI GI	g5053113
BLAST score	282
E value	1.0e-46
Match length	115
% identity	69
NCBI Description	(AF156101) phosphatase PP1 [Chlamydomonas reinhardtii]
Seq. No.	389576
Contig ID	16307_1.R1084
5'-most EST	LIB3433-022-P1-K1-E10

Seq. No.	389577
Contig ID	16308_1.R1084
5'-most EST	LIB3433-036-P1-K1-D5

Seq. No.	389578
Contig ID	16311_1.R1084
5'-most EST	uC-osroM202029b01b1
Method	BLASTX
NCBI GI	g1203832
BLAST score	2434
E value	0.0e+00
Match length	545
% identity	85
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No.	389579
Contig ID	16313_1.R1084
5'-most EST	LIB3433-036-P1-K1-E1

Seq. No.	389580
Contig ID	16323_1.R1084
5'-most EST	uC-osf1cyp014h10b1

Seq. No.	389581
Contig ID	16325_1.R1084
5'-most EST	LIB3433-036-P1-K1-F1
Method	BLASTN
NCBI GI	g4097013
BLAST score	38
E value	1.0e-11
Match length	41
% identity	98
NCBI Description	Expression vector pBMRz, complete cds

Seq. No.	389582
Contig ID	16325_2.R1084
5'-most EST	LIB3434-054-P1-K1-D7

Seq. No.	389583
Contig ID	16329_1.R1084
5'-most EST	LIB3433-036-P1-K1-F2
Method	BLASTX
NCBI GI	g3283072
BLAST score	127
E value	3.0e-13
Match length	88
% identity	48
NCBI Description	(AF056022) p60 katanin [Homo sapiens]

Seq. No.	389584
Contig ID	16330_1.R1084
5'-most EST	LIB3433-036-P1-K1-F3

Seq. No.	389585

Contig ID	16334_1.R1084
5'-most EST	LIB3434-014-P1-K1-A4

Seq. No.	389586
Contig ID	16335_1.R1084
5'-most EST	uC-osflM202052f07b1
Method	BLASTX
NCBI GI	g736721
BLAST score	451
E value	1.0e-44
Match length	156
% identity	59
NCBI Description	(D49833) stearoyl-acyl carrier protein desaturse [Sesamum indicum]

Seq. No.	389587
Contig ID	16335_2.R1084
5'-most EST	uC-osrocyp030f07b1
Method	BLASTX
NCBI GI	g4263704
BLAST score	372
E value	2.0e-35
Match length	190
% identity	41
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	389588
Contig ID	16340_1.R1084
5'-most EST	LIB3433-036-P1-K1-G12

Seq. No.	389589
Contig ID	16349_1.R1084
5'-most EST	g428923
Method	BLASTX
NCBI GI	g542176
BLAST score	750
E value	2.0e-79
Match length	260
% identity	61
NCBI Description	probable finger protein WZF1 - wheat >gi_485814_dbj_BAA03901_ (D16415) WZF1 [Triticum aestivum] >gi_485816_dbj_BAA03902_ (D16416) WZF1 [Triticum aestivum]

Seq. No.	389590
Contig ID	16361_1.R1084
5'-most EST	LIB3433-037-P1-K1-A2

Seq. No.	389591
Contig ID	16364_1.R1084
5'-most EST	uC-osflcyp008f04b1
Method	BLASTX
NCBI GI	g731529
BLAST score	156
E value	5.0e-10
Match length	120
% identity	34

NCBI Description	HYPOTHETICAL 92.5 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION >gi_1077719_pir__S50660 hypothetical protein YER157w - yeast (Saccharomyces cerevisiae) >gi_603397 (U18917) Yer157wp [Saccharomyces cerevisiae]

Seq. No.	389592
Contig ID	16366_1.R1084
5'-most EST	LIB3433-037-P1-K1-A7

Seq. No.	389593
Contig ID	16368_1.R1084
5'-most EST	LIB3433-037-P1-K1-B1
Method	BLASTX
NCBI GI	g3643596
BLAST score	402
E value	7.0e-39
Match length	124
% identity	64
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389594
Contig ID	16369_1.R1084
5'-most EST	LIB3433-060-P1-K1-E7
Method	BLASTX
NCBI GI	g2244840
BLAST score	165
E value	3.0e-11
Match length	113
% identity	37
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389595
Contig ID	16372_1.R1084
5'-most EST	LIB3433-017-Q6-K1-D2
Method	BLASTX
NCBI GI	g4874274
BLAST score	642
E value	2.0e-71
Match length	173
% identity	73
NCBI Description	(AC007354) Similar to gb_X02844 lipase precursor from Staphylococcus hyicus. ESTs gb_AI239406 and gb_T76725 come from this gene. [Arabidopsis thaliana]

Seq. No.	389596
Contig ID	16373_1.R1084
5'-most EST	LIB3433-040-P1-K1-H1
Method	BLASTX
NCBI GI	g5123712
BLAST score	521
E value	5.0e-53
Match length	138
% identity	68
NCBI Description	(AL079347) putative protein [Arabidopsis thaliana]

Seq. No.	389597
Contig ID	16375_1.R1084

5'-most EST	LIB3433-037-P1-K1-B6
Method	BLASTX
NCBI GI	g2317901
BLAST score	537
E value	5.0e-55
Match length	134
% identity	75
NCBI Description	(U89959) Similar to vesicle transport protein, PIR Accession Number A55931 [Arabidopsis thaliana]

Seq. No.	389598
Contig ID	16381_1.R1084
5'-most EST	LIB3433-037-P1-K1-C11
Method	BLASTX
NCBI GI	g4580397
BLAST score	308
E value	6.0e-28
Match length	183
% identity	36
NCBI Description	(AC007171) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	389599
Contig ID	16382_1.R1084
5'-most EST	LIB3433-037-P1-K1-C12
Method	BLASTX
NCBI GI	g2739376
BLAST score	865
E value	7.0e-93
Match length	270
% identity	60
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	389600
Contig ID	16389_1.R1084
5'-most EST	g3761075

Seq. No.	389601
Contig ID	16403_1.R1084
5'-most EST	g428282
Method	BLASTX
NCBI GI	g4006878
BLAST score	884
E value	4.0e-95
Match length	243
% identity	63
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	389602
Contig ID	16404_1.R1084
5'-most EST	LIB3433-037-P1-K1-E11

Seq. No.	389603
Contig ID	16410_1.R1084
5'-most EST	LIB3433-037-P1-K1-E6
Method	BLASTX
NCBI GI	g1854443
BLAST score	452

E value	2.0e-76
Match length	261
% identity	64
NCBI Description	(D83970) CPRD8 protein [Vigna unguiculata]

Seq. No.	389604
Contig ID	16410_2.R1084
5'-most EST	LIB3433-023-P1-K1-E6
Method	BLASTX
NCBI GI	g3882356
BLAST score	215
E value	2.0e-39
Match length	160
% identity	62
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana]

Seq. No.	389605
Contig ID	16413_1.R1084
5'-most EST	uC-osrocyp030h01b1
Method	BLASTX
NCBI GI	g4680199
BLAST score	174
E value	3.0e-12
Match length	100
% identity	33
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	389606
Contig ID	16416_1.R1084
5'-most EST	uC-osrocyp010e04b1
Method	BLASTX
NCBI GI	g2230757
BLAST score	666
E value	7.0e-70
Match length	196
% identity	66
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	389607
Contig ID	16421_1.R1084
5'-most EST	LIB3433-037-P1-K1-F5
Method	BLASTX
NCBI GI	g3075402
BLAST score	171
E value	6.0e-12
Match length	76
% identity	46
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	389608
Contig ID	16427_1.R1084
5'-most EST	LIB3477-001-P1-K1-G5
Method	BLASTX
NCBI GI	g2290382
BLAST score	159
E value	3.0e-10

Match length	90
% identity	41
NCBI Description	(U89985) serine/threonine protein phosphatase PPT1 [Neurospora crassa]

Seq. No.	389609
Contig ID	16429_1.R1084
5'-most EST	uC-osflcyp073h10b1
Method	BLASTX
NCBI GI	g719291
BLAST score	605
E value	1.0e-62
Match length	210
% identity	60
NCBI Description	(U19134) unknown [Arabidopsis thaliana] >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]

Seq. No.	389610
Contig ID	16437_1.R1084
5'-most EST	g4969326

Seq. No.	389611
Contig ID	16442_1.R1084
5'-most EST	g2312548
Method	BLASTX
NCBI GI	g3395431
BLAST score	185
E value	3.0e-13
Match length	75
% identity	47
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	389612
Contig ID	16447_1.R1084
5'-most EST	g3767738
Method	BLASTX
NCBI GI	g3695021
BLAST score	156
E value	3.0e-10
Match length	48
% identity	65
NCBI Description	(AF055849) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389613
Contig ID	16449_1.R1084
5'-most EST	uC-osroM202040b08b1
Method	BLASTX
NCBI GI	g2894599
BLAST score	446
E value	1.0e-43
Match length	248
% identity	46
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	389614
Contig ID	16451_1.R1084
5'-most EST	LIB3433-038-P1-K1-A6

Method	BLASTX
NCBI GI	g4895183
BLAST score	767
E value	2.0e-81
Match length	215
% identity	66
NCBI Description	(AC007661) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389615
Contig ID	16452_1.R1084
5'-most EST	uC-osflm202101c09b1
Method	BLASTX
NCBI GI	g4559380
BLAST score	1106
E value	1.0e-121
Match length	317
% identity	62
NCBI Description	(AC006526) putative auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	389616
Contig ID	16452_2.R1084
5'-most EST	LIB3433-038-P1-K1-A5
Method	BLASTX
NCBI GI	g4559380
BLAST score	295
E value	2.0e-26
Match length	92
% identity	61
NCBI Description	(AC006526) putative auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	389617
Contig ID	16455_1.R1084
5'-most EST	LIB3475-010-P1-K1-B12
Method	BLASTX
NCBI GI	g4335747
BLAST score	676
E value	5.0e-71
Match length	207
% identity	64
NCBI Description	(AC006284) putative A3 protein [Vigna unguiculata] (integral membrane protein) [Arabidopsis thaliana]

Seq. No.	389618
Contig ID	16462_1.R1084
5'-most EST	LIB3433-053-P1-K1-G5
Method	BLASTX
NCBI GI	g2914706
BLAST score	264
E value	6.0e-42
Match length	189
% identity	51
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	389619
Contig ID	16462_2.R1084

5'-most EST	g5002976
Method	BLASTX
NCBI GI	g2914706
BLAST score	410
E value	1.0e-39
Match length	161
% identity	50
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	389620
Contig ID	16462_3.R1084
5'-most EST	g2309714
Method	BLASTX
NCBI GI	g2924792
BLAST score	362
E value	3.0e-34
Match length	142
% identity	50
NCBI Description	(AC002334) similar to synaptobrevin [Arabidopsis thaliana]

Seq. No.	389621
Contig ID	16463_1.R1084
5'-most EST	LIB3433-038-P1-K1-B4

Seq. No.	389622
Contig ID	16474_1.R1084
5'-most EST	g2310756
Method	BLASTX
NCBI GI	g5091556
BLAST score	317
E value	7.0e-29
Match length	97
% identity	63
NCBI Description	(AC007067) T10O24.25 [Arabidopsis thaliana]

Seq. No.	389623
Contig ID	16488_1.R1084
5'-most EST	LIB3433-038-P1-K1-D7
Method	BLASTX
NCBI GI	g2459429
BLAST score	163
E value	3.0e-20
Match length	151
% identity	36
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	389624
Contig ID	16490_1.R1084
5'-most EST	LIB3433-045-P1-K1-G7
Method	BLASTX
NCBI GI	g4584525
BLAST score	392
E value	7.0e-38
Match length	96
% identity	74
NCBI Description	(AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	389625
Contig ID	16493_1.R1084
5'-most EST	LIB3433-045-P1-K1-E6
Method	BLASTX
NCBI GI	g2342690
BLAST score	447
E value	2.0e-44
Match length	146
% identity	59
NCBI Description	(AC000106) Similar to Homo copine I (gb_U83246). [Arabidopsis thaliana]

Seq. No.	389626
Contig ID	16494_1.R1084
5'-most EST	LIB3433-038-P1-K1-E4

Seq. No.	389627
Contig ID	16495_1.R1084
5'-most EST	LIB3433-038-P1-K1-E5
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	3.0e-11
Match length	37
% identity	60
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389628
Contig ID	16496_1.R1084
5'-most EST	g1854146
Method	BLASTX
NCBI GI	g3513727
BLAST score	489
E value	2.0e-52
Match length	198
% identity	34
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	389629
Contig ID	16497_1.R1084
5'-most EST	g3764122
Method	BLASTX
NCBI GI	g4090884
BLAST score	885
E value	3.0e-95
Match length	219
% identity	76
NCBI Description	(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]

Seq. No.	389630
Contig ID	16497_2.R1084

5'-most EST	g5003079
Method	BLASTX
NCBI GI	g2914706
BLAST score	609
E value	3.0e-63
Match length	125
% identity	89
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	389631
Contig ID	16498_1.R1084
5'-most EST	uC-osrocyp012g09b1
Method	BLASTX
NCBI GI	g5669093
BLAST score	223
E value	9.0e-19
Match length	166
% identity	36
NCBI Description	(AF130307) glutathione-dependent formaldehyde dehydrogenase [Acinetobacter baumannii]

Seq. No.	389632
Contig ID	16507_1.R1084
5'-most EST	uC-osflM202052b12b1
Method	BLASTX
NCBI GI	g4895238
BLAST score	454
E value	8.0e-45
Match length	214
% identity	50
NCBI Description	(AC007659) unknown protein [Arabidopsis thaliana]

Seq. No.	389633
Contig ID	16511_2.R1084
5'-most EST	uC-osflM2020117h04a1

Seq. No.	389634
Contig ID	16513_1.R1084
5'-most EST	LIB3434-019-P1-K1-H12
Method	BLASTX
NCBI GI	g4539009
BLAST score	545
E value	1.0e-55
Match length	154
% identity	66
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	389635
Contig ID	16516_1.R1084
5'-most EST	LIB3479-005-Q6-K1-B6
Method	BLASTX
NCBI GI	g1076316
BLAST score	197
E value	1.0e-14
Match length	172
% identity	29
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana

>gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	389636
Contig ID	16522_1.R1084
5'-most EST	g427246
Method	BLASTX
NCBI GI	g3885334
BLAST score	245
E value	2.0e-32
Match length	100
% identity	73
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	389637
Contig ID	16528_1.R1084
5'-most EST	g4878245

Seq. No.	389638
Contig ID	16535_1.R1084
5'-most EST	uC-osrocyp033d11b1
Method	BLASTX
NCBI GI	g4914332
BLAST score	647
E value	4.0e-67
Match length	347
% identity	48
NCBI Description	(AC005489) F14N23.18 [Arabidopsis thaliana]

Seq. No.	389639
Contig ID	16540_1.R1084
5'-most EST	LIB3433-039-P1-K1-A9
Method	BLASTN
NCBI GI	g4206065
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Homo sapiens map 7qter; 41.64cR from WI-8540 repeat region, complete sequence

Seq. No.	389640
Contig ID	16543_1.R1084
5'-most EST	g2800392
Method	BLASTX
NCBI GI	g4584546
BLAST score	500
E value	3.0e-50
Match length	140
% identity	62
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	389641
Contig ID	16547_1.R1084
5'-most EST	LIB3433-039-P1-K1-B1
Method	BLASTX

NCBI GI	g3249066
BLAST score	415
E value	3.0e-40
Match length	200
% identity	49
NCBI Description	(AC004473) Similar to S. cerevisiae SIK1P protein gb_984964. ESTs gb_F15433 and gb_AA395158 come from this gene. [Arabidopsis thaliana]

Seq. No.	389642
Contig ID	16548_1.R1084
5'-most EST	LIB3433-039-P1-K1-B10
Method	BLASTX
NCBI GI	g4371292
BLAST score	288
E value	1.0e-25
Match length	123
% identity	48
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	389643
Contig ID	16558_1.R1084
5'-most EST	LIB3433-016-Q6-K6-A3

Seq. No.	389644
Contig ID	16558_2.R1084
5'-most EST	uC-osroM202011e04a1

Seq. No.	389645
Contig ID	16575_1.R1084
5'-most EST	LIB3433-039-P1-K1-D3
Method	BLASTX
NCBI GI	g3551958
BLAST score	159
E value	1.0e-10
Match length	47
% identity	62
NCBI Description	(AF082032) senescence-associated protein 12 [Hemerocallis hybrid cultivar]

Seq. No.	389646
Contig ID	16576_1.R1084
5'-most EST	LIB3433-039-P1-K1-D4
Method	BLASTX
NCBI GI	g416564
BLAST score	893
E value	1.0e-112
Match length	221
% identity	88
NCBI Description	ABCISIC ACID-INDUCIBLE PROTEIN KINASE >gi_422013_pir__A46408 abscisic acid-inducible serine/threonine protein kinase homolog - wheat (fragment) >gi_170664_gb_AAA96325.1_AAA96325 (M94726) protein kinase [Triticum aestivum]

Seq. No.	389647
Contig ID	16577_1.R1084

5'-most EST	g3090518
Seq. No.	389648
Contig ID	16600_1.R1084
5'-most EST	LIB3433-039-P1-K1-F4
Method	BLASTX
NCBI GI	g730557
BLAST score	454
E value	6.0e-45
Match length	117
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_2119150_pir__S60476 ribosomal protein L34 - garden pea >gi_498908 (U10047) ribosomal protein L34 homolog [Pisum sativum]
Seq. No.	389649
Contig ID	16605_1.R1084
5'-most EST	g3763522
Method	BLASTX
NCBI GI	g113357
BLAST score	816
E value	2.0e-87
Match length	243
% identity	57
NCBI Description	ALCOHOL DEHYDROGENASE 1 >gi_82347_pir__S01893 alcohol dehydrogenase (EC 1.1.1.1) 1 - barley >gi_18875_emb_CAA30600_ (X07774) alcohol dehydrogenase 1 (AA 1-379) [Hordeum vulgare] >gi_226107_prf__1410317A alcohol dehydrogenase 1 [Hordeum vulgare var. distichum]
Seq. No.	389650
Contig ID	16607_1.R1084
5'-most EST	uC-osflcyp097c02b1
Method	BLASTX
NCBI GI	g2130080
BLAST score	210
E value	2.0e-16
Match length	93
% identity	44
NCBI Description	Nramp1 protein - rice >gi_1470320_bbs_177441 (S81897) OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa]
Seq. No.	389651
Contig ID	16611_1.R1084
5'-most EST	LIB3434-013-P1-K1-H7
Method	BLASTX
NCBI GI	g478409
BLAST score	562
E value	2.0e-57
Match length	185
% identity	58
NCBI Description	peroxidase (EC 1.11.1.7), cationic - adzuki bean >gi_218328_dbj_BAA01950_ (D11337) peroxidase [Vigna angularis]

Seq. No.	389652
Contig ID	16612_1.R1084
5'-most EST	LIB3433-039-P1-K1-G4
Method	BLASTX
NCBI GI	g4972072
BLAST score	270
E value	4.0e-23
Match length	141
% identity	44
NCBI Description	(AL078467) putative RING zinc finger protein [Arabidopsis thaliana]

Seq. No.	389653
Contig ID	16614_1.R1084
5'-most EST	g3760574

Seq. No.	389654
Contig ID	16620_1.R1084
5'-most EST	LIB3434-057-P1-K1-F4
Method	BLASTX
NCBI GI	g3395427
BLAST score	171
E value	5.0e-12
Match length	75
% identity	48
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	389655
Contig ID	16622_1.R1084
5'-most EST	g3768371

Seq. No.	389656
Contig ID	16622_2.R1084
5'-most EST	LIB3433-039-P1-K1-H4
Method	BLASTX
NCBI GI	g2492952
BLAST score	416
E value	8.0e-62
Match length	181
% identity	70
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	389657
Contig ID	16622_3.R1084
5'-most EST	g2442693
Method	BLASTX
NCBI GI	g2492953
BLAST score	360
E value	5.0e-34
Match length	162
% identity	66
NCBI Description	CHORISMATE SYNTHASE 2 PRECURSOR

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 2)
>gi_542027_pir__S40409 chorismate synthase (EC 4.6.1.4) 2
precursor - tomato >gi_410484_emb_CAA79854_ (Z21791)
chorismate synthase 2 [Lycopersicon esculentum]

Seq. No.	389658
Contig ID	16624_1.R1084
5'-most EST	g4715746
Method	BLASTX
NCBI GI	g1806144
BLAST score	700
E value	1.0e-109
Match length	350
% identity	64
NCBI Description	(X97316) cdc2MsE [Medicago sativa]

Seq. No.	389659
Contig ID	16633_1.R1084
5'-most EST	uC-osflcyp152d10a1
Method	BLASTX
NCBI GI	g1752734
BLAST score	180
E value	5.0e-13
Match length	42
% identity	79
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No.	389660
Contig ID	16634_1.R1084
5'-most EST	LIB3433-040-P1-K1-A3

Seq. No.	389661
Contig ID	16636_1.R1084
5'-most EST	LIB3433-040-P1-K1-A5

Seq. No.	389662
Contig ID	16639_1.R1084
5'-most EST	g4714619

Seq. No.	389663
Contig ID	16640_1.R1084
5'-most EST	g428826
Method	BLASTX
NCBI GI	g6041796
BLAST score	276
E value	5.0e-24
Match length	174
% identity	39
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]

Seq. No.	389664
Contig ID	16649_1.R1084
5'-most EST	LIB3433-040-P1-K1-B8

Seq. No.	389665
Contig ID	16650_1.R1084
5'-most EST	LIB3477-007-P1-K1-D2

Method	BLASTX
NCBI GI	g5080816
BLAST score	730
E value	2.0e-77
Match length	185
% identity	71
NCBI Description	(AC007258) Putative ATPase [Arabidopsis thaliana]

Seq. No.	389666
Contig ID	16651_1.R1084
5'-most EST	LIB3433-040-P1-K1-C1
Method	BLASTX
NCBI GI	g5922612
BLAST score	649
E value	7.0e-68
Match length	138
% identity	56
NCBI Description	(AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa]

Seq. No.	389667
Contig ID	16651_2.R1084
5'-most EST	uC-osflcyp102c03a1
Method	BLASTN
NCBI GI	g5922603
BLAST score	283
E value	1.0e-158
Match length	331
% identity	97
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No.	389668
Contig ID	16664_1.R1084
5'-most EST	LIB3433-040-P1-K1-D11
Method	BLASTX
NCBI GI	g2660670
BLAST score	317
E value	6.0e-29
Match length	95
% identity	65
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	389669
Contig ID	16665_1.R1084
5'-most EST	LIB3434-025-P1-K1-G8
Method	BLASTX
NCBI GI	g2583133
BLAST score	734
E value	1.0e-77
Match length	218
% identity	68
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	389670

Contig ID	16667_1.R1084
5'-most EST	uC-osroM202038h05b1
Method	BLASTX
NCBI GI	g6041850
BLAST score	416
E value	2.0e-40
Match length	179
% identity	28
NCBI Description	(AC009853) unknown protein [Arabidopsis thaliana]

Seq. No.	389671
Contig ID	16675_1.R1084
5'-most EST	g702005

Seq. No.	389672
Contig ID	16684_1.R1084
5'-most EST	LIB3433-040-P1-K1-E9
Method	BLASTX
NCBI GI	g3668097
BLAST score	554
E value	1.0e-56
Match length	143
% identity	75
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	389673
Contig ID	16687_1.R1084
5'-most EST	LIB3433-040-P1-K1-F11
Method	BLASTX
NCBI GI	g4186184
BLAST score	199
E value	4.0e-15
Match length	134
% identity	31
NCBI Description	(AF111168) unknown [Homo sapiens] >gi_5262359_emb_CAB45684.1_ (AJ243310) C14orf3 protein [Homo sapiens]

Seq. No.	389674
Contig ID	16688_1.R1084
5'-most EST	g2309912
Method	BLASTX
NCBI GI	g5902371
BLAST score	559
E value	6.0e-57
Match length	145
% identity	68
NCBI Description	(AC009322) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	389675
Contig ID	16691_1.R1084
5'-most EST	g426850
Method	BLASTX
NCBI GI	g4585976
BLAST score	558
E value	4.0e-57

Match length	150
% identity	68
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	389676
Contig ID	16692_1.R1084
5'-most EST	g3763181

Seq. No.	389677
Contig ID	16693_1.R1084
5'-most EST	LIB3433-051-P1-K1-E6
Method	BLASTX
NCBI GI	g2809251
BLAST score	449
E value	2.0e-51
Match length	181
% identity	58
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No.	389678
Contig ID	16696_1.R1084
5'-most EST	LIB3479-006-Q6-K1-B12
Method	BLASTX
NCBI GI	g3790587
BLAST score	198
E value	1.0e-14
Match length	198
% identity	37
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No.	389679
Contig ID	16696_2.R1084
5'-most EST	g2428274
Method	BLASTX
NCBI GI	g3790587
BLAST score	557
E value	5.0e-57
Match length	163
% identity	72
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No.	389680
Contig ID	16697_1.R1084
5'-most EST	uC-osflm202102h09b1
Method	BLASTX
NCBI GI	g2673920
BLAST score	164
E value	5.0e-11
Match length	91
% identity	47
NCBI Description	(AC002561) similar to Drosophila couch potato protein [Arabidopsis thaliana]

Seq. No.	389681
Contig ID	16704_1.R1084

5'-most EST	g2427738
Method	BLASTX
NCBI GI	g1903364
BLAST score	284
E value	4.0e-25
Match length	106
% identity	53
NCBI Description	(AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No.	389682
Contig ID	16707_1.R1084
5'-most EST	LIB3433-040-P1-K1-G9

Seq. No.	389683
Contig ID	16713_1.R1084
5'-most EST	g5039041
Method	BLASTX
NCBI GI	g2239083
BLAST score	184
E value	2.0e-13
Match length	70
% identity	44
NCBI Description	(Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	389684
Contig ID	16717_1.R1084
5'-most EST	LIB3433-040-P1-K1-H9

Seq. No.	389685
Contig ID	16721_2.R1084
5'-most EST	LIB3433-041-P1-K1-A12
Method	BLASTX
NCBI GI	g4454033
BLAST score	572
E value	1.0e-58
Match length	236
% identity	50
NCBI Description	(AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No.	389686
Contig ID	16724_1.R1084
5'-most EST	uC-osroM202001c03b1
Method	BLASTX
NCBI GI	g283391
BLAST score	317
E value	6.0e-47
Match length	174
% identity	53
NCBI Description	ADP-ribosylation factor - yeast (Candida albicans) >gi_254344_bbs_111914 (S43354) ADP-ribosylation factor, Arf [Candida albicans, Peptide, 179 aa] [Candida albicans]

Seq. No.	389687
Contig ID	16731_1.R1084
5'-most EST	uC-osrocyp027g01b1
Method	BLASTX
NCBI GI	g2335201
BLAST score	1117
E value	1.0e-122
Match length	281
% identity	76
NCBI Description	(AF013581) chitinase [Oryza sativa]

Seq. No.	389688
Contig ID	16732_1.R1084
5'-most EST	LIB3479-001-Q6-K1-B5
Method	BLASTX
NCBI GI	g3252815
BLAST score	478
E value	6.0e-48
Match length	118
% identity	72
NCBI Description	(AC004705) vacuolar sorting receptor-like protein [Arabidopsis thaliana] >gi_3810588 (AC005398) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No.	389689
Contig ID	16732_2.R1084
5'-most EST	LIB3433-041-P1-K1-B4
Method	BLASTX
NCBI GI	g3252813
BLAST score	883
E value	1.0e-166
Match length	350
% identity	75
NCBI Description	(AC004705) vacuolar sorting receptor-like protein [Arabidopsis thaliana] >gi_3810586 (AC005398) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No.	389690
Contig ID	16740_1.R1084
5'-most EST	g5771192

Seq. No.	389691
Contig ID	16741_1.R1084
5'-most EST	LIB3433-045-P1-K1-B1
Method	BLASTX
NCBI GI	g1781326
BLAST score	135
E value	2.0e-15
Match length	170
% identity	36
NCBI Description	(Y10464) peroxidase [Spinacia oleracea]

Seq. No.	389692
Contig ID	16741_2.R1084
5'-most EST	uC-osflcyp130c02a1
Method	BLASTX
NCBI GI	g2117620

BLAST score 195
E value 1.0e-14
Match length 84
% identity 51
NCBI Description peroxidase (EC 1.11.1.7) 1A - alfalfa >gi_971558_emb_CAA62225_ (X90692) peroxidase1A [Medicago sativa]

Seq. No. 389693
Contig ID 16748_1.R1084
5'-most EST g3767776

Seq. No. 389694
Contig ID 16753_1.R1084
5'-most EST uC-osrocyp011a03b1
Method BLASTX
NCBI GI g4586058
BLAST score 645
E value 6.0e-67
Match length 337
% identity 44
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 389695
Contig ID 16755_1.R1084
5'-most EST g5003814
Method BLASTX
NCBI GI g4689366
BLAST score 195
E value 1.0e-15
Match length 67
% identity 60
NCBI Description (AF134155) RING finger protein [Arabidopsis thaliana]

Seq. No. 389696
Contig ID 16758_1.R1084
5'-most EST LIB3434-042-P1-K1-E10

Seq. No. 389697
Contig ID 16760_1.R1084
5'-most EST LIB3433-041-P1-K1-E2

Seq. No. 389698
Contig ID 16761_1.R1084
5'-most EST g2310651
Method BLASTX
NCBI GI g4538993
BLAST score 803
E value 1.0e-85
Match length 216
% identity 70
NCBI Description (AL049481) putative host response protein [Arabidopsis thaliana]

Seq. No. 389699
Contig ID 16768_1.R1084
5'-most EST g568732

Method	BLASTX
NCBI GI	g833835
BLAST score	249
E value	5.0e-39
Match length	172
% identity	50
NCBI Description	(U26025) amygdalin hydrolase isoform AH I precursor [Prunus serotina]

Seq. No.	389700
Contig ID	16769_1.R1084
5'-most EST	g4714084

Seq. No.	389701
Contig ID	16776_1.R1084
5'-most EST	uC-osflcyp024e02b1
Method	BLASTX
NCBI GI	g2914700
BLAST score	1657
E value	0.0e+00
Match length	457
% identity	77
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	389702
Contig ID	16777_1.R1084
5'-most EST	LIB3475-001-P1-K2-E3
Method	BLASTX
NCBI GI	g5262775
BLAST score	1346
E value	1.0e-149
Match length	463
% identity	57
NCBI Description	(AL080282) putative protein [Arabidopsis thaliana]

Seq. No.	389703
Contig ID	16778_1.R1084
5'-most EST	LIB3433-041-P1-K1-G11
Method	BLASTX
NCBI GI	g4406775
BLAST score	194
E value	2.0e-14
Match length	88
% identity	45
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	389704
Contig ID	16779_1.R1084
5'-most EST	LIB3433-041-P1-K1-G12
Method	BLASTX
NCBI GI	g4539422
BLAST score	261
E value	1.0e-22
Match length	97
% identity	56
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	389705
Contig ID	16782_1.R1084
5'-most EST	uC-osflcyp126g06b1
Method	BLASTX
NCBI GI	g6006862
BLAST score	646
E value	3.0e-67
Match length	388
% identity	44
NCBI Description	(AC009540) unknown protein [Arabidopsis thaliana]

Seq. No.	389706
Contig ID	16786_1.R1084
5'-most EST	g286367
Method	BLASTX
NCBI GI	g3421087
BLAST score	1145
E value	1.0e-126
Match length	237
% identity	94
NCBI Description	(AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana] >gi_6056394_gb_AAF02858.1_AC009324_7 (AC009324) 20S proteasome subunit PAE1 [Arabidopsis thaliana]

Seq. No.	389707
Contig ID	16788_1.R1084
5'-most EST	LIB3433-041-P1-K1-H3
Method	BLASTX
NCBI GI	g3355484
BLAST score	388
E value	2.0e-40
Match length	148
% identity	37
NCBI Description	(AC004218) putative geranylgeranyl transferase type I beta subunit [Arabidopsis thaliana]

Seq. No.	389708
Contig ID	16795_1.R1084
5'-most EST	g2311455
Method	BLASTX
NCBI GI	g2829275
BLAST score	631
E value	1.0e-65
Match length	134
% identity	88
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	389709
Contig ID	16796_1.R1084
5'-most EST	g2428086
Method	BLASTX

NCBI GI	g1370603
BLAST score	1120
E value	1.0e-141
Match length	314
% identity	82
NCBI Description	(X98245) annexin p35 [Zea mays]

Seq. No.	389710
Contig ID	16796_2.R1084
5'-most EST	LIB3479-010-Q6-K1-D3
Method	BLASTX
NCBI GI	g3378208
BLAST score	210
E value	7.0e-24
Match length	127
% identity	51
NCBI Description	(AF079232) annexin p34 [Lycopersicon esculentum]

Seq. No.	389711
Contig ID	16802_1.R1084
5'-most EST	LIB3434-016-P1-K1-E9

Seq. No.	389712
Contig ID	16810_1.R1084
5'-most EST	LIB3433-042-P1-K1-C1

Seq. No.	389713
Contig ID	16819_1.R1084
5'-most EST	uC-osroM202024e06b1
Method	BLASTX
NCBI GI	g4587515
BLAST score	805
E value	1.0e-85
Match length	411
% identity	44
NCBI Description	(AC007060) EST gb_Z37678 comes from this gene. [Arabidopsis thaliana]

Seq. No.	389714
Contig ID	16820_1.R1084
5'-most EST	g3767809

Seq. No.	389715
Contig ID	16826_1.R1084
5'-most EST	uC-osroM202030c05b1

Seq. No.	389716
Contig ID	16828_1.R1084
5'-most EST	LIB3433-050-P1-K1-E8
Method	BLASTX
NCBI GI	g2204226
BLAST score	560
E value	3.0e-57
Match length	175
% identity	63
NCBI Description	(Y13848) alpha-galactosidase [Hordeum vulgare]

Seq. No.	389717
Contig ID	16835_1.R1084
5'-most EST	LIB3433-042-P1-K1-E2

Seq. No.	389718
Contig ID	16838_1.R1084
5'-most EST	LIB3433-042-P1-K1-E6
Method	BLASTX
NCBI GI	g1497987
BLAST score	210
E value	5.0e-33
Match length	98
% identity	73
NCBI Description	(U62798) SCARECROW [Arabidopsis thaliana]

Seq. No.	389719
Contig ID	16840_1.R1084
5'-most EST	LIB3434-009-P1-K1-A5
Method	BLASTX
NCBI GI	g5672692
BLAST score	1061
E value	1.0e-116
Match length	243
% identity	78
NCBI Description	(AB028448) nuclease I [Hordeum vulgare]

Seq. No.	389720
Contig ID	16843_1.R1084
5'-most EST	g1632270

Seq. No.	389721
Contig ID	16847_1.R1084
5'-most EST	LIB3433-042-P1-K1-F3

Seq. No.	389722
Contig ID	16849_1.R1084
5'-most EST	g2428908
Method	BLASTN
NCBI GI	g3047100
BLAST score	33
E value	1.0e-08
Match length	61
% identity	89
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	389723
Contig ID	16851_1.R1084
5'-most EST	LIB3433-044-P1-K1-C5

Seq. No.	389724
Contig ID	16852_1.R1084
5'-most EST	g426609
Method	BLASTX
NCBI GI	g4262167
BLAST score	400
E value	8.0e-39
Match length	159

% identity	53
NCBI Description	(AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No.	389725
Contig ID	16860_1.R1084
5'-most EST	g2442382
Method	BLASTX
NCBI GI	g2498077
BLAST score	699
E value	1.0e-73
Match length	148
% identity	84
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase [Saccharum officinarum]

Seq. No.	389726
Contig ID	16862_1.R1084
5'-most EST	g3760224

Seq. No.	389727
Contig ID	16870_1.R1084
5'-most EST	LIB3433-042-P1-K1-H8

Seq. No.	389728
Contig ID	16875_1.R1084
5'-most EST	g3763290
Method	BLASTX
NCBI GI	g3402817
BLAST score	320
E value	3.0e-29
Match length	67
% identity	93
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	389729
Contig ID	16878_1.R1084
5'-most EST	uC-osflcyp011c09b1
Method	BLASTX
NCBI GI	g2462748
BLAST score	848
E value	4.0e-91
Match length	185
% identity	87
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	389730
Contig ID	16880_1.R1084
5'-most EST	LIB3433-043-P1-K1-A9
Method	BLASTX
NCBI GI	g4263704
BLAST score	153
E value	8.0e-10
Match length	57
% identity	47

NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	389731
Contig ID	16881_1.R1084
5'-most EST	LIB3477-009-P1-K1-A12
Method	BLASTX
NCBI GI	g3461814
BLAST score	536
E value	3.0e-54
Match length	282
% identity	40
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389732
Contig ID	16887_1.R1084
5'-most EST	LIB3434-047-P1-K1-D6
Method	BLASTX
NCBI GI	g5059115
BLAST score	1276
E value	1.0e-141
Match length	334
% identity	72
NCBI Description	(AF132212) OPDA-reductase homolog [Arabidopsis thaliana]

Seq. No.	389733
Contig ID	16910_1.R1084
5'-most EST	g572487
Method	BLASTN
NCBI GI	g5803242
BLAST score	44
E value	3.0e-15
Match length	151
% identity	87
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	389734
Contig ID	16912_1.R1084
5'-most EST	LIB3433-043-P1-K1-E1
Method	BLASTX
NCBI GI	g2497883
BLAST score	228
E value	2.0e-18
Match length	59
% identity	73
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi_1362174_pir__S57768 metallothionein-like protein - rice >gi_687638 (U18404) metallothionein-like protein [Oryza sativa] >gi_1815626 (U43529) metallothionein-like type 1 [Oryza sativa] >gi_4097154_gb_AAD10376.1_ (U46159) type 1 rice metallothionein-like gene; Method: conceptual translation supplied by author. [Oryza sativa]

Seq. No.	389735
Contig ID	16913_1.R1084
5'-most EST	LIB3433-043-P1-K1-E10

Seq. No.	389736
Contig ID	16916_1.R1084
5'-most EST	uC-osflM202134e10a1
Method	BLASTX
NCBI GI	g4567279
BLAST score	587
E value	1.0e-60
Match length	133
% identity	86
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	389737
Contig ID	16917_1.R1084
5'-most EST	g3763168
Method	BLASTX
NCBI GI	g209078
BLAST score	218
E value	3.0e-17
Match length	45
% identity	89
NCBI Description	(M37847) alpha-peptide [Cloning vector] >gi_3603281 (AF053122) alpha-peptide [Cloning vector pCD341] >gi_3603293 (AF053123) alpha-peptide [Cloning vector pCD342]

Seq. No.	389738
Contig ID	16926_1.R1084
5'-most EST	g2312695
Method	BLASTX
NCBI GI	g2129752
BLAST score	318
E value	5.0e-29
Match length	127
% identity	50
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_ (Z35475) thioredoxin [Arabidopsis thaliana]

Seq. No.	389739
Contig ID	16929_1.R1084
5'-most EST	g2799946
Method	BLASTX
NCBI GI	g4506745
BLAST score	318
E value	5.0e-35
Match length	120
% identity	65
NCBI Description	ribosomal protein S9 >gi_1173285_sp_P46781_RS9_HUMAN 40S RIBOSOMAL PROTEIN S9 >gi_1362936_pir__S55917 ribosomal protein S9 - human >gi_550023 (U14971) ribosomal protein S9 [Homo sapiens] >gi_1096943_prf__2113200F ribosomal protein S9 [Homo sapiens]

Seq. No.	389740
Contig ID	16934_1.R1084
5'-most EST	g3763075
Method	BLASTX

NCBI GI g3915847
BLAST score 641
E value 7.0e-67
Match length 162
% identity 80
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 389741
Contig ID 16934_2.R1084
5'-most EST uC-osroM202039d08b1
Method BLASTX
NCBI GI g3915847
BLAST score 992
E value 1.0e-108
Match length 234
% identity 83
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 389742
Contig ID 16940_1.R1084
5'-most EST LIB3433-043-P1-K1-G4

Seq. No. 389743
Contig ID 16943_1.R1084
5'-most EST g3764147
Method BLASTX
NCBI GI g4680661
BLAST score 582
E value 2.0e-59
Match length 433
% identity 30
NCBI Description (AF132945) CGI-11 protein [Homo sapiens]

Seq. No. 389744
Contig ID 16953_1.R1084
5'-most EST g5002831
Method BLASTX
NCBI GI g2245131
BLAST score 717
E value 2.0e-75
Match length 240
% identity 65
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 389745
Contig ID 16960_1.R1084
5'-most EST LIB3479-008-Q6-K1-G10
Method BLASTX
NCBI GI g4558673
BLAST score 288
E value 1.0e-25
Match length 76
% identity 64
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana] >gi_4726112_gb_AAD28312.1_AC006436_3 (AC006436)

hypothetical protein [Arabidopsis thaliana]

Seq. No.	389746
Contig ID	16964_1.R1084
5'-most EST	LIB3433-025-P1-K1-F7
Method	BLASTX
NCBI GI	g2708749
BLAST score	236
E value	2.0e-19
Match length	115
% identity	41
NCBI Description	(AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No.	389747
Contig ID	16969_1.R1084
5'-most EST	g2311477
Method	BLASTX
NCBI GI	g3687251
BLAST score	328
E value	3.0e-48
Match length	142
% identity	71
NCBI Description	(AC005169) unknown protein [Arabidopsis thaliana]

Seq. No.	389748
Contig ID	16969_2.R1084
5'-most EST	uC-osflcyp155h04b1
Method	BLASTX
NCBI GI	g3687251
BLAST score	245
E value	1.0e-20
Match length	89
% identity	58
NCBI Description	(AC005169) unknown protein [Arabidopsis thaliana]

Seq. No.	389749
Contig ID	16970_1.R1084
5'-most EST	uC-osflcyp081f03b1
Method	BLASTX
NCBI GI	g1710521
BLAST score	567
E value	4.0e-58
Match length	144
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L24 >gi_1154859_emb_CAA63960_ (X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No.	389750
Contig ID	16970_2.R1084
5'-most EST	g427178
Method	BLASTX
NCBI GI	g1710521
BLAST score	557
E value	5.0e-57
Match length	113
% identity	95

NCBI Description	60S RIBOSOMAL PROTEIN L24 >gi_1154859_emb_CAA63960_ (X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No.	389751
Contig ID	16970_3.R1084
5'-most EST	LIB3433-048-P1-K1-E4
Method	BLASTX
NCBI GI	g1710521
BLAST score	576
E value	3.0e-59
Match length	148
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L24 >gi_1154859_emb_CAA63960_ (X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No.	389752
Contig ID	16974_1.R1084
5'-most EST	LIB3433-044-P1-K1-C1

Seq. No.	389753
Contig ID	16982_1.R1084
5'-most EST	LIB3477-003-P1-K1-E8

Seq. No.	389754
Contig ID	16983_1.R1084
5'-most EST	LIB3474-005-P1-K1-H3
Method	BLASTX
NCBI GI	g1197461
BLAST score	1156
E value	1.0e-127
Match length	247
% identity	88
NCBI Description	(X78819) casein kinase I [Arabidopsis thaliana]

Seq. No.	389755
Contig ID	16985_1.R1084
5'-most EST	g428982
Method	BLASTX
NCBI GI	g5919185
BLAST score	292
E value	5.0e-26
Match length	114
% identity	54
NCBI Description	(AF183809) arabinogalactan protein Pop14A9 [Populus alba x Populus tremula]

Seq. No.	389756
Contig ID	16986_1.R1084
5'-most EST	LIB3433-044-P1-K1-D11
Method	BLASTX
NCBI GI	g3142296
BLAST score	157
E value	3.0e-10
Match length	64
% identity	52
NCBI Description	(AC002411) Contains similarity to hypothetical mitochondrial import receptor subunit gb_Z98597 from S.

pombe. ESTs gb_T45575 and gb_Z26435 and gb_AA394576 come from this gene. [Arabidopsis thaliana]

Seq. No.	389757
Contig ID	16987_1.R1084
5'-most EST	uC-osflcyp022a06b1

Seq. No.	389758
Contig ID	16990_1.R1084
5'-most EST	g3769062
Method	BLASTX
NCBI GI	g5263330
BLAST score	289
E value	9.0e-26
Match length	67
% identity	81
NCBI Description	(AC007727) Contains similarity to gb_AJ000644 SPOP (speckle-type POZ protein) from Homo sapiens and contains a PF_00651 BTB/POZ domain. ESTs gb_T75841, gb_R89974, gb_R30221, gb_N96386, gb_T76457, gb_AI100013 and gb

Seq. No.	389759
Contig ID	16993_1.R1084
5'-most EST	uC-osroM202016b04b1

Seq. No.	389760
Contig ID	16996_1.R1084
5'-most EST	g3767089
Method	BLASTX
NCBI GI	g2407800
BLAST score	525
E value	3.0e-53
Match length	117
% identity	88
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	389761
Contig ID	16996_2.R1084
5'-most EST	g699795
Method	BLASTX
NCBI GI	g2407800
BLAST score	522
E value	5.0e-53
Match length	117
% identity	88
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	389762
Contig ID	17002_1.R1084
5'-most EST	g2310130
Method	BLASTX
NCBI GI	g3150404
BLAST score	143
E value	6.0e-16
Match length	176
% identity	18
NCBI Description	(AC004165) putative mitochondrial carrier protein

[Arabidopsis thaliana]

Seq. No.	389763
Contig ID	17012_1.R1084
5'-most EST	g2280830
Method	BLASTX
NCBI GI	g1762945
BLAST score	410
E value	1.0e-39
Match length	142
% identity	54
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No.	389764
Contig ID	17014_1.R1084
5'-most EST	g700464
Method	BLASTX
NCBI GI	g4490316
BLAST score	378
E value	2.0e-49
Match length	192
% identity	57
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	389765
Contig ID	17022_1.R1084
5'-most EST	g2309684
Method	BLASTX
NCBI GI	g400054
BLAST score	593
E value	8.0e-73
Match length	268
% identity	57
NCBI Description	DIHYDROXY-ACID DEHYDRATASE (DAD) >gi_486729_pir__S35137 probable phosphogluconate dehydratase (EC 4.2.1.12) - Lactococcus lactis subsp. lactis >gi_2565156 (U92974) IlvD [Lactococcus lactis]

Seq. No.	389766
Contig ID	17023_1.R1084
5'-most EST	LIB3433-045-P1-K1-A1
Method	BLASTX
NCBI GI	g4508073
BLAST score	202
E value	1.0e-15
Match length	132
% identity	34
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	389767
Contig ID	17027_1.R1084
5'-most EST	uC-osrocyp037d10b1
Method	BLASTX
NCBI GI	g4972109
BLAST score	249
E value	1.0e-20

Match length	176
% identity	33
NCBI Description	(AL078579) putative acyl-CoA binding protein [Arabidopsis thaliana]

Seq. No.	389768
Contig ID	17031_1.R1084
5'-most EST	LIB3433-045-P1-K1-A8
Method	BLASTX
NCBI GI	g3297819
BLAST score	889
E value	5.0e-96
Match length	182
% identity	91
NCBI Description	(AL031032) protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	389769
Contig ID	17039_1.R1084
5'-most EST	LIB3433-045-P1-K1-B5

Seq. No.	389770
Contig ID	17043_1.R1084
5'-most EST	LIB3433-045-P1-K1-C1

Seq. No.	389771
Contig ID	17045_1.R1084
5'-most EST	LIB3433-045-P1-K1-C11
Method	BLASTX
NCBI GI	g5091623
BLAST score	324
E value	9.0e-30
Match length	122
% identity	55
NCBI Description	(AC007454) Similar to gb_U93048 somatic embryogenesis receptor-like kinase from Daucus carota, contains 4 PF_00560 Leucine Rich Repeat domains and a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No.	389772
Contig ID	17047_1.R1084
5'-most EST	LIB3433-045-P1-K1-G1

Seq. No.	389773
Contig ID	17051_1.R1084
5'-most EST	uC-osrocyp013e02b1
Method	BLASTX
NCBI GI	g2979565
BLAST score	481
E value	5.0e-48
Match length	125
% identity	74
NCBI Description	(AC003680) putative sin3 associated polypeptide (SAP18) [Arabidopsis thaliana]

Seq. No.	389774
Contig ID	17052_1.R1084

5'-most EST	LIB3433-045-P1-K1-C7
Method	BLASTX
NCBI GI	g4469022
BLAST score	448
E value	2.0e-44
Match length	164
% identity	52
NCBI Description	(AL035602) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	389775
Contig ID	17054_1.R1084
5'-most EST	LIB3434-053-P1-K1-A3
Method	BLASTX
NCBI GI	g4567310
BLAST score	172
E value	8.0e-12
Match length	82
% identity	48
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	389776
Contig ID	17058_1.R1084
5'-most EST	g4715356
Method	BLASTN
NCBI GI	g6006355
BLAST score	544
E value	0.0e+00
Match length	596
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	389777
Contig ID	17060_1.R1084
5'-most EST	LIB3433-045-P1-K1-D3

Seq. No.	389778
Contig ID	17063_1.R1084
5'-most EST	LIB3433-045-P1-K1-D7
Method	BLASTX
NCBI GI	g5902363
BLAST score	789
E value	6.0e-84
Match length	252
% identity	63
NCBI Description	(AC009322) Putative coatomer protein complex, subunit beta 2 (beta prime) [Arabidopsis thaliana]

Seq. No.	389779
Contig ID	17063_2.R1084
5'-most EST	g3760099

Seq. No.	389780
Contig ID	17066_1.R1084
5'-most EST	g568602
Method	BLASTX
NCBI GI	g1168470

BLAST score	413
E value	6.0e-44
Match length	118
% identity	77
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	389781
Contig ID	17070_1.R1084
5'-most EST	LIB3433-045-P1-K1-E3
Method	BLASTX
NCBI GI	g2498731
BLAST score	363
E value	4.0e-59
Match length	173
% identity	69
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	389782
Contig ID	17071_1.R1084
5'-most EST	uC-osrocyp009c08a1

Seq. No.	389783
Contig ID	17082_1.R1084
5'-most EST	g2443158

Seq. No.	389784
Contig ID	17083_1.R1084
5'-most EST	LIB3433-045-P1-K1-F5

Seq. No.	389785
Contig ID	17087_1.R1084
5'-most EST	LIB3433-019-P1-K1-A3
Method	BLASTX
NCBI GI	g4104058
BLAST score	169
E value	1.0e-11
Match length	70
% identity	47
NCBI Description	(AF031195) blue copper-binding protein homolog [Triticum aestivum]

Seq. No.	389786
Contig ID	17089_1.R1084
5'-most EST	LIB3433-045-P1-K1-G10

Seq. No.	389787
Contig ID	17090_1.R1084
5'-most EST	uC-osflcyp054g05b1

Seq. No.	389788

Contig ID 17093_1.R1084
5'-most EST g3769260

Seq. No. 389789
Contig ID 17095_1.R1084
5'-most EST LIB3475-001-P1-K2-F6

Seq. No. 389790
Contig ID 17099_1.R1084
5'-most EST LIB3433-045-P1-K1-G9
Method BLASTX
NCBI GI g5915836
BLAST score 465
E value 3.0e-46
Match length 152
% identity 57
NCBI Description CYTOCHROME P450 71D7 >gi_1762144 (U48435) putative cytochrome P450 [Solanum chacoense]

Seq. No. 389791
Contig ID 17099_2.R1084
5'-most EST uC-osroM202007h06a1
Method BLASTX
NCBI GI g5915839
BLAST score 405
E value 3.0e-39
Match length 122
% identity 57
NCBI Description CYTOCHROME P450 71D10 >gi_2739000_gb_AAB94588_ (AF022459) CYP71D10p [Glycine max]

Seq. No. 389792
Contig ID 17101_1.R1084
5'-most EST g5003942

Seq. No. 389793
Contig ID 17105_1.R1084
5'-most EST uC-osflcyp026d05b1

Seq. No. 389794
Contig ID 17106_1.R1084
5'-most EST LIB3433-056-P1-K1-E9
Method BLASTX
NCBI GI g464707
BLAST score 639
E value 1.0e-66
Match length 152
% identity 78
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A

[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	389795
Contig ID	17106_2.R1084
5'-most EST	g3763415
Method	BLASTX
NCBI GI	g464707
BLAST score	424
E value	2.0e-41
Match length	102
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	389796
Contig ID	17106_3.R1084
5'-most EST	uC-osflM202049e04b1
Method	BLASTX
NCBI GI	g464707
BLAST score	476
E value	8.0e-48
Match length	111
% identity	78
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	389797
Contig ID	17114_1.R1084
5'-most EST	g571905
Method	BLASTX
NCBI GI	g5734639
BLAST score	528
E value	1.0e-53
Match length	166
% identity	61
NCBI Description	(AP000391) ESTs AU056036(S20239),C72753(E2173), AU056035(S20239) correspond to a region of the predicted gene.; Similar to putative cytochrome P-450 (AC003680) [Oryza sativa]

Seq. No.	389798
Contig ID	17119_1.R1084
5'-most EST	g2317305
Method	BLASTX
NCBI GI	g4512659
BLAST score	536
E value	5.0e-94
Match length	240
% identity	70
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	389799
Contig ID	17122_1.R1084
5'-most EST	g642039

Seq. No.	389800
Contig ID	17137_1.R1084
5'-most EST	uC-osflcyp055d08b1
Method	BLASTX
NCBI GI	g3023271
BLAST score	2011
E value	0.0e+00
Match length	381
% identity	99
NCBI Description	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH) (FALDH) (GSH-FDH) >gi_1675394 (U77637) class III ADH enzyme [Oryza sativa]

Seq. No.	389801
Contig ID	17138_1.R1084
5'-most EST	LIB3433-046-P1-K1-C4
Method	BLASTX
NCBI GI	g4895194
BLAST score	224
E value	3.0e-18
Match length	118
% identity	38
NCBI Description	(AC007661) putative peptide transporter protein [Arabidopsis thaliana]

Seq. No.	389802

Contig ID	17145_1.R1084
5'-most EST	LIB3433-046-P1-K1-D11

Seq. No.	389803
Contig ID	17155_1.R1084
5'-most EST	LIB3433-046-P1-K1-E10

Seq. No.	389804
Contig ID	17156_1.R1084
5'-most EST	LIB3433-046-P1-K1-E12

Seq. No.	389805
Contig ID	17161_1.R1084
5'-most EST	g2310189
Method	BLASTX
NCBI GI	g3335336
BLAST score	313
E value	3.0e-42
Match length	166
% identity	56
NCBI Description	(AC004512) Contains similarity to DnaJ gene YM8520.10 gb_825566 from from S. cerevisiae cosmid gb_Z49705. ESTs gb_Z47720 and gb_Z29879 come from this gene. [Arabidopsis thaliana]

Seq. No.	389806
Contig ID	17162_1.R1084
5'-most EST	LIB3433-046-P1-K1-E8
Method	BLASTX
NCBI GI	g729051
BLAST score	429
E value	3.0e-42
Match length	96
% identity	52
NCBI Description	CALTRACTIN (CENTRIN) >gi_444342_prf__1906390A caltractin-like protein [Atriplex nummularia]

Seq. No.	389807
Contig ID	17173_1.R1084
5'-most EST	LIB3433-046-P1-K1-F8
Method	BLASTX
NCBI GI	g2289003
BLAST score	312
E value	1.0e-28
Match length	127
% identity	54
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No.	389808
Contig ID	17175_1.R1084
5'-most EST	LIB3433-046-P1-K1-G1
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	6.0e-10
Match length	35

% identity	42
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389809
Contig ID	17176_1.R1084
5'-most EST	LIB3433-046-P1-K1-G10
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	5.0e-10
Match length	35
% identity	37
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	389810
Contig ID	17179_1.R1084
5'-most EST	LIB3433-053-P1-K1-B12
Method	BLASTX
NCBI GI	g4039152
BLAST score	169
E value	1.0e-11
Match length	53
% identity	58
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_ (AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	389811
Contig ID	17180_1.R1084
5'-most EST	uC-osrocyp012a10b1
Method	BLASTX
NCBI GI	g1781336
BLAST score	874
E value	6.0e-94
Match length	303
% identity	57
NCBI Description	(Y10469) peroxidase [Spinacia oleracea]

Seq. No.	389812
Contig ID	17184_1.R1084
5'-most EST	LIB3434-048-P1-K1-B5
Method	BLASTN
NCBI GI	g6088090
BLAST score	426
E value	0.0e+00
Match length	522
% identity	96
NCBI Description	Oryza sativa DNA, chromosome 6, 1.6cM, RFLP marker, clone:G8018

Seq. No.	389813
Contig ID	17186_1.R1084
5'-most EST	LIB3434-058-P1-K1-E10
Method	BLASTX
NCBI GI	g1620371
BLAST score	627
E value	3.0e-65

Match length	171
% identity	65
NCBI Description	(Y08782) peroxidase ATP23a [Arabidopsis thaliana]

Seq. No.	389814
Contig ID	17189_1.R1084
5'-most EST	uC-osf1M202020f06b1

Seq. No.	389815
Contig ID	17190_1.R1084
5'-most EST	g2428840
Method	BLASTX
NCBI GI	g5103835
BLAST score	424
E value	4.0e-56
Match length	130
% identity	86
NCBI Description	(AC007591) ESTs gb_T22508, gb_H36196 and gb_AI100134 come from this gene. [Arabidopsis thaliana]

Seq. No.	389816
Contig ID	17191_1.R1084
5'-most EST	LIB3433-047-P1-K1-A12
Method	BLASTX
NCBI GI	g1363488
BLAST score	511
E value	1.0e-51
Match length	153
% identity	60
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	389817
Contig ID	17192_1.R1084
5'-most EST	LIB3433-047-P1-K1-A2
Method	BLASTX
NCBI GI	g3063467
BLAST score	482
E value	4.0e-48
Match length	126
% identity	75
NCBI Description	(AC003981) F22O13.29 [Arabidopsis thaliana]

Seq. No.	389818
Contig ID	17194_1.R1084
5'-most EST	LIB3433-047-P1-K1-A7
Method	BLASTX
NCBI GI	g3377842
BLAST score	205
E value	4.0e-18
Match length	60
% identity	82
NCBI Description	(AF076274) No definition line found [Arabidopsis thaliana]

Seq. No.	389819

Contig ID	17197_1.R1084
5'-most EST	g4714485
Method	BLASTX
NCBI GI	g3309086
BLAST score	481
E value	3.0e-48
Match length	166
% identity	47
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana] >gi_4938495_emb_CAB43853.1_ (AL078465) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No.	389820
Contig ID	17201_1.R1084
5'-most EST	LIB3433-047-P1-K1-B3
Method	BLASTX
NCBI GI	g4704662
BLAST score	382
E value	1.0e-36
Match length	90
% identity	78
NCBI Description	(AF116860) uracil phosphoribosyltransferase 1 [Arabidopsis thaliana]

Seq. No.	389821
Contig ID	17204_1.R1084
5'-most EST	g2428754

Seq. No.	389822
Contig ID	17209_1.R1084
5'-most EST	g2800728
Method	BLASTN
NCBI GI	g984755
BLAST score	80
E value	9.0e-37
Match length	88
% identity	99
NCBI Description	O.sativa mRNA for chilling-inducible protein

Seq. No.	389823
Contig ID	17218_1.R1084
5'-most EST	LIB3433-047-P1-K1-D10
Method	BLASTX
NCBI GI	g4101591
BLAST score	360
E value	4.0e-34
Match length	134
% identity	57
NCBI Description	(AF005051) aspartyl aminopeptidase [Mus musculus]

Seq. No.	389824
Contig ID	17231_1.R1084
5'-most EST	LIB3433-056-P1-K1-F8

Seq. No.	389825
Contig ID	17237_2.R1084
5'-most EST	LIB3434-029-P1-K1-B12

Method	BLASTX
NCBI GI	g2150000
BLAST score	244
E value	1.0e-20
Match length	68
% identity	63
NCBI Description	(AF000939) aleurone ribonuclease [Hordeum vulgare]

Seq. No.	389826
Contig ID	17240_1.R1084
5'-most EST	LIB3433-047-P1-K1-F2
Method	BLASTX
NCBI GI	g2832623
BLAST score	352
E value	6.0e-33
Match length	115
% identity	54
NCBI Description	(AL021711) protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	389827
Contig ID	17241_1.R1084
5'-most EST	LIB3433-015-Q6-K1-G9

Seq. No.	389828
Contig ID	17247_1.R1084
5'-most EST	uC-osflM202069d01a1
Method	BLASTX
NCBI GI	g3935157
BLAST score	148
E value	2.0e-09
Match length	34
% identity	85
NCBI Description	(AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No.	389829
Contig ID	17247_2.R1084
5'-most EST	g5803339
Method	BLASTX
NCBI GI	g4263722
BLAST score	408
E value	7.0e-40
Match length	99
% identity	75
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.	389830
Contig ID	17252_1.R1084
5'-most EST	g2799128
Method	BLASTX
NCBI GI	g1066163
BLAST score	328
E value	2.0e-33
Match length	86
% identity	76
NCBI Description	(X93015) glyoxysomal beta-ketoacyl-thiolase [Brassica napus]

Seq. No.	389831
Contig ID	17252_2.R1084
5'-most EST	uC-osflcyp050b11b1
Method	BLASTX
NCBI GI	g393707
BLAST score	1382
E value	1.0e-153
Match length	446
% identity	60
NCBI Description	(X67696) acetyl-CoA acyltransferase [Cucumis sativus]

Seq. No.	389832
Contig ID	17253_1.R1084
5'-most EST	LIB3433-047-P1-K1-G8
Method	BLASTX
NCBI GI	g2493132
BLAST score	1304
E value	1.0e-144
Match length	256
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B SUBUNIT) >gi_167110 (L11873) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No.	389833
Contig ID	17257_1.R1084
5'-most EST	LIB3433-047-P1-K1-H11
Method	BLASTX
NCBI GI	g2352492
BLAST score	219
E value	4.0e-21
Match length	92
% identity	59
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	389834
Contig ID	17260_1.R1084
5'-most EST	LIB3433-047-P1-K1-H3
Method	BLASTX
NCBI GI	g3641252
BLAST score	237
E value	1.0e-19
Match length	104
% identity	46
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	389835
Contig ID	17262_1.R1084
5'-most EST	LIB3434-033-P1-K1-B8
Method	BLASTX
NCBI GI	g3914899
BLAST score	357
E value	3.0e-53

Match length	132
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal protein S4 type I [Zea mays]

Seq. No.	389836
Contig ID	17264_1.R1084
5'-most EST	g5004128
Method	BLASTX
NCBI GI	g2129622
BLAST score	571
E value	1.0e-58
Match length	122
% identity	86
NCBI Description	immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406 (U52046) immunophilin [Arabidopsis thaliana]

Seq. No.	389837
Contig ID	17270_1.R1084
5'-most EST	g568847

Seq. No.	389838
Contig ID	17272_1.R1084
5'-most EST	g2799017
Method	BLASTX
NCBI GI	g4678349
BLAST score	165
E value	4.0e-24
Match length	133
% identity	25
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	389839
Contig ID	17272_2.R1084
5'-most EST	g2798833
Method	BLASTN
NCBI GI	g1698774
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Filamentous phage display expression cloning vector pZGT5 with murine Ig kappa light chain fragment insert, complete sequence

Seq. No.	389840
Contig ID	17272_3.R1084
5'-most EST	uC-osflcyp033h08b1

Seq. No.	389841
Contig ID	17273_1.R1084
5'-most EST	g2311738

Seq. No.	389842
Contig ID	17276_1.R1084
5'-most EST	uC-osflcyp052c09b1
Method	BLASTX

NCBI GI g3599491
BLAST score 591
E value 7.0e-61
Match length 166
% identity 67
NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No. 389843
Contig ID 17278_1.R1084
5'-most EST LIB3433-048-P1-K1-B6

Seq. No. 389844
Contig ID 17283_1.R1084
5'-most EST LIB3433-048-P1-K1-C10

Seq. No. 389845
Contig ID 17290_1.R1084
5'-most EST LIB3433-048-P1-K1-D10
Method BLASTX
NCBI GI g3402675
BLAST score 211
E value 3.0e-16
Match length 115
% identity 43
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 389846
Contig ID 17292_1.R1084
5'-most EST LIB3434-023-P1-K1-D6
Method BLASTX
NCBI GI g2651300
BLAST score 368
E value 9.0e-35
Match length 201
% identity 41
NCBI Description (AC002336) putative initiator tRNA phosphoribosyl-transferase [Arabidopsis thaliana]

Seq. No. 389847
Contig ID 17295_1.R1084
5'-most EST uC-osflm202104f01b1
Method BLASTX
NCBI GI g4519258
BLAST score 150
E value 3.0e-09
Match length 155
% identity 30
NCBI Description (AB017914) L-zip+NBS+LRR [Oryza sativa]

Seq. No. 389848
Contig ID 17296_1.R1084
5'-most EST LIB3433-048-P1-K1-E11
Method BLASTX
NCBI GI g4582787
BLAST score 568
E value 2.0e-58
Match length 120

% identity	93
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No.	389849
Contig ID	17301_1.R1084
5'-most EST	LIB3434-010-P1-K1-F5

Seq. No.	389850
Contig ID	17316_1.R1084
5'-most EST	g3763310
Method	BLASTX
NCBI GI	g5596645
BLAST score	171
E value	9.0e-12
Match length	42
% identity	67
NCBI Description	(Z82266) similar to RNA polymerases I, II and III shared polypeptide (approx 7kd) [Caenorhabditis elegans]

Seq. No.	389851
Contig ID	17317_1.R1084
5'-most EST	LIB3433-048-P1-K1-G12
Method	BLASTX
NCBI GI	g3421384
BLAST score	498
E value	3.0e-50
Match length	164
% identity	64
NCBI Description	(AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq. No.	389852
Contig ID	17325_1.R1084
5'-most EST	LIB3433-048-P1-K1-H12

Seq. No.	389853
Contig ID	17332_1.R1084
5'-most EST	LIB3434-057-P1-K1-G7
Method	BLASTX
NCBI GI	g4567304
BLAST score	412
E value	5.0e-40
Match length	251
% identity	53
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	389854
Contig ID	17345_1.R1084
5'-most EST	g701649

Seq. No.	389855
Contig ID	17356_1.R1084
5'-most EST	g428415

Seq. No.	389856
Contig ID	17357_1.R1084
5'-most EST	g2431215

Seq. No.	389857
Contig ID	17359_1.R1084
5'-most EST	LIB3434-005-P1-K1-A10
Method	BLASTX
NCBI GI	g5053010
BLAST score	147
E value	6.0e-09
Match length	160
% identity	24
NCBI Description	(AF154120) sorting nexin 1 [Mus musculus]

Seq. No.	389858
Contig ID	17363_1.R1084
5'-most EST	uC-osflcyp137g10a1

Seq. No.	389859
Contig ID	17367_1.R1084
5'-most EST	uC-osflcyp026a05b1

Seq. No.	389860
Contig ID	17369_1.R1084
5'-most EST	g2442433
Method	BLASTX
NCBI GI	g2129742
BLAST score	266
E value	5.0e-23
Match length	74
% identity	64
NCBI Description	stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	389861
Contig ID	17369_2.R1084
5'-most EST	g3762446
Method	BLASTX
NCBI GI	g2129742
BLAST score	267
E value	5.0e-23
Match length	74
% identity	64
NCBI Description	stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	389862
Contig ID	17382_1.R1084
5'-most EST	LIB3433-060-P1-K1-A3

Seq. No.	389863

Contig ID	17383_1.R1084
5'-most EST	LIB3434-035-P1-K1-D8
Method	BLASTX
NCBI GI	g2129840
BLAST score	307
E value	1.0e-27
Match length	128
% identity	52
NCBI Description	nucleosome assembly protein 1 - soybean >gi_1161252 (L38856) nucleosome assembly protein 1 [Glycine max]

Seq. No.	389864
Contig ID	17389_1.R1084
5'-most EST	LIB3433-049-P1-K1-G2

Seq. No.	389865
Contig ID	17411_1.R1084
5'-most EST	LIB3433-050-P1-K1-A3
Method	BLASTX
NCBI GI	g5777631
BLAST score	467
E value	1.0e-46
Match length	152
% identity	61
NCBI Description	(AJ245900) CAA303719.1 protein [Oryza sativa]

Seq. No.	389866
Contig ID	17415_1.R1084
5'-most EST	g2799396
Method	BLASTN
NCBI GI	g2280519
BLAST score	43
E value	1.0e-14
Match length	51
% identity	98
NCBI Description	Nicotiana tabacum mRNA for BYJ6, partial cds

Seq. No.	389867
Contig ID	17416_1.R1084
5'-most EST	uC-osflcyp078b04b1
Method	BLASTX
NCBI GI	g3914431
BLAST score	818
E value	1.0e-111
Match length	239
% identity	83
NCBI Description	PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha subunit [Spinacia oleracea]

Seq. No.	389868
Contig ID	17416_2.R1084
5'-most EST	uC-osflM202054h10b1
Method	BLASTX
NCBI GI	g3914431
BLAST score	307

E value	7.0e-28
Match length	124
% identity	56
NCBI Description	PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha subunit [Spinacia oleracea]

Seq. No.	389869
Contig ID	17417_2.R1084
5'-most EST	LIB3433-050-P1-K1-B10
Method	BLASTX
NCBI GI	g4759160
BLAST score	202
E value	5.0e-29
Match length	114
% identity	58
NCBI Description	small nuclear ribonucleoprotein D3 polypeptide (18kD) >gi_1173456_sp_P43331_SMD3_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	389870
Contig ID	17420_1.R1084
5'-most EST	LIB3433-023-P1-K1-G7
Method	BLASTX
NCBI GI	g6091722
BLAST score	438
E value	3.0e-43
Match length	106
% identity	76
NCBI Description	(AC010797) putative ribosomal protein L13 [Arabidopsis thaliana]

Seq. No.	389871
Contig ID	17431_1.R1084
5'-most EST	LIB3433-050-P1-K1-C3

Seq. No.	389872
Contig ID	17436_1.R1084
5'-most EST	uC-osflcyp112h03b1
Method	BLASTX
NCBI GI	g5880464
BLAST score	162
E value	8.0e-11
Match length	40
% identity	68
NCBI Description	(AF088901) actin bundling protein ABP135 [Lilium longiflorum]

Seq. No.	389873
Contig ID	17442_1.R1084
5'-most EST	g426092
Method	BLASTX
NCBI GI	g118304
BLAST score	543
E value	6.0e-69

Match length	405
% identity	40
NCBI Description	DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE) >gi_77626_pir__A31133 diaminopimelate decarboxylase (EC 4.1.1.20) - Pseudomonas aeruginosa

Seq. No.	389874
Contig ID	17444_1.R1084
5'-most EST	LIB3433-050-P1-K1-D6

Seq. No.	389875
Contig ID	17453_1.R1084
5'-most EST	uC-osflcyp124e11b1
Method	BLASTX
NCBI GI	g4325371
BLAST score	282
E value	5.0e-25
Match length	114
% identity	53
NCBI Description	(AF128396) contains similarity to Medicago truncatula N7 protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No.	389876
Contig ID	17461_1.R1084
5'-most EST	g1632282

Seq. No.	389877
Contig ID	17463_1.R1084
5'-most EST	LIB3479-008-Q6-K1-H2
Method	BLASTX
NCBI GI	g1703089
BLAST score	158
E value	2.0e-10
Match length	95
% identity	38
NCBI Description	ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE) (APH) (ACYLAMINOACYL-PEPTIDASE) (DNF15S2 PROTEIN) >gi_2118063_pir__JC4655 acylaminoacyl-peptidase (EC 3.4.19.1) - human >gi_556514_dbj_BAA07476_ (D38441) acylamino acid-releasing enzyme [Homo sapiens]

Seq. No.	389878
Contig ID	17465_1.R1084
5'-most EST	LIB3433-050-P1-K1-F4
Method	BLASTX
NCBI GI	g1825727
BLAST score	262
E value	2.0e-22
Match length	81
% identity	58
NCBI Description	(U88308) C32E8.5 gene product [Caenorhabditis elegans]

Seq. No.	389879
Contig ID	17469_1.R1084
5'-most EST	g2442271

Seq. No. 389880

Contig ID	17471_1.R1084
5'-most EST	LIB3433-050-P1-K1-G11
Method	BLASTX
NCBI GI	g2462748
BLAST score	729
E value	5.0e-77
Match length	170
% identity	80
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	389881
Contig ID	17476_1.R1084
5'-most EST	uC-osrocyp011g06b1
Method	BLASTX
NCBI GI	g6063540
BLAST score	1017
E value	1.0e-141
Match length	264
% identity	97
NCBI Description	(AP000615) similar to OsMlo-h1. (Z95353) [Oryza sativa]

Seq. No.	389882
Contig ID	17481_1.R1084
5'-most EST	g287032
Method	BLASTX
NCBI GI	g3033396
BLAST score	247
E value	8.0e-21
Match length	86
% identity	52
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	389883
Contig ID	17488_1.R1084
5'-most EST	uC-osroM202032e06b1
Method	BLASTX
NCBI GI	g3005931
BLAST score	959
E value	1.0e-104
Match length	268
% identity	39
NCBI Description	(AJ005016) ABC transporter [Homo sapiens]

Seq. No.	389884
Contig ID	17495_1.R1084
5'-most EST	LIB3433-051-P1-K1-A4
Method	BLASTX
NCBI GI	g5081779
BLAST score	589
E value	9.0e-61
Match length	139
% identity	80
NCBI Description	(AF150630) cellulose synthase [Gossypium hirsutum]

Seq. No.	389885
Contig ID	17496_1.R1084

5'-most EST	uC-osflcyp110b10b1
Method	BLASTX
NCBI GI	g3641837
BLAST score	948
E value	1.0e-102
Match length	300
% identity	64
NCBI Description	(AL023094) Nonclathrin coat protein gamma-like protein [Arabidopsis thaliana]

Seq. No.	389886
Contig ID	17499_1.R1084
5'-most EST	g4879694
Method	BLASTX
NCBI GI	g1890575
BLAST score	746
E value	3.0e-79
Match length	150
% identity	89
NCBI Description	(X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]

Seq. No.	389887
Contig ID	17499_2.R1084
5'-most EST	g287283
Method	BLASTX
NCBI GI	g1890577
BLAST score	489
E value	2.0e-97
Match length	192
% identity	89
NCBI Description	(X93175) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]

Seq. No.	389888
Contig ID	17500_1.R1084
5'-most EST	uC-osflcyp179b02b1
Method	BLASTX
NCBI GI	g4105782
BLAST score	911
E value	2.0e-98
Match length	215
% identity	79
NCBI Description	(AF049922) PGP169-12 [Petunia x hybrida]

Seq. No.	389889
Contig ID	17508_1.R1084
5'-most EST	LIB3433-051-P1-K1-B5
Method	BLASTX
NCBI GI	g4982479
BLAST score	529
E value	9.0e-54
Match length	171
% identity	60
NCBI Description	(AF069441) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	389890
Contig ID	17510_2.R1084
5'-most EST	g572154
Seq. No.	389891
Contig ID	17513_1.R1084
5'-most EST	LIB3433-051-P1-K1-C10
Seq. No.	389892
Contig ID	17516_1.R1084
5'-most EST	g2280671
Method	BLASTX
NCBI GI	g2760830
BLAST score	511
E value	9.0e-52
Match length	109
% identity	83
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
Seq. No.	389893
Contig ID	17517_1.R1084
5'-most EST	LIB3433-051-P1-K1-C3
Seq. No.	389894
Contig ID	17521_1.R1084
5'-most EST	uC-osrocyp005a10a1
Method	BLASTX
NCBI GI	g4454482
BLAST score	680
E value	2.0e-71
Match length	268
% identity	52
NCBI Description	(AC006234) hypothetical protein [Arabidopsis thaliana]
Seq. No.	389895
Contig ID	17524_1.R1084
5'-most EST	g5607323
Seq. No.	389896
Contig ID	17525_1.R1084
5'-most EST	LIB3433-053-P1-K1-F3
Seq. No.	389897
Contig ID	17527_1.R1084
5'-most EST	uC-osrocyp008h07b1
Method	BLASTX
NCBI GI	g1076809
BLAST score	1254
E value	1.0e-138
Match length	268
% identity	91
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - maize >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase [Zea mays]
Seq. No.	389898

Contig ID	17527_3.R1084
5'-most EST	g2427524
Method	BLASTX
NCBI GI	g1076809
BLAST score	947
E value	1.0e-103
Match length	198
% identity	93
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - maize >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase [Zea mays]

Seq. No.	389899
Contig ID	17529_1.R1084
5'-most EST	LIB3434-048-P1-K1-G6

Seq. No.	389900
Contig ID	17530_1.R1084
5'-most EST	LIB3433-051-P1-K1-D5

Seq. No.	389901
Contig ID	17533_1.R1084
5'-most EST	LIB3433-051-P1-K1-E1
Method	BLASTX
NCBI GI	g2598575
BLAST score	336
E value	3.0e-31
Match length	119
% identity	60
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	389902
Contig ID	17536_1.R1084
5'-most EST	LIB3433-051-P1-K1-E12
Method	BLASTX
NCBI GI	g4914371
BLAST score	270
E value	3.0e-23
Match length	178
% identity	31
NCBI Description	(AC007584) unknown protein [Arabidopsis thaliana]

Seq. No.	389903
Contig ID	17539_1.R1084
5'-most EST	LIB3434-029-P1-K1-E11

Seq. No.	389904
Contig ID	17542_1.R1084
5'-most EST	LIB3433-051-P1-K1-E8

Seq. No.	389905
Contig ID	17561_1.R1084
5'-most EST	uC-osroM202029c06a1
Method	BLASTX
NCBI GI	g584861
BLAST score	198
E value	3.0e-15

Match length	72
% identity	54
NCBI Description	CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4) >gi_480396_pir__S36806 cytochrome P450 71A2 - eggplant >gi_408140_emb_CAA50645_ (X71654) P450 hydroxylase [Solanum melongena] >gi_441185_dbj_BAA03635_ (D14990) Cytochrome P-450EG4 [Solanum melongena]

Seq. No.	389906
Contig ID	17564_1.R1084
5'-most EST	LIB3433-051-P1-K1-G8

Seq. No.	389907
Contig ID	17567_1.R1084
5'-most EST	LIB3433-051-P1-K1-H6

Seq. No.	389908
Contig ID	17569_1.R1084
5'-most EST	g2312307
Method	BLASTX
NCBI GI	g4206196
BLAST score	272
E value	3.0e-29
Match length	175
% identity	45
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389909
Contig ID	17570_1.R1084
5'-most EST	uC-osf1cyp012e02b1
Method	BLASTX
NCBI GI	g4886271
BLAST score	545
E value	9.0e-56
Match length	145
% identity	70
NCBI Description	(AL050300) putative protein [Arabidopsis thaliana]

Seq. No.	389910
Contig ID	17574_1.R1084
5'-most EST	uC-osroM202039h11a1

Seq. No.	389911
Contig ID	17581_1.R1084
5'-most EST	LIB3433-052-P1-K1-A4
Method	BLASTN
NCBI GI	g2463510
BLAST score	74
E value	4.0e-33
Match length	162
% identity	24
NCBI Description	Z.mays small nuclear RNA genes snoR1.1, snoR2.2, snoR3.2, U14.1a, U14.1b, U14.1c and U14.1d

Seq. No.	389912
Contig ID	17582_1.R1084
5'-most EST	LIB3434-027-P1-K1-C4

Method	BLASTX
NCBI GI	g4582434
BLAST score	426
E value	1.0e-41
Match length	93
% identity	90
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	389913
Contig ID	17585_1.R1084
5'-most EST	LIB3433-052-P1-K1-A8

Seq. No.	389914
Contig ID	17586_1.R1084
5'-most EST	g700445
Method	BLASTX
NCBI GI	g3183106
BLAST score	473
E value	5.0e-47
Match length	213
% identity	45
NCBI Description	PROBABLE OXALYL-COA DECARBOXYLASE >gi_1788716 (AE000325) putative enzyme [Escherichia coli]

Seq. No.	389915
Contig ID	17588_1.R1084
5'-most EST	LIB3433-059-P1-K1-B4
Method	BLASTX
NCBI GI	g2795803
BLAST score	292
E value	6.0e-42
Match length	247
% identity	21
NCBI Description	(AC003674) putative beta-1,3-endoglucanase [Arabidopsis thaliana] >gi_3355491 (AC004218) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	389916
Contig ID	17595_1.R1084
5'-most EST	LIB3475-005-P1-K1-H9
Method	BLASTX
NCBI GI	g2493318
BLAST score	234
E value	4.0e-19
Match length	99
% identity	47
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	389917
Contig ID	17603_1.R1084
5'-most EST	LIB3433-052-P1-K1-D1
Method	BLASTX
NCBI GI	g4587550
BLAST score	172
E value	5.0e-12

Match length	65
% identity	51
NCBI Description	(AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No.	389918
Contig ID	17607_1.R1084
5'-most EST	uC-osflcyp159h04b1
Method	BLASTX
NCBI GI	g1352468
BLAST score	397
E value	2.0e-77
Match length	189
% identity	85
NCBI Description	BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) >gi_1122439 (U16123) invertase [Zea mays]

Seq. No.	389919
Contig ID	17608_1.R1084
5'-most EST	g428121
Method	BLASTX
NCBI GI	g4538911
BLAST score	329
E value	3.0e-30
Match length	174
% identity	40
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389920
Contig ID	17612_1.R1084
5'-most EST	g2310139

Seq. No.	389921
Contig ID	17615_1.R1084
5'-most EST	uC-osflcyp012a02b1

Seq. No.	389922
Contig ID	17619_1.R1084
5'-most EST	g3768692
Method	BLASTX
NCBI GI	g1362093
BLAST score	562
E value	2.0e-57
Match length	169
% identity	66
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	389923
Contig ID	17621_1.R1084
5'-most EST	g427372
Method	BLASTX
NCBI GI	g4454466
BLAST score	184
E value	3.0e-13
Match length	57

% identity	58
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	389924
Contig ID	17624_1.R1084
5'-most EST	LIB3433-052-P1-K1-F7
Method	BLASTX
NCBI GI	g3660471
BLAST score	926
E value	1.0e-118
Match length	226
% identity	92
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No.	389925
Contig ID	17629_1.R1084
5'-most EST	LIB3433-052-P1-K1-F9

Seq. No.	389926
Contig ID	17636_1.R1084
5'-most EST	LIB3433-052-P1-K1-G5
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	4.0e-10
Match length	35
% identity	37
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	389927
Contig ID	17637_1.R1084
5'-most EST	uC-osflcyp152g04b1
Method	BLASTX
NCBI GI	g4455210
BLAST score	690
E value	3.0e-78
Match length	239
% identity	63
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	389928
Contig ID	17639_1.R1084
5'-most EST	g700415

Seq. No.	389929
Contig ID	17652_1.R1084
5'-most EST	g2280769
Method	BLASTX
NCBI GI	g4469025
BLAST score	177
E value	9.0e-13
Match length	54
% identity	46
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	389930
Contig ID	17652_2.R1084
5'-most EST	g286393
Method	BLASTX
NCBI GI	g4469025
BLAST score	329
E value	1.0e-30
Match length	76
% identity	58
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	389931
Contig ID	17656_1.R1084
5'-most EST	LIB3433-053-P1-K1-A3
Method	BLASTX
NCBI GI	g2119757
BLAST score	549
E value	4.0e-56
Match length	121
% identity	79
NCBI Description	glucose starvation-induced protein precursor (clone pZSS2) - maize >gi_559534_emb_CAA57674_ (X82184) defence-related protein [Zea mays]

Seq. No.	389932
Contig ID	17657_1.R1084
5'-most EST	g3759945
Method	BLASTN
NCBI GI	g433815
BLAST score	322
E value	0.0e+00
Match length	605
% identity	28
NCBI Description	O.sativa gene for hydroxyproline-rich glycoprotein

Seq. No.	389933
Contig ID	17663_1.R1084
5'-most EST	g4716036
Method	BLASTX
NCBI GI	g4539348
BLAST score	217
E value	2.0e-17
Match length	91
% identity	57
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	389934
Contig ID	17676_1.R1084
5'-most EST	LIB3433-053-P1-K1-C11
Method	BLASTX
NCBI GI	g2459429
BLAST score	566
E value	3.0e-58
Match length	135
% identity	77
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	389935
Contig ID	17677_1.R1084
5'-most EST	g5455556
Method	BLASTX
NCBI GI	g567893
BLAST score	201
E value	7.0e-24
Match length	70
% identity	75
NCBI Description	(L37382) beta-galactosidase-complementation protein [Cloning vector]

Seq. No.	389936
Contig ID	17677_2.R1084
5'-most EST	g286618
Method	BLASTN
NCBI GI	g5922603
BLAST score	51
E value	2.0e-19
Match length	71
% identity	17
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No.	389937
Contig ID	17679_1.R1084
5'-most EST	g701909
Method	BLASTX
NCBI GI	g2244840
BLAST score	135
E value	1.0e-11
Match length	109
% identity	48
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389938
Contig ID	17684_1.R1084
5'-most EST	g428549
Method	BLASTX
NCBI GI	g549736
BLAST score	185
E value	2.0e-13
Match length	98
% identity	45
NCBI Description	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION >gi_539212_pir__S38002 hypothetical protein YKL172w - yeast (Saccharomyces cerevisiae) >gi_407510_emb_CAA81515_ (Z26878) unknown [Saccharomyces cerevisiae] >gi_486302_emb_CAA82014_ (Z28172) ORF YKL172w [Saccharomyces cerevisiae] >gi_1582533_prf__2118403G ORF [Saccharomyces cerevisiae]

Seq. No.	389939
Contig ID	17691_1.R1084
5'-most EST	g5003030
Method	BLASTX
NCBI GI	g2160177
BLAST score	310

E value	5.0e-28
Match length	134
% identity	43
NCBI Description	(AC000132) EST gb_R64758 comes from this gene. [Arabidopsis thaliana]

Seq. No.	389940
Contig ID	17707_1.R1084
5'-most EST	LIB3433-053-P1-K1-E8
Method	BLASTX
NCBI GI	g2129742
BLAST score	263
E value	1.0e-22
Match length	71
% identity	65
NCBI Description	stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	389941
Contig ID	17708_1.R1084
5'-most EST	LIB3434-042-P1-K1-D4
Method	BLASTX
NCBI GI	g1888551
BLAST score	364
E value	2.0e-34
Match length	143
% identity	50
NCBI Description	(U89895) pathogenesis-related protein class 1 [Oryza sativa]

Seq. No.	389942
Contig ID	17718_1.R1084
5'-most EST	LIB3433-053-P1-K1-F9
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	8.0e-10
Match length	35
% identity	42
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389943
Contig ID	17719_1.R1084
5'-most EST	g568082
Method	BLASTX
NCBI GI	g3914685
BLAST score	804
E value	9.0e-86
Match length	171
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal protein L17 [Zea mays]

Seq. No.	389944
Contig ID	17720_1.R1084
5'-most EST	LIB3433-053-P1-K1-G10
Method	BLASTX
NCBI GI	g5107180
BLAST score	312
E value	2.0e-28
Match length	75
% identity	71
NCBI Description	(AF150096) small zinc finger-like protein [Lycopersicon esculentum]

Seq. No.	389945
Contig ID	17721_1.R1084
5'-most EST	LIB3433-053-P1-K1-G11
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	50
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389946
Contig ID	17726_1.R1084
5'-most EST	g2428816
Method	BLASTX
NCBI GI	g4557647
BLAST score	149
E value	3.0e-09
Match length	56
% identity	50
NCBI Description	heat shock factor binding protein 1 >gi_3283409 (AF068754) heat shock factor binding protein 1 HSBP1 [Homo sapiens]

Seq. No.	389947
Contig ID	17728_1.R1084
5'-most EST	LIB3434-013-P1-K1-B4
Method	BLASTX
NCBI GI	g1370601
BLAST score	824
E value	2.0e-88
Match length	184
% identity	43
NCBI Description	(X98244) annexin p33 [Zea mays]

Seq. No.	389948
Contig ID	17742_1.R1084
5'-most EST	LIB3433-026-P1-K1-A1

Seq. No.	389949
Contig ID	17746_1.R1084
5'-most EST	g568521
Method	BLASTX
NCBI GI	g4263787
BLAST score	229
E value	6.0e-29

Match length	95
% identity	73
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	389950
Contig ID	17747_1.R1084
5'-most EST	LIB3433-054-P1-K1-A7
Method	BLASTN
NCBI GI	g6015437
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389951
Contig ID	17748_1.R1084
5'-most EST	LIB3433-054-P1-K1-A8
Method	BLASTX
NCBI GI	g3600031
BLAST score	299
E value	2.0e-33
Match length	154
% identity	53
NCBI Description	(AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolases [Arabidopsis thaliana]

Seq. No.	389952
Contig ID	17750_1.R1084
5'-most EST	g5607540
Method	BLASTN
NCBI GI	g1184323
BLAST score	82
E value	7.0e-38
Match length	119
% identity	94
NCBI Description	Cloning vector pCRSCRIPT Direct, complete sequence

Seq. No.	389953
Contig ID	17752_1.R1084
5'-most EST	g2442744
Method	BLASTX
NCBI GI	g2388585
BLAST score	479
E value	5.0e-48
Match length	142
% identity	68
NCBI Description	(AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb_U88169). [Arabidopsis thaliana]

Seq. No.	389954
Contig ID	17756_2.R1084
5'-most EST	LIB3433-054-P1-K1-B4

Seq. No.	389955
Contig ID	17758_1.R1084
5'-most EST	uC-osf1M202069b07a1

Seq. No.	389956
Contig ID	17762_1.R1084
5'-most EST	g3768097

Seq. No.	389957
Contig ID	17764_1.R1084
5'-most EST	LIB3434-058-P1-K1-A5
Method	BLASTX
NCBI GI	g3617770
BLAST score	811
E value	8.0e-87
Match length	202
% identity	74
NCBI Description	(Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	389958
Contig ID	17765_1.R1084
5'-most EST	uC-osflcyp033d07b1

Seq. No.	389959
Contig ID	17766_1.R1084
5'-most EST	LIB3433-054-P1-K1-C8
Method	BLASTX
NCBI GI	g4539301
BLAST score	303
E value	1.0e-27
Match length	75
% identity	76
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	389960
Contig ID	17769_1.R1084
5'-most EST	g700567
Method	BLASTX
NCBI GI	g4263779
BLAST score	149
E value	3.0e-09
Match length	141
% identity	27
NCBI Description	(AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	389961
Contig ID	17774_1.R1084
5'-most EST	g2310203
Method	BLASTX
NCBI GI	g3337356
BLAST score	1435
E value	1.0e-159
Match length	305
% identity	90
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	389962
Contig ID	17775_1.R1084

5'-most EST	LIB3433-017-Q6-K1-B6
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	4.0e-11
Match length	49
% identity	49
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	389963
Contig ID	17779_1.R1084
5'-most EST	LIB3434-029-P1-K1-E3
Method	BLASTX
NCBI GI	g5080825
BLAST score	896
E value	1.0e-96
Match length	273
% identity	60
NCBI Description	(AC007258) Putative Aldo/keto reductase [Arabidopsis thaliana]

Seq. No.	389964
Contig ID	17780_1.R1084
5'-most EST	LIB3433-054-P1-K1-D4
Method	BLASTX
NCBI GI	g4887131
BLAST score	554
E value	1.0e-56
Match length	174
% identity	61
NCBI Description	(AF134732) 60S ribosomal protein L1 [Prunus armeniaca]

Seq. No.	389965
Contig ID	17795_1.R1084
5'-most EST	LIB3433-054-P1-K1-E9

Seq. No.	389966
Contig ID	17809_1.R1084
5'-most EST	g2312879

Seq. No.	389967
Contig ID	17812_1.R1084
5'-most EST	uC-osroM202017c12b1
Method	BLASTX
NCBI GI	g4263704
BLAST score	411
E value	1.0e-40
Match length	171
% identity	54
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	389968
Contig ID	17823_1.R1084
5'-most EST	LIB3433-054-P1-K1-H4
Method	BLASTX
NCBI GI	g4895248

BLAST score	1461
E value	1.0e-163
Match length	322
% identity	86
NCBI Description	(AC007659) putative mitochondrial elongation factor G [Arabidopsis thaliana]

Seq. No.	389969
Contig ID	17824_1.R1084
5'-most EST	LIB3433-054-P1-K1-H7

Seq. No.	389970
Contig ID	17842_1.R1084
5'-most EST	LIB3433-055-P1-K1-B2
Method	BLASTX
NCBI GI	g3461820
BLAST score	130
E value	4.0e-15
Match length	149
% identity	34
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	389971
Contig ID	17849_1.R1084
5'-most EST	LIB3433-055-P1-K1-C1
Method	BLASTX
NCBI GI	g3421104
BLAST score	751
E value	1.0e-79
Match length	193
% identity	80
NCBI Description	(AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis thaliana]

Seq. No.	389972
Contig ID	17853_1.R1084
5'-most EST	g428647
Method	BLASTX
NCBI GI	g3033397
BLAST score	1188
E value	1.0e-131
Match length	293
% identity	75
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	389973
Contig ID	17854_1.R1084
5'-most EST	uC-osflcyp055g06b1
Method	BLASTX
NCBI GI	g4206122
BLAST score	808
E value	2.0e-86
Match length	208
% identity	75
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	389974
Contig ID	17865_1.R1084
5'-most EST	LIB3433-055-P1-K1-D2
Method	BLASTX
NCBI GI	g1723239
BLAST score	263
E value	8.0e-23
Match length	111
% identity	49
NCBI Description	HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I >gi_1177358_emb_CAA93234_ (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]

Seq. No.	389975
Contig ID	17868_1.R1084
5'-most EST	LIB3433-055-P1-K1-D5
Method	BLASTX
NCBI GI	g5051782
BLAST score	887
E value	1.0e-95
Match length	266
% identity	62
NCBI Description	(AL078637) serine/threonine kinase-like protein [Arabidopsis thaliana]

Seq. No.	389976
Contig ID	17868_2.R1084
5'-most EST	uC-osflcyp168a04b1

Seq. No.	389977
Contig ID	17871_1.R1084
5'-most EST	LIB3433-055-P1-K1-D8

Seq. No.	389978
Contig ID	17872_1.R1084
5'-most EST	LIB3433-055-P1-K1-D9
Method	BLASTX
NCBI GI	g2388580
BLAST score	1173
E value	1.0e-129
Match length	259
% identity	81
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	389979
Contig ID	17876_1.R1084
5'-most EST	g2311001
Method	BLASTX
NCBI GI	g5091616
BLAST score	522
E value	1.0e-52
Match length	352
% identity	40
NCBI Description	(AC007454) F23M19.3 [Arabidopsis thaliana]

Seq. No.	389980

Contig ID	17879_1.R1084
5'-most EST	LIB3433-055-P1-K1-E4
Seq. No.	389981
Contig ID	17882_1.R1084
5'-most EST	LIB3434-044-P1-K1-B10
Seq. No.	389982
Contig ID	17884_1.R1084
5'-most EST	LIB3433-056-P1-K1-F9
Seq. No.	389983
Contig ID	17885_1.R1084
5'-most EST	uC-osflcyp152a03b1
Method	BLASTX
NCBI GI	g1762945
BLAST score	416
E value	2.0e-40
Match length	148
% identity	53
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]
Seq. No.	389984
Contig ID	17885_2.R1084
5'-most EST	LIB3434-042-P1-K1-H4
Method	BLASTX
NCBI GI	g1762945
BLAST score	375
E value	8.0e-36
Match length	143
% identity	48
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]
Seq. No.	389985
Contig ID	17896_1.R1084
5'-most EST	g1944237
Method	BLASTX
NCBI GI	g2119076
BLAST score	255
E value	1.0e-21
Match length	102
% identity	57
NCBI Description	ribosomal protein S10 - potato mitochondrion
Seq. No.	389986
Contig ID	17907_1.R1084
5'-most EST	uC-osflcyp009a08b1
Seq. No.	389987
Contig ID	17909_1.R1084
5'-most EST	LIB3433-055-P1-K1-H2
Method	BLASTX
NCBI GI	g3766535
BLAST score	547
E value	8.0e-56

Match length 155
% identity 68
NCBI Description (Y11687) 14-3-3 protein [Solanum tuberosum]

Seq. No. 389988
Contig ID 17914_1.R1084
5'-most EST uC-osflcyp079e01a1

Seq. No. 389989
Contig ID 17915_1.R1084
5'-most EST LIB3433-055-P1-K1-H9
Method BLASTX
NCBI GI g2832300
BLAST score 470
E value 7.0e-53
Match length 160
% identity 66
NCBI Description (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus roseus]

Seq. No. 389990
Contig ID 17918_1.R1084
5'-most EST LIB3433-056-P1-K1-A8
Method BLASTX
NCBI GI g3461839
BLAST score 346
E value 2.0e-32
Match length 158
% identity 49
NCBI Description (AC005315) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 389991
Contig ID 17923_1.R1084
5'-most EST uC-osflcyp029b10b1
Method BLASTX
NCBI GI g2224911
BLAST score 758
E value 2.0e-80
Match length 172
% identity 84
NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No. 389992
Contig ID 17927_1.R1084
5'-most EST g4715313
Method BLASTX
NCBI GI g4371285
BLAST score 420
E value 2.0e-41
Match length 106
% identity 77
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 389993
Contig ID 17933_1.R1084

5'-most EST	LIB3433-019-P1-K1-C5
Method	BLASTX
NCBI GI	g2772934
BLAST score	682
E value	2.0e-71
Match length	213
% identity	59
NCBI Description	(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis thaliana]

Seq. No.	389994
Contig ID	17941_1.R1084
5'-most EST	LIB3433-056-P1-K1-C9
Method	BLASTX
NCBI GI	g3858935
BLAST score	440
E value	1.0e-46
Match length	134
% identity	73
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	389995
Contig ID	17943_1.R1084
5'-most EST	LIB3433-056-P1-K1-D11

Seq. No.	389996
Contig ID	17951_1.R1084
5'-most EST	g4969028
Method	BLASTX
NCBI GI	g4680212
BLAST score	195
E value	1.0e-14
Match length	42
% identity	83
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	389997
Contig ID	17952_1.R1084
5'-most EST	g2428473

Seq. No.	389998
Contig ID	17955_1.R1084
5'-most EST	LIB3434-034-P1-K1-E8
Method	BLASTX
NCBI GI	g4836805
BLAST score	196
E value	8.0e-15
Match length	82
% identity	43
NCBI Description	(AF146793) protein B [Mus musculus]

Seq. No.	389999
Contig ID	17962_1.R1084
5'-most EST	LIB3433-056-P1-K1-F2

Method	BLASTX
NCBI GI	g2828296
BLAST score	465
E value	2.0e-46
Match length	129
% identity	42
NCBI Description	(AL021687) RNase L inhibitor-like protein [Arabidopsis thaliana]

Seq. No.	390000
Contig ID	17970_1.R1084
5'-most EST	LIB3433-056-P1-K1-G10
Method	BLASTX
NCBI GI	g3108209
BLAST score	462
E value	5.0e-46
Match length	116
% identity	70
NCBI Description	(AF028809) eukaryotic cap-binding protein [Arabidopsis thaliana]

Seq. No.	390001
Contig ID	17975_1.R1084
5'-most EST	g428580
Method	BLASTX
NCBI GI	g2494132
BLAST score	320
E value	2.0e-38
Match length	127
% identity	62
NCBI Description	(AC002376) Contains similarity to human dimethylaniline monooxygenase (gb_M64082). [Arabidopsis thaliana]

Seq. No.	390002
Contig ID	17976_1.R1084
5'-most EST	g3766763

Seq. No.	390003
Contig ID	17979_1.R1084
5'-most EST	g3766586
Method	BLASTX
NCBI GI	g5833467
BLAST score	450
E value	9.0e-53
Match length	145
% identity	70
NCBI Description	(AF158602) monodehydroascorbate reductase [Zantedeschia aethiopica]

Seq. No.	390004
Contig ID	17990_1.R1084
5'-most EST	LIB3433-017-Q6-K1-E10
Method	BLASTX
NCBI GI	g4006893
BLAST score	930
E value	1.0e-100
Match length	218

% identity	76
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	390005
Contig ID	17993_1.R1084
5'-most EST	g287156
Method	BLASTX
NCBI GI	g5106764
BLAST score	976
E value	1.0e-106
Match length	420
% identity	51
NCBI Description	(AF073329) eukaryotic translation initiation factor 3 large subunit [Zea mays]

Seq. No.	390006
Contig ID	17997_1.R1084
5'-most EST	LIB3433-057-P1-K1-A9
Method	BLASTX
NCBI GI	g1888357
BLAST score	559
E value	3.0e-57
Match length	169
% identity	65
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	390007
Contig ID	17999_1.R1084
5'-most EST	g2280781

Seq. No.	390008
Contig ID	18001_1.R1084
5'-most EST	LIB3434-004-P1-K1-B1
Method	BLASTX
NCBI GI	g5230728
BLAST score	1036
E value	1.0e-113
Match length	248
% identity	79
NCBI Description	(AF089851) peroxisomal copper-containing amine oxidase [Glycine max]

Seq. No.	390009
Contig ID	18002_1.R1084
5'-most EST	g286842
Method	BLASTX
NCBI GI	g2981475
BLAST score	841
E value	3.0e-90
Match length	219
% identity	72
NCBI Description	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]

Seq. No.	390010

Contig ID	18005_1.R1084
5'-most EST	LIB3433-057-P1-K1-B6
Seq. No.	390011
Contig ID	18014_1.R1084
5'-most EST	LIB3433-057-P1-K1-C4
Seq. No.	390012
Contig ID	18022_1.R1084
5'-most EST	LIB3433-057-P1-K1-D11
Method	BLASTX
NCBI GI	g4760370
BLAST score	492
E value	2.0e-49
Match length	155
% identity	68
NCBI Description	(AF082565) ATP dependent copper transporter [Arabidopsis thaliana] >gi_4760380_gb_AAD29115.1_ (AF091112) ATP dependent copper transporter [Arabidopsis thaliana]
Seq. No.	390013
Contig ID	18024_1.R1084
5'-most EST	g4716445
Method	BLASTX
NCBI GI	g4105798
BLAST score	567
E value	4.0e-58
Match length	248
% identity	48
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.	390014
Contig ID	18027_1.R1084
5'-most EST	LIB3434-042-P1-K1-B5
Method	BLASTX
NCBI GI	g4874273
BLAST score	381
E value	2.0e-75
Match length	225
% identity	63
NCBI Description	(AC007354) Similar to gi_3128199 F4I1.5 putative proteinase from Arabidopsis thaliana BAC gb_AC004521
Seq. No.	390015
Contig ID	18037_1.R1084
5'-most EST	LIB3433-057-P1-K1-E7
Method	BLASTX
NCBI GI	g4490308
BLAST score	473
E value	2.0e-89
Match length	242
% identity	72
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]
Seq. No.	390016
Contig ID	18039_1.R1084
5'-most EST	g428171

Method	BLASTX
NCBI GI	g1171577
BLAST score	209
E value	6.0e-16
Match length	241
% identity	29
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.	390017
Contig ID	18046_1.R1084
5'-most EST	LIB3434-024-P1-K1-E3

Seq. No.	390018
Contig ID	18047_1.R1084
5'-most EST	uC-osflcyp037h09b1
Method	BLASTX
NCBI GI	g3894172
BLAST score	331
E value	2.0e-30
Match length	208
% identity	37
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	390019
Contig ID	18055_1.R1084
5'-most EST	LIB3474-006-P1-K1-A9
Method	BLASTX
NCBI GI	g4966343
BLAST score	691
E value	9.0e-73
Match length	204
% identity	63
NCBI Description	(AC006341) Is a member of PF_00481 Protein phosphatase 2C family. [Arabidopsis thaliana]

Seq. No.	390020
Contig ID	18058_1.R1084
5'-most EST	uC-osflcyp086a11a1

Seq. No.	390021
Contig ID	18059_1.R1084
5'-most EST	LIB3477-005-P1-K1-C7
Method	BLASTX
NCBI GI	g1076715
BLAST score	413
E value	4.0e-40
Match length	104
% identity	69
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	390022
Contig ID	18061_1.R1084
5'-most EST	g2310508
Method	BLASTX
NCBI GI	g4056568

BLAST score	589
E value	1.0e-120
Match length	328
% identity	30
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	390023
Contig ID	18064_1.R1084
5'-most EST	LIB3433-057-P1-K1-H2
Method	BLASTX
NCBI GI	g2245000
BLAST score	246
E value	1.0e-20
Match length	72
% identity	62
NCBI Description	(Z97341) LET1 like protein [Arabidopsis thaliana]

Seq. No.	390024
Contig ID	18066_1.R1084
5'-most EST	LIB3433-057-P1-K1-H4

Seq. No.	390025
Contig ID	18068_1.R1084
5'-most EST	LIB3433-057-P1-K1-H6
Method	BLASTX
NCBI GI	g3123244
BLAST score	183
E value	1.0e-14
Match length	132
% identity	40
NCBI Description	ALPHA-MANNOSIDASE IIX (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX) >gi_1132479_dbj_BAA09510_ (D55649) alpha mannosidase II isozyme [Homo sapiens]

Seq. No.	390026
Contig ID	18069_1.R1084
5'-most EST	g701968
Method	BLASTX
NCBI GI	g2129550
BLAST score	761
E value	1.0e-122
Match length	292
% identity	76
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	390027
Contig ID	18071_1.R1084
5'-most EST	LIB3433-057-P1-K1-H9
Method	BLASTX

NCBI GI	g6063548
BLAST score	534
E value	2.0e-54
Match length	102
% identity	100
NCBI Description	(AP000615) ESTs AU078175(C51476),AU068986(C51476) correspond to a region of the predicted gene.; similar to NADH dehydrogenase. (AC006532) [Oryza sativa]

Seq. No.	390028
Contig ID	18072_1.R1084
5'-most EST	g3763205
Method	BLASTN
NCBI GI	g2645165
BLAST score	89
E value	4.0e-42
Match length	111
% identity	95
NCBI Description	Oryza sativa mRNA, similar to ribosomal protein

Seq. No.	390029
Contig ID	18074_1.R1084
5'-most EST	g5002870
Method	BLASTX
NCBI GI	g4827050
BLAST score	246
E value	1.0e-20
Match length	68
% identity	65
NCBI Description	ubiquitin specific protease 14 (tRNA-guanine transglycosylase) >gi_1729927_sp_P54578_TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi_940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]

Seq. No.	390030
Contig ID	18075_1.R1084
5'-most EST	g4880889

Seq. No.	390031
Contig ID	18079_1.R1084
5'-most EST	g2317393
Method	BLASTX
NCBI GI	g1504052
BLAST score	665
E value	1.0e-69
Match length	137
% identity	94
NCBI Description	(D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No.	390032
Contig ID	18080_1.R1084
5'-most EST	g286658

Seq. No.	390033
Contig ID	18081_1.R1084
5'-most EST	g3107321

Method	BLASTX
NCBI GI	g5441874
BLAST score	723
E value	9.0e-79
Match length	223
% identity	66
NCBI Description	(AP000366) Similar to maize transposon MuDR mudrA-like protein. (AC002340) [Oryza sativa]

Seq. No.	390034
Contig ID	18084_1.R1084
5'-most EST	g3768766
Method	BLASTX
NCBI GI	g2494075
BLAST score	878
E value	8.0e-95
Match length	175
% identity	96
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE [NADP+]) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1084478_pir__S43833 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - maize >gi_474408_emb_CAA53075_ (X75326) glyceraldehyde-3-phosphate dehydrogenase (GAPN) [Zea mays]

Seq. No.	390035
Contig ID	18089_1.R1084
5'-most EST	LIB3433-058-P1-K1-C11
Method	BLASTX
NCBI GI	g141435
BLAST score	244
E value	3.0e-20
Match length	110
% identity	43
NCBI Description	DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi_98360_pir__E37854 folate biosynthesis protein 1 (sul 3' region) - Bacillus subtilis >gi_143411 (M34053) ORF1 [Bacillus subtilis] >gi_467467_dbj_BAA05313_ (D26185) unknown [Bacillus subtilis] >gi_2632345_emb_CAB11854_ (Z99104) dihydroneopterin aldolase [Bacillus subtilis]

Seq. No.	390036
Contig ID	18091_1.R1084
5'-most EST	LIB3433-058-P1-K1-C3
Method	BLASTX
NCBI GI	g4165550
BLAST score	258
E value	1.0e-43
Match length	116
% identity	85
NCBI Description	(AJ004915) apgm [Malus domestica]

Seq. No.	390037
Contig ID	18094_1.R1084
5'-most EST	LIB3479-011-Q6-K1-A6

Method	BLASTX
NCBI GI	g6016872
BLAST score	316
E value	2.0e-43
Match length	130
% identity	75
NCBI Description	(AP000570) EST AU058127(S5254) corresponds to a region of the predicted gene.; Similar to dynein light chain 1, cytoplasmic. (Q24117) [Oryza sativa]

Seq. No.	390038
Contig ID	18104_1.R1084
5'-most EST	LIB3433-058-P1-K1-D5
Method	BLASTX
NCBI GI	g3421413
BLAST score	925
E value	1.0e-100
Match length	192
% identity	89
NCBI Description	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No.	390039
Contig ID	18112_1.R1084
5'-most EST	g5004732
Method	BLASTX
NCBI GI	g464621
BLAST score	626
E value	6.0e-65
Match length	217
% identity	60
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	390040
Contig ID	18112_3.R1084
5'-most EST	g4714290
Method	BLASTX
NCBI GI	g464621
BLAST score	453
E value	6.0e-45
Match length	121
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	390041
Contig ID	18121_1.R1084
5'-most EST	uC-osroM202021c06b1

Seq. No.	390042
Contig ID	18123_1.R1084

5'-most EST	LIB3434-038-P1-K1-B9
Method	BLASTX
NCBI GI	g2150000
BLAST score	541
E value	3.0e-55
Match length	153
% identity	61
NCBI Description	(AF000939) aleurone ribonuclease [Hordeum vulgare]

Seq. No.	390043
Contig ID	18128_1.R1084
5'-most EST	LIB3433-058-P1-K1-F8
Method	BLASTX
NCBI GI	g5932536
BLAST score	695
E value	3.0e-73
Match length	174
% identity	76
NCBI Description	(AC009465) unknown protein [Arabidopsis thaliana]

Seq. No.	390044
Contig ID	18145_1.R1084
5'-most EST	LIB3433-058-P1-K1-H5

Seq. No.	390045
Contig ID	18146_1.R1084
5'-most EST	LIB3433-058-P1-K1-H6

Seq. No.	390046
Contig ID	18146_2.R1084
5'-most EST	g702522

Seq. No.	390047
Contig ID	18148_1.R1084
5'-most EST	g2311414

Seq. No.	390048
Contig ID	18160_1.R1084
5'-most EST	g5038986
Method	BLASTX
NCBI GI	g5915819
BLAST score	554
E value	1.0e-56
Match length	159
% identity	64
NCBI Description	FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTOCHROME P450 75A6) >gi_1785488_dbj_BAA03440_ (D14590) flavonoid 3',5'-hydroxylase [Campanula medium]

Seq. No.	390049
Contig ID	18161_1.R1084
5'-most EST	LIB3433-059-P1-K1-B11
Method	BLASTX
NCBI GI	g3868853
BLAST score	410
E value	1.0e-39
Match length	105

% identity	70
NCBI Description	(AB013853) GPI-anchored protein [Vigna radiata]

Seq. No.	390050
Contig ID	18172_1.R1084
5'-most EST	LIB3433-059-P1-K1-C10

Seq. No.	390051
Contig ID	18175_2.R1084
5'-most EST	g2312250
Method	BLASTX
NCBI GI	g4262186
BLAST score	563
E value	5.0e-58
Match length	151
% identity	73
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	390052
Contig ID	18179_1.R1084
5'-most EST	g2311421
Method	BLASTX
NCBI GI	g464981
BLAST score	711
E value	2.0e-77
Match length	148
% identity	96
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	390053
Contig ID	18179_2.R1084
5'-most EST	LIB3434-040-P1-K1-F6
Method	BLASTX
NCBI GI	g464981
BLAST score	419
E value	1.0e-40
Match length	82
% identity	95
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	390054
Contig ID	18181_1.R1084
5'-most EST	g2427719

Seq. No.	390055
Contig ID	18183_1.R1084
5'-most EST	uC-osf1M202051g11b1
Method	BLASTX
NCBI GI	g3758827
BLAST score	431
E value	1.0e-44
Match length	135

% identity	67
NCBI Description	(AJ011921) amino acid selective channel protein [Hordeum vulgare]

Seq. No.	390056
Contig ID	18187_1.R1084
5'-most EST	g2427834
Method	BLASTX
NCBI GI	g6016679
BLAST score	326
E value	5.0e-30
Match length	156
% identity	46
NCBI Description	(AC009991) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	390057
Contig ID	18205_1.R1084
5'-most EST	uC-osroM202036b08b1
Method	BLASTX
NCBI GI	g5042456
BLAST score	811
E value	6.0e-87
Match length	178
% identity	89
NCBI Description	(AC007789) putative pathogenesis related protein [Oryza sativa]

Seq. No.	390058
Contig ID	18209_1.R1084
5'-most EST	g3766561

Seq. No.	390059
Contig ID	18211_1.R1084
5'-most EST	uC-osroM202022a05b1
Method	BLASTX
NCBI GI	g1946372
BLAST score	225
E value	2.0e-18
Match length	59
% identity	85
NCBI Description	(U93215) yeast hypothetical protein YDB1_SCHPO isolog [Arabidopsis thaliana]

Seq. No.	390060
Contig ID	18215_1.R1084
5'-most EST	LIB3433-059-P1-K1-G1

Seq. No.	390061
Contig ID	18216_1.R1084
5'-most EST	uC-osrocyp010c08a1

Seq. No.	390062
Contig ID	18218_1.R1084
5'-most EST	uC-osflM202016h08b1
Method	BLASTX
NCBI GI	g4539459

BLAST score	313
E value	2.0e-28
Match length	93
% identity	66
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	390063
Contig ID	18249_1.R1084
5'-most EST	LIB3433-060-P1-K1-B1
Method	BLASTX
NCBI GI	g4455213
BLAST score	629
E value	1.0e-65
Match length	149
% identity	79
NCBI Description	(AL035440) glutamine amidotransferase/cyclase [Arabidopsis thaliana]

Seq. No.	390064
Contig ID	18254_1.R1084
5'-most EST	LIB3433-060-P1-K1-B4
Method	BLASTX
NCBI GI	g1669655
BLAST score	553
E value	2.0e-56
Match length	269
% identity	44
NCBI Description	(X95962) CER3 [Arabidopsis thaliana]

Seq. No.	390065
Contig ID	18257_1.R1084
5'-most EST	LIB3475-007-P1-K1-B10
Method	BLASTX
NCBI GI	g6056194
BLAST score	128
E value	5.0e-12
Match length	92
% identity	40
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	390066
Contig ID	18264_1.R1084
5'-most EST	g701473
Method	BLASTX
NCBI GI	g6056200
BLAST score	231
E value	2.0e-28
Match length	126
% identity	65
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	390067
Contig ID	18266_1.R1084
5'-most EST	g2428364
Method	BLASTX
NCBI GI	g1151244
BLAST score	553

E value	4.0e-87
Match length	308
% identity	52
NCBI Description	(U43377) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	390068
Contig ID	18268_1.R1084
5'-most EST	LIB3434-013-P1-K1-H8
Method	BLASTX
NCBI GI	g1323742
BLAST score	296
E value	3.0e-26
Match length	158
% identity	39
NCBI Description	(U32427) unknown [Triticum aestivum]

Seq. No.	390069
Contig ID	18270_1.R1084
5'-most EST	LIB3433-060-P1-K1-C8
Method	BLASTX
NCBI GI	g4100325
BLAST score	490
E value	5.0e-59
Match length	209
% identity	62
NCBI Description	(U96736) SL-TPS/P [Selaginella lepidophylla]

Seq. No.	390070
Contig ID	18278_1.R1084
5'-most EST	g3548931

Seq. No.	390071
Contig ID	18281_1.R1084
5'-most EST	LIB3433-060-P1-K1-D8
Method	BLASTX
NCBI GI	g4741923
BLAST score	190
E value	5.0e-14
Match length	52
% identity	60
NCBI Description	(AF130849) PIT1 [Arabidopsis thaliana]

Seq. No.	390072
Contig ID	18282_1.R1084
5'-most EST	uC-osflM202094d12b1
Method	BLASTX
NCBI GI	g3805765
BLAST score	1125
E value	1.0e-123
Match length	330
% identity	65
NCBI Description	(AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No.	390073
Contig ID	18284_1.R1084
5'-most EST	g2800776
Method	BLASTN

NCBI GI	g416316
BLAST score	52
E value	4.0e-20
Match length	52
% identity	100
NCBI Description	Yeast integrative vector pRS405 with LEU2 marker, complete sequence

Seq. No.	390074
Contig ID	18293_1.R1084
5'-most EST	g568384
Method	BLASTX
NCBI GI	g100226
BLAST score	281
E value	8.0e-25
Match length	171
% identity	37
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	390075
Contig ID	18302_1.R1084
5'-most EST	LIB3433-060-P1-K1-F7
Method	BLASTX
NCBI GI	g4539465
BLAST score	217
E value	2.0e-17
Match length	123
% identity	40
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	390076
Contig ID	18303_1.R1084
5'-most EST	uC-osroM202023f11b1
Method	BLASTX
NCBI GI	g294845
BLAST score	496
E value	1.0e-93
Match length	294
% identity	61
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	390077
Contig ID	18308_1.R1084
5'-most EST	LIB3434-017-P1-K1-G11
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	36
% identity	59
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	390078

Contig ID	18310_1.R1084
5'-most EST	uC-osflcyp026e05b1
Method	BLASTX
NCBI GI	g2213583
BLAST score	508
E value	3.0e-51
Match length	229
% identity	44
NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No.	390079
Contig ID	18316_1.R1084
5'-most EST	LIB3434-018-P1-K1-F4
Method	BLASTX
NCBI GI	g1351974
BLAST score	574
E value	3.0e-59
Match length	114
% identity	97
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325 ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_ (X80042) ADP-ribosylation factor [Zea mays]

Seq. No.	390080
Contig ID	18323_1.R1084
5'-most EST	g2309925
Method	BLASTX
NCBI GI	g5902359
BLAST score	832
E value	6.0e-89
Match length	227
% identity	69
NCBI Description	(AC009322) Heat-shock protein [Arabidopsis thaliana]

Seq. No.	390081
Contig ID	18333_1.R1084
5'-most EST	g4716634
Method	BLASTX
NCBI GI	g2982311
BLAST score	163
E value	6.0e-15
Match length	109
% identity	47
NCBI Description	(AF051240) probable ubiquitin-conjugating enzyme E2 [Picea mariana]

Seq. No.	390082
Contig ID	18338_1.R1084
5'-most EST	g2312290

Seq. No.	390083
Contig ID	18343_1.R1084
5'-most EST	uC-osflM202053g11b1
Method	BLASTX
NCBI GI	g5257264
BLAST score	560

E value	4.0e-65
Match length	207
% identity	69
NCBI Description	(AP000364) ESTs AU064813(E40579),D24600(R2232) correspond to a region of the predicted gene.; Similar to Human mRNA for KIAA0255 gene. (D87444) [Oryza sativa]

Seq. No.	390084
Contig ID	18345_1.R1084
5'-most EST	g4716093
Method	BLASTX
NCBI GI	g4138583
BLAST score	673
E value	1.0e-70
Match length	178
% identity	76
NCBI Description	(Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No.	390085
Contig ID	18348_1.R1084
5'-most EST	LIB3433-061-P1-K1-B9
Method	BLASTX
NCBI GI	g5733831
BLAST score	351
E value	7.0e-33
Match length	221
% identity	38
NCBI Description	(AF026267) ethylene receptor homolog [Nicotiana tabacum]

Seq. No.	390086
Contig ID	18355_1.R1084
5'-most EST	uC-osroM202035c12b1
Method	BLASTX
NCBI GI	g1684851
BLAST score	191
E value	2.0e-14
Match length	64
% identity	59
NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No.	390087
Contig ID	18359_1.R1084
5'-most EST	LIB3433-061-P1-K1-D10

Seq. No.	390088
Contig ID	18375_1.R1084
5'-most EST	uC-osflcyp080f03b1
Method	BLASTX
NCBI GI	g1168654
BLAST score	291
E value	6.0e-26
Match length	73
% identity	67
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) - garden asparagus >gi_452712_emb_CAA54525_ (X77319) beta-galactosidase [Asparagus officinalis]

Seq. No. 390089
Contig ID 18377_1.R1084
5'-most EST LIB3434-015-P1-K1-E12

Seq. No. 390090
Contig ID 18382_1.R1084
5'-most EST LIB3433-061-P1-K1-F12
Method BLASTX
NCBI GI g1871192
BLAST score 147
E value 9.0e-09
Match length 87
% identity 41
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 390091
Contig ID 18393_1.R1084
5'-most EST uC-osflcyp021e12b1

Seq. No. 390092
Contig ID 18401_1.R1084
5'-most EST LIB3433-061-P1-K1-H10

Seq. No. 390093
Contig ID 18404_1.R1084
5'-most EST LIB3434-005-P1-K1-H12
Method BLASTX
NCBI GI g4091008
BLAST score 874
E value 3.0e-94
Match length 200
% identity 78
NCBI Description (AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No. 390094
Contig ID 18409_1.R1084
5'-most EST g3107777
Method BLASTX
NCBI GI g3157933
BLAST score 192
E value 3.0e-14
Match length 91
% identity 43
NCBI Description (AC002131) Contains similarity to box helicases gb_U29097 from C. elegans and to the ENBP1 gene product gb_X95995 from Vicia sativa. [Arabidopsis thaliana]

Seq. No. 390095
Contig ID 18416_1.R1084
5'-most EST uC-osflcyp128d04a1

Seq. No. 390096
Contig ID 18418_1.R1084
5'-most EST LIB3433-015-Q6-K1-A9
Method BLASTX

NCBI GI	g5541704
BLAST score	476
E value	2.0e-47
Match length	103
% identity	88
NCBI Description	(AL096860) 40S RIBOSOMAL PROTEIN S20 homolog [Arabidopsis thaliana]

Seq. No.	390097
Contig ID	18418_2.R1084
5'-most EST	LIB3434-024-P1-K1-B11
Method	BLASTX
NCBI GI	g5541704
BLAST score	476
E value	2.0e-47
Match length	103
% identity	88
NCBI Description	(AL096860) 40S RIBOSOMAL PROTEIN S20 homolog [Arabidopsis thaliana]

Seq. No.	390098
Contig ID	18419_1.R1084
5'-most EST	LIB3433-015-Q6-K1-B1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	47
% identity	65
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	390099
Contig ID	18420_1.R1084
5'-most EST	uC-osflm202108a06b1
Method	BLASTX
NCBI GI	g4204286
BLAST score	151
E value	2.0e-09
Match length	125
% identity	39
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	390100
Contig ID	18421_1.R1084
5'-most EST	g3107821
Method	BLASTX
NCBI GI	g3885329
BLAST score	1061
E value	1.0e-116
Match length	259
% identity	80
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	390101
Contig ID	18421_2.R1084
5'-most EST	uC-osflcyp156h08b1
Method	BLASTX

NCBI GI	g3885329
BLAST score	713
E value	2.0e-75
Match length	163
% identity	83
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	390102
Contig ID	18423_1.R1084
5'-most EST	LIB3433-015-Q6-K1-B3
Method	BLASTX
NCBI GI	g4544445
BLAST score	579
E value	1.0e-59
Match length	185
% identity	54
NCBI Description	(AC006592) putative pyrophosphate--fructose 6-phosphate 1-phosphotransferase [Arabidopsis thaliana]

Seq. No.	390103
Contig ID	18424_1.R1084
5'-most EST	g2428320
Method	BLASTX
NCBI GI	g4512712
BLAST score	344
E value	9.0e-32
Match length	167
% identity	43
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	390104
Contig ID	18425_1.R1084
5'-most EST	LIB3433-015-Q6-K6-B5
Method	BLASTX
NCBI GI	g1173624
BLAST score	488
E value	3.0e-49
Match length	141
% identity	64
NCBI Description	(U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid SM9108']

Seq. No.	390105
Contig ID	18427_1.R1084
5'-most EST	LIB3433-015-Q6-K1-B7
Method	BLASTX
NCBI GI	g4406810
BLAST score	339
E value	9.0e-32
Match length	90
% identity	64
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	390106
Contig ID	18430_1.R1084
5'-most EST	LIB3433-015-Q6-K6-C1
Method	BLASTN

NCBI GI g3983664
BLAST score 100
E value 7.0e-49
Match length 344
% identity 83
NCBI Description Oryza sativa mRNA for importin-beta2, partial cds

Seq. No. 390107
Contig ID 18431_1.R1084
5'-most EST LIB3433-015-Q6-K6-C10

Seq. No. 390108
Contig ID 18432_1.R1084
5'-most EST LIB3433-015-Q6-K1-C11
Method BLASTX
NCBI GI g4580461
BLAST score 421
E value 4.0e-41
Match length 103
% identity 81
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 390109
Contig ID 18433_1.R1084
5'-most EST LIB3433-015-Q6-K1-C12

Seq. No. 390110
Contig ID 18441_1.R1084
5'-most EST LIB3433-015-Q6-K1-D10

Seq. No. 390111
Contig ID 18443_1.R1084
5'-most EST LIB3433-015-Q6-K7-D12

Seq. No. 390112
Contig ID 18445_1.R1084
5'-most EST LIB3433-015-Q6-K1-D3
Method BLASTX
NCBI GI g2760839
BLAST score 313
E value 2.0e-28
Match length 102
% identity 61
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 390113
Contig ID 18446_1.R1084
5'-most EST LIB3433-015-Q6-K6-D4

Seq. No. 390114
Contig ID 18448_1.R1084
5'-most EST LIB3433-015-Q6-K1-D6
Method BLASTX
NCBI GI g1076746
BLAST score 425
E value 1.0e-41
Match length 169

% identity	72
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	390115
Contig ID	18450_1.R1084
5'-most EST	LIB3433-015-Q6-K1-D9
Method	BLASTN
NCBI GI	g5777612
BLAST score	87
E value	6.0e-41
Match length	191
% identity	49
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	390116
Contig ID	18452_1.R1084
5'-most EST	LIB3433-015-Q6-K1-E10
Method	BLASTX
NCBI GI	g3377822
BLAST score	548
E value	5.0e-56
Match length	152
% identity	69
NCBI Description	(AF076275) contains similarity to Caenorhabditis elegans MEL-26 (GB:U67737) [Arabidopsis thaliana]

Seq. No.	390117
Contig ID	18454_1.R1084
5'-most EST	g4716011

Seq. No.	390118
Contig ID	18457_1.R1084
5'-most EST	LIB3433-015-Q6-K1-E4
Method	BLASTX
NCBI GI	g3257095
BLAST score	190
E value	5.0e-14
Match length	122
% identity	30
NCBI Description	(AP000003) 840aa long hypothetical cell division control protein (transitional endoplasmic reticulum ATPase) [Pyrococcus horikoshii]

Seq. No.	390119
Contig ID	18458_1.R1084
5'-most EST	LIB3433-015-Q6-K1-E5
Method	BLASTX
NCBI GI	g2244940
BLAST score	479
E value	8.0e-48
Match length	172
% identity	64
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390120

Contig ID	18464_1.R1084
5'-most EST	LIB3433-015-Q6-K7-F12
Method	BLASTX
NCBI GI	g3599483
BLAST score	166
E value	3.0e-12
Match length	170
% identity	35
NCBI Description	(AF085276) MEI-W68 [Drosophila melanogaster]

Seq. No.	390121
Contig ID	18466_1.R1084
5'-most EST	LIB3433-015-Q6-K6-F3

Seq. No.	390122
Contig ID	18471_1.R1084
5'-most EST	LIB3434-009-P1-K1-A2
Method	BLASTX
NCBI GI	g3341679
BLAST score	803
E value	7.0e-86
Match length	209
% identity	72
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	390123
Contig ID	18475_1.R1084
5'-most EST	g2800636
Method	BLASTX
NCBI GI	g2088653
BLAST score	430
E value	7.0e-42
Match length	176
% identity	48
NCBI Description	(AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]

Seq. No.	390124
Contig ID	18477_1.R1084
5'-most EST	LIB3433-015-Q6-K7-G4
Method	BLASTX
NCBI GI	g5080810
BLAST score	561
E value	3.0e-59
Match length	191
% identity	63
NCBI Description	(AC007258) Very similar to helicases [Arabidopsis thaliana]

Seq. No.	390125
Contig ID	18478_1.R1084
5'-most EST	LIB3433-015-Q6-K6-G6

Seq. No.	390126
Contig ID	18479_1.R1084
5'-most EST	uC-osflcyp178f04a1
Method	BLASTX

NCBI GI	g4572671
BLAST score	170
E value	1.0e-11
Match length	92
% identity	49
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	390127
Contig ID	18481_1.R1084
5'-most EST	LIB3433-015-Q6-K6-H10
Method	BLASTX
NCBI GI	g3513727
BLAST score	499
E value	4.0e-50
Match length	160
% identity	41
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	390128
Contig ID	18485_1.R1084
5'-most EST	LIB3434-043-P1-K1-G1
Method	BLASTX
NCBI GI	g1592812
BLAST score	175
E value	6.0e-12
Match length	120
% identity	39
NCBI Description	(X95957) 22 kDa polypeptide [Nicotiana tabacum]

Seq. No.	390129
Contig ID	18486_1.R1084
5'-most EST	LIB3433-015-Q6-K1-H6

Seq. No.	390130
Contig ID	18496_1.R1084
5'-most EST	LIB3433-019-P1-K1-A6
Method	BLASTN
NCBI GI	g6015437
BLAST score	33
E value	7.0e-09
Match length	37
% identity	62
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	390131
Contig ID	18501_1.R1084
5'-most EST	LIB3434-011-P1-K1-B8

Seq. No.	390132
Contig ID	18504_1.R1084
5'-most EST	g702132
Method	BLASTX

NCBI GI g3935181
BLAST score 843
E value 9.0e-91
Match length 171
% identity 87
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No. 390133
Contig ID 18506_1.R1084
5'-most EST g4715763

Seq. No. 390134
Contig ID 18509_1.R1084
5'-most EST g2431182
Method BLASTX
NCBI GI g6016736
BLAST score 255
E value 2.0e-21
Match length 114
% identity 47
NCBI Description (AC009325) unknown protein [Arabidopsis thaliana]

Seq. No. 390135
Contig ID 18510_1.R1084
5'-most EST g3766570
Method BLASTX
NCBI GI g2911071
BLAST score 267
E value 3.0e-23
Match length 165
% identity 41
NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No. 390136
Contig ID 18517_1.R1084
5'-most EST LIB3475-001-P1-K2-A1

Seq. No. 390137
Contig ID 18526_1.R1084
5'-most EST LIB3433-019-P1-K1-D5

Seq. No. 390138
Contig ID 18529_1.R1084
5'-most EST LIB3433-019-P1-K1-D8

Seq. No. 390139
Contig ID 18533_1.R1084
5'-most EST g2310743
Method BLASTX
NCBI GI g2342735
BLAST score 408
E value 2.0e-39
Match length 134
% identity 66
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 390140

Contig ID	18541_1.R1084
5'-most EST	uC-osflcyp011h08b1

Seq. No.	390141
Contig ID	18542_1.R1084
5'-most EST	LIB3475-009-P1-K1-C10
Method	BLASTX
NCBI GI	g3377810
BLAST score	402
E value	5.0e-39
Match length	323
% identity	36
NCBI Description	(AF076275) contains similarity to glutaredoxins [Arabidopsis thaliana]

Seq. No.	390142
Contig ID	18544_1.R1084
5'-most EST	LIB3433-019-P1-K1-F10

Seq. No.	390143
Contig ID	18544_2.R1084
5'-most EST	uC-osroM202025f07b1

Seq. No.	390144
Contig ID	18555_1.R1084
5'-most EST	g3761245
Method	BLASTX
NCBI GI	g3819164
BLAST score	190
E value	4.0e-14
Match length	87
% identity	56
NCBI Description	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]

Seq. No.	390145
Contig ID	18556_1.R1084
5'-most EST	g287191
Method	BLASTX
NCBI GI	g4914455
BLAST score	1109
E value	1.0e-121
Match length	242
% identity	87
NCBI Description	(AL050400) fibrillarin-like protein [Arabidopsis thaliana]

Seq. No.	390146
Contig ID	18566_1.R1084
5'-most EST	LIB3433-019-P1-K1-H11

Seq. No.	390147
Contig ID	18570_1.R1084
5'-most EST	LIB3433-024-P1-K1-D5
Method	BLASTX
NCBI GI	g2431767
BLAST score	205
E value	7.0e-16

Match length	67
% identity	61
NCBI Description	(U62751) acidic ribosomal protein P3a [Zea mays]

Seq. No.	390148
Contig ID	18570_2.R1084
5'-most EST	g5667371
Method	BLASTX
NCBI GI	g2431767
BLAST score	179
E value	7.0e-13
Match length	98
% identity	44
NCBI Description	(U62751) acidic ribosomal protein P3a [Zea mays]

Seq. No.	390149
Contig ID	18581_1.R1084
5'-most EST	LIB3433-021-P1-K1-A3
Method	BLASTN
NCBI GI	g6015437
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	390150
Contig ID	18594_1.R1084
5'-most EST	LIB3433-021-P1-K1-B7

Seq. No.	390151
Contig ID	18598_1.R1084
5'-most EST	LIB3433-021-P1-K1-C2
Method	BLASTX
NCBI GI	g3335375
BLAST score	458
E value	1.0e-45
Match length	154
% identity	61
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	390152
Contig ID	18601_1.R1084
5'-most EST	LIB3433-021-P1-K1-C5

Seq. No.	390153
Contig ID	18602_1.R1084
5'-most EST	LIB3433-021-P1-K1-C6

Seq. No.	390154
Contig ID	18608_1.R1084
5'-most EST	uC-osf1M202095h01b1

Seq. No.	390155
Contig ID	18609_1.R1084
5'-most EST	LIB3433-021-P1-K1-D5
Method	BLASTX

NCBI GI	g2190012
BLAST score	409
E value	1.0e-39
Match length	125
% identity	62
NCBI Description	(AB004242) din1 [Raphanus sativus]

Seq. No.	390156
Contig ID	18617_1.R1084
5'-most EST	LIB3434-024-P1-K1-C3
Method	BLASTX
NCBI GI	g854361
BLAST score	738
E value	2.0e-78
Match length	152
% identity	97
NCBI Description	(X58877) beta-glucanase [Oryza sativa]

Seq. No.	390157
Contig ID	18631_1.R1084
5'-most EST	g3060991
Method	BLASTX
NCBI GI	g2244837
BLAST score	632
E value	7.0e-80
Match length	196
% identity	77
NCBI Description	(Z97337) proteasome chain protein [Arabidopsis thaliana] >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]

Seq. No.	390158
Contig ID	18632_1.R1084
5'-most EST	LIB3477-009-P1-K1-G2
Method	BLASTN
NCBI GI	g169818
BLAST score	82
E value	5.0e-38
Match length	82
% identity	100
NCBI Description	Rice 25S ribosomal RNA gene

Seq. No.	390159
Contig ID	18636_1.R1084
5'-most EST	LIB3433-021-P1-K1-G12
Method	BLASTX
NCBI GI	g3935150
BLAST score	204
E value	2.0e-30
Match length	107
% identity	42
NCBI Description	(AC005106) T25N20.14 [Arabidopsis thaliana]

Seq. No.	390160
Contig ID	18638_1.R1084
5'-most EST	LIB3433-021-P1-K1-G3

Method	BLASTX
NCBI GI	g2852449
BLAST score	685
E value	4.0e-72
Match length	165
% identity	79
NCBI Description	(D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No.	390161
Contig ID	18640_1.R1084
5'-most EST	LIB3433-021-P1-K1-G5
Method	BLASTX
NCBI GI	g2132171
BLAST score	234
E value	1.0e-24
Match length	143
% identity	45
NCBI Description	hypothetical protein YPL063w - yeast (Saccharomyces cerevisiae) >gi_1079679 (U39205) similar to Caenorhabditis elegans CELF45E12_5 F45E12.1 gene product, encoded by GenBank Accession Number U29536 [Saccharomyces cerevisiae]

Seq. No.	390162
Contig ID	18650_1.R1084
5'-most EST	g568433

Seq. No.	390163
Contig ID	18656_1.R1084
5'-most EST	LIB3433-024-P1-K1-A4
Method	BLASTX
NCBI GI	g4490721
BLAST score	459
E value	1.0e-45
Match length	110
% identity	79
NCBI Description	(AL035709) squalene epoxidase-like protein [Arabidopsis thaliana]

Seq. No.	390164
Contig ID	18660_1.R1084
5'-most EST	g3760556

Seq. No.	390165
Contig ID	18664_1.R1084
5'-most EST	g2442288
Method	BLASTX
NCBI GI	g3451075
BLAST score	216
E value	3.0e-17
Match length	91
% identity	56
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	390166
Contig ID	18664_2.R1084
5'-most EST	LIB3433-024-P1-K1-B12

Method	BLASTX
NCBI GI	g3451075
BLAST score	361
E value	4.0e-34
Match length	124
% identity	57
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	390167
Contig ID	18665_1.R1084
5'-most EST	LIB3433-024-P1-K1-B2
Method	BLASTX
NCBI GI	g5231113
BLAST score	655
E value	2.0e-68
Match length	228
% identity	59
NCBI Description	(AF141202) EIN2 [Arabidopsis thaliana] >gi_5231115_gb_AAD41077.1_AF141203_1 (AF141203) EIN2 [Arabidopsis thaliana]

Seq. No.	390168
Contig ID	18666_1.R1084
5'-most EST	g2309810
Method	BLASTX
NCBI GI	g4803927
BLAST score	695
E value	6.0e-73
Match length	211
% identity	63
NCBI Description	(AC006264) signal sequence receptor, alpha subunit (SSR-alpha) [Arabidopsis thaliana]

Seq. No.	390169
Contig ID	18668_1.R1084
5'-most EST	uC-osroM202001g11b1

Seq. No.	390170
Contig ID	18668_2.R1084
5'-most EST	uC-osflcyp033a02b1

Seq. No.	390171
Contig ID	18672_1.R1084
5'-most EST	LIB3433-024-P1-K1-C1

Seq. No.	390172
Contig ID	18680_1.R1084
5'-most EST	g2798301
Method	BLASTX
NCBI GI	g4580517
BLAST score	380
E value	2.0e-50
Match length	159
% identity	63
NCBI Description	(AF036302) scarecrow-like 5 [Arabidopsis thaliana]

Seq. No. 390173

Contig ID	18693_1.R1084
5'-most EST	LIB3433-024-P1-K1-E11
Method	BLASTX
NCBI GI	g6006869
BLAST score	207
E value	4.0e-16
Match length	147
% identity	39
NCBI Description	(AC009540) putative cationic amino acid transporter [Arabidopsis thaliana]

Seq. No.	390174
Contig ID	18699_1.R1084
5'-most EST	LIB3433-024-P1-K1-E7
Method	BLASTX
NCBI GI	g5042455
BLAST score	909
E value	2.0e-98
Match length	177
% identity	97
NCBI Description	(AC007789) NADP-dependent isocitrate dehydrogenase [Oryza sativa]

Seq. No.	390175
Contig ID	18705_1.R1084
5'-most EST	LIB3433-024-P1-K1-F2
Method	BLASTX
NCBI GI	g3335341
BLAST score	397
E value	2.0e-38
Match length	150
% identity	57
NCBI Description	(AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.	390176
Contig ID	18714_1.R1084
5'-most EST	LIB3433-024-P1-K1-G11

Seq. No.	390177
Contig ID	18717_1.R1084
5'-most EST	uC-osroM202040f11b1

Seq. No.	390178
Contig ID	18722_1.R1084
5'-most EST	g427060

Seq. No.	390179
Contig ID	18724_2.R1084
5'-most EST	LIB3434-014-P1-K1-C2
Method	BLASTX
NCBI GI	g3341697
BLAST score	470
E value	1.0e-46
Match length	148
% identity	61
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390180
Contig ID	18731_1.R1084
5'-most EST	g286933
Method	BLASTX
NCBI GI	g399940
BLAST score	764
E value	2.0e-81
Match length	193
% identity	78
NCBI Description	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR >gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

Seq. No.	390181
Contig ID	18741_1.R1084
5'-most EST	uC-osroM202008c06a1

Seq. No.	390182
Contig ID	18742_1.R1084
5'-most EST	g5004670
Method	BLASTX
NCBI GI	g2499327
BLAST score	225
E value	1.0e-18
Match length	52
% identity	92
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	390183
Contig ID	18744_1.R1084
5'-most EST	LIB3433-022-P1-K1-B7
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	6.0e-10
Match length	39
% identity	97
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	390184
Contig ID	18747_1.R1084
5'-most EST	uC-osf1cyp124a08b1
Method	BLASTX
NCBI GI	g2194132
BLAST score	819
E value	1.0e-87
Match length	279
% identity	62
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	390185
Contig ID	18749_2.R1084

5'-most EST	uC-osflcyp125g11b1
Seq. No.	390186
Contig ID	18762_1.R1084
5'-most EST	g3763598
Seq. No.	390187
Contig ID	18766_1.R1084
5'-most EST	LIB3433-022-P1-K1-C9
Method	BLASTX
NCBI GI	g2827528
BLAST score	216
E value	4.0e-17
Match length	56
% identity	66
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.	390188
Contig ID	18785_1.R1084
5'-most EST	g4879141
Method	BLASTX
NCBI GI	g4678350
BLAST score	349
E value	6.0e-33
Match length	74
% identity	84
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]
Seq. No.	390189
Contig ID	18790_1.R1084
5'-most EST	LIB3434-059-P1-K1-D12
Seq. No.	390190
Contig ID	18792_1.R1084
5'-most EST	LIB3433-022-P1-K1-F12
Method	BLASTX
NCBI GI	g114089
BLAST score	506
E value	5.0e-51
Match length	141
% identity	71
NCBI Description	RAS-RELATED PROTEIN ARA-4 >gi_81633_pir__JS0641 GTP-binding protein ara-4 - Arabidopsis thaliana >gi_217839_dbj_BAA00831_ (D01026) small GTP-binding protein [Arabidopsis thaliana] >gi_3763922 (AC004450) GTP-binding protein [Arabidopsis thaliana]
Seq. No.	390191
Contig ID	18794_1.R1084
5'-most EST	g3060977
Seq. No.	390192
Contig ID	18802_1.R1084
5'-most EST	g3767884
Method	BLASTX
NCBI GI	g3319340
BLAST score	282

E value 5.0e-25
Match length 137
% identity 43
NCBI Description (AF077407) contains similarity to E. coli cation transport protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No. 390193
Contig ID 18802_2.R1084
5'-most EST g4715700
Method BLASTX
NCBI GI g3319340
BLAST score 230
E value 2.0e-18
Match length 62
% identity 61
NCBI Description (AF077407) contains similarity to E. coli cation transport protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No. 390194
Contig ID 18804_1.R1084
5'-most EST LIB3434-029-P1-K1-A1

Seq. No. 390195
Contig ID 18813_1.R1084
5'-most EST g4715958

Seq. No. 390196
Contig ID 18815_1.R1084
5'-most EST LIB3433-022-P1-K1-H2

Seq. No. 390197
Contig ID 18818_1.R1084
5'-most EST uC-osflcyp085g03b1
Method BLASTX
NCBI GI g2317725
BLAST score 285
E value 3.0e-25
Match length 169
% identity 37
NCBI Description (AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]

Seq. No. 390198
Contig ID 18824_1.R1084
5'-most EST LIB3433-023-P1-K1-A11
Method BLASTX
NCBI GI g3264767
BLAST score 225
E value 4.0e-18
Match length 53
% identity 77
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 390199
Contig ID 18826_1.R1084
5'-most EST g569503

Seq. No.	390200
Contig ID	18828_1.R1084
5'-most EST	g1944243

Seq. No.	390201
Contig ID	18829_1.R1084
5'-most EST	uC-osflcyp143b07b1
Method	BLASTX
NCBI GI	g3850063
BLAST score	294
E value	3.0e-26
Match length	204
% identity	35
NCBI Description	(AJ223830) ARE1 [Rattus norvegicus]

Seq. No.	390202
Contig ID	18837_1.R1084
5'-most EST	LIB3433-023-P1-K1-B6
Method	BLASTX
NCBI GI	g1345881
BLAST score	405
E value	3.0e-62
Match length	134
% identity	90
NCBI Description	CYTOCHROME B5 >gi_1076743_pir__S46307 cytochrome b5 - rice >gi_414705_emb_CAA53366_ (X75670) cytochrome b5 [Oryza sativa]

Seq. No.	390203
Contig ID	18845_1.R1084
5'-most EST	g3763117
Method	BLASTX
NCBI GI	g3850571
BLAST score	317
E value	6.0e-29
Match length	64
% identity	92
NCBI Description	(AC005278) Similar to gb_U85207 snRNP core Sm protein homolog Sm-X5 from Mus musculus. EST gb_AA612141 comes from this gene. [Arabidopsis thaliana]

Seq. No.	390204
Contig ID	18845_3.R1084
5'-most EST	LIB3433-023-P1-K1-C3
Method	BLASTX
NCBI GI	g3850571
BLAST score	317
E value	2.0e-39
Match length	92
% identity	92
NCBI Description	(AC005278) Similar to gb_U85207 snRNP core Sm protein homolog Sm-X5 from Mus musculus. EST gb_AA612141 comes from this gene. [Arabidopsis thaliana]

Seq. No.	390205
Contig ID	18847_1.R1084
5'-most EST	uC-osflcyp112d08b1

Method	BLASTX
NCBI GI	g4581520
BLAST score	396
E value	5.0e-38
Match length	235
% identity	45
NCBI Description	(AL049559) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	390206
Contig ID	18851_1.R1084
5'-most EST	LIB3433-023-P1-K1-C9
Method	BLASTX
NCBI GI	g2773249
BLAST score	205
E value	5.0e-16
Match length	84
% identity	44
NCBI Description	(AF039707) glutamate carboxypeptidase II [Rattus norvegicus]

Seq. No.	390207
Contig ID	18852_1.R1084
5'-most EST	uC-osroM202041b10b1

Seq. No.	390208
Contig ID	18856_1.R1084
5'-most EST	LIB3433-023-P1-K1-D3

Seq. No.	390209
Contig ID	18859_1.R1084
5'-most EST	g4881120
Method	BLASTX
NCBI GI	g2344898
BLAST score	439
E value	2.0e-46
Match length	130
% identity	72
NCBI Description	(AC002388) 60S ribosomal protein L30 isolog [Arabidopsis thaliana]

Seq. No.	390210
Contig ID	18859_2.R1084
5'-most EST	g5003683
Method	BLASTX
NCBI GI	g2344898
BLAST score	511
E value	7.0e-52
Match length	128
% identity	75
NCBI Description	(AC002388) 60S ribosomal protein L30 isolog [Arabidopsis thaliana]

Seq. No.	390211
Contig ID	18862_1.R1084
5'-most EST	LIB3433-023-P1-K1-D9
Method	BLASTX
NCBI GI	g1491615

BLAST score	186
E value	1.0e-13
Match length	79
% identity	46
NCBI Description	(X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No.	390212
Contig ID	18868_1.R1084
5'-most EST	LIB3434-033-P1-K1-D11
Method	BLASTX
NCBI GI	g575605
BLAST score	293
E value	5.0e-26
Match length	143
% identity	46
NCBI Description	(D42065) cationic peroxidase isozyme 40K precursor [Nicotiana tabacum]

Seq. No.	390213
Contig ID	18869_1.R1084
5'-most EST	LIB3433-023-P1-K1-E5
Method	BLASTX
NCBI GI	g113240
BLAST score	318
E value	3.0e-29
Match length	77
% identity	87
NCBI Description	ACTIN 2 >gi_71636_pir__ATRZ2 actin 2 - rice >gi_20329_emb_CAA33873_ (X15864) actin [Oryza sativa]

Seq. No.	390214
Contig ID	18872_1.R1084
5'-most EST	LIB3433-023-P1-K1-E8
Method	BLASTX
NCBI GI	g626598
BLAST score	275
E value	7.0e-24
Match length	166
% identity	39
NCBI Description	hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) >gi_500710 (U10400) Ysc84p [Saccharomyces cerevisiae]

Seq. No.	390215
Contig ID	18882_1.R1084
5'-most EST	g3767455
Method	BLASTX
NCBI GI	g2506276
BLAST score	489
E value	8.0e-55
Match length	171
% identity	72
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain - Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60

alpha subunit [Arabidopsis thaliana]
>gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco
binding protein alpha subunit [Arabidopsis thaliana]

Seq. No.	390216
Contig ID	18887_1.R1084
5'-most EST	uC-osrocyp003g11a1

Seq. No.	390217
Contig ID	18888_1.R1084
5'-most EST	g2280953
Method	BLASTX
NCBI GI	g115524
BLAST score	376
E value	1.0e-35
Match length	149
% identity	33
NCBI Description	CALMODULIN >gi_71687_pir__MCPO calmodulin - potato >gi_169477 (J04559) calmodulin [Solanum tuberosum]

Seq. No.	390218
Contig ID	18890_1.R1084
5'-most EST	LIB3433-023-P1-K1-G4

Seq. No.	390219
Contig ID	18894_1.R1084
5'-most EST	g3760701

Seq. No.	390220
Contig ID	18894_2.R1084
5'-most EST	g5455554
Method	BLASTN
NCBI GI	g1684627
BLAST score	75
E value	1.0e-33
Match length	81
% identity	98
NCBI Description	Artificial sequences, plasmid vector pGreen-2

Seq. No.	390221
Contig ID	18896_1.R1084
5'-most EST	LIB3433-023-P1-K1-H1

Seq. No.	390222
Contig ID	18930_1.R1084
5'-most EST	LIB3433-025-P1-K1-B9
Method	BLASTX
NCBI GI	g1944319
BLAST score	325
E value	1.0e-45
Match length	154
% identity	61
NCBI Description	(D31700) cysteine proteinase inhibitor [Glycine max] >gi_1944342_dbj_BAA19610_ (D64115) cysteine proteinase inhibitor [Glycine max]

Seq. No. 390223

Contig ID	18933_1.R1084
5'-most EST	g572480
Seq. No.	390224
Contig ID	18941_1.R1084
5'-most EST	g4879745
Method	BLASTX
NCBI GI	g4522004
BLAST score	188
E value	2.0e-13
Match length	67
% identity	63
NCBI Description	(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]
Seq. No.	390225
Contig ID	18950_1.R1084
5'-most EST	LIB3433-025-P1-K1-D7
Seq. No.	390226
Contig ID	18952_1.R1084
5'-most EST	uC-osrocyp010h03a1
Method	BLASTX
NCBI GI	g1129134
BLAST score	190
E value	6.0e-14
Match length	41
% identity	78
NCBI Description	(X94105) old yellow enzyme NADPH dehydrogenase [Chenopodium rubrum]
Seq. No.	390227
Contig ID	18953_1.R1084
5'-most EST	g568290
Seq. No.	390228
Contig ID	18959_1.R1084
5'-most EST	g2799440
Seq. No.	390229
Contig ID	18962_1.R1084
5'-most EST	g3759667
Method	BLASTX
NCBI GI	g3746882
BLAST score	266
E value	6.0e-23
Match length	106
% identity	46
NCBI Description	(AF086708) 26S proteasome subunit 11 [Homo sapiens]
Seq. No.	390230
Contig ID	18962_2.R1084
5'-most EST	g3760720
Method	BLASTX
NCBI GI	g3746882
BLAST score	211
E value	2.0e-16

Match length	94
% identity	41
NCBI Description	(AF086708) 26S proteasome subunit 11 [Homo sapiens]

Seq. No.	390231
Contig ID	18963_1.R1084
5'-most EST	uC-osroM202039b04b1
Method	BLASTX
NCBI GI	g4506221
BLAST score	476
E value	2.0e-47
Match length	193
% identity	49
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 >gi_1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit p55 [Homo sapiens]

Seq. No.	390232
Contig ID	18966_1.R1084
5'-most EST	LIB3433-025-P1-K1-F12
Method	BLASTX
NCBI GI	g2275213
BLAST score	271
E value	2.0e-23
Match length	83
% identity	60
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390233
Contig ID	18978_1.R1084
5'-most EST	LIB3433-025-P1-K1-G4
Method	BLASTX
NCBI GI	g2529663
BLAST score	689
E value	2.0e-72
Match length	174
% identity	72
NCBI Description	(AC002535) putative lysophospholipase [Arabidopsis thaliana] >gi_3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	390234
Contig ID	18981_1.R1084
5'-most EST	uC-osf1M202014g06b1
Method	BLASTX
NCBI GI	g3047083
BLAST score	543
E value	2.0e-55
Match length	125
% identity	81
NCBI Description	(AF058914) similar to FLAP endonuclease-1 (SW:P39748) [Arabidopsis thaliana]

Seq. No.	390235
Contig ID	18987_1.R1084
5'-most EST	uC-osroM202037c04b1
Method	BLASTX

NCBI GI	g5031275
BLAST score	812
E value	9.0e-87
Match length	203
% identity	72
NCBI Description	(AF139496) unknown [Prunus armeniaca]

Seq. No.	390236
Contig ID	18989_1.R1084
5'-most EST	g2311870
Method	BLASTX
NCBI GI	g409007
BLAST score	344
E value	4.0e-32
Match length	81
% identity	79
NCBI Description	BBI-M=Bowman-Birk trypsin inhibitor-related protein [Zea mays=corn, Peptide, 102 aa] >gi_447268_prf__1914141A trypsin inhibitor-related protein [Zea mays]

Seq. No.	390237
Contig ID	18998_1.R1084
5'-most EST	LIB3433-003-Q6-K6-D3

Seq. No.	390238
Contig ID	19001_1.R1084
5'-most EST	LIB3433-026-P1-K1-A5

Seq. No.	390239
Contig ID	19002_1.R1084
5'-most EST	LIB3433-026-P1-K1-A9
Method	BLASTX
NCBI GI	g2244965
BLAST score	144
E value	1.0e-08
Match length	77
% identity	39
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390240
Contig ID	19004_1.R1084
5'-most EST	LIB3477-011-P1-K1-B9
Method	BLASTX
NCBI GI	g4835247
BLAST score	226
E value	3.0e-21
Match length	78
% identity	69
NCBI Description	(AL049862) putative tRNA synthetase [Arabidopsis thaliana]

Seq. No.	390241
Contig ID	19006_1.R1084
5'-most EST	LIB3434-010-P1-K1-G6
Method	BLASTX
NCBI GI	g730558
BLAST score	457
E value	2.0e-45

Match length	95
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal protein L34 - common tobacco >gi_2129964_pir__S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi_436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]

Seq. No.	390242
Contig ID	19006_2.R1084
5'-most EST	g2442252
Method	BLASTX
NCBI GI	g730558
BLAST score	454
E value	6.0e-45
Match length	95
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal protein L34 - common tobacco >gi_2129964_pir__S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi_436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]

Seq. No.	390243
Contig ID	19007_1.R1084
5'-most EST	LIB3433-026-P1-K1-B2
Method	BLASTX
NCBI GI	g3334112
BLAST score	371
E value	3.0e-35
Match length	81
% identity	86
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1938236_emb_CAA70200_ (Y08996) acyl-CoA-binding protein [Ricinus communis]

Seq. No.	390244
Contig ID	19010_1.R1084
5'-most EST	uC-osroM202017e04b1
Method	BLASTX
NCBI GI	g3850999
BLAST score	1391
E value	1.0e-154
Match length	310
% identity	89
NCBI Description	(AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1 [Zea mays]

Seq. No.	390245
Contig ID	19017_1.R1084
5'-most EST	LIB3433-026-P1-K1-C11

Seq. No.	390246
Contig ID	19023_1.R1084
5'-most EST	uC-osflcyp112h12b1

Seq. No.	390247
Contig ID	19029_1.R1084
5'-most EST	g5667343
Method	BLASTX
NCBI GI	g4850408
BLAST score	368
E value	7.0e-35
Match length	169
% identity	44
NCBI Description	(AC007357) Contains PF_00097 Zinc finger (C3HC4) ring finger motif. [Arabidopsis thaliana]

Seq. No.	390248
Contig ID	19032_1.R1084
5'-most EST	g699990
Method	BLASTX
NCBI GI	g4455192
BLAST score	493
E value	7.0e-77
Match length	304
% identity	31
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	390249
Contig ID	19047_1.R1084
5'-most EST	uC-osflcyp013e05b1
Method	BLASTX
NCBI GI	g4960154
BLAST score	276
E value	7.0e-24
Match length	55
% identity	95
NCBI Description	(AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]

Seq. No.	390250
Contig ID	19047_2.R1084
5'-most EST	LIB3477-001-P1-K1-F3
Method	BLASTX
NCBI GI	g4960156
BLAST score	511
E value	1.0e-51
Match length	153
% identity	68
NCBI Description	(AF153284) putative progesterone-binding protein homolog [Arabidopsis thaliana]

Seq. No.	390251
Contig ID	19055_1.R1084
5'-most EST	LIB3433-026-P1-K1-F5
Method	BLASTX
NCBI GI	g4512711
BLAST score	188
E value	2.0e-13
Match length	163
% identity	35
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	390252
Contig ID	19059_1.R1084
5'-most EST	uC-osroM202004h03a2

Seq. No.	390253
Contig ID	19067_1.R1084
5'-most EST	g1632116

Seq. No.	390254
Contig ID	19069_1.R1084
5'-most EST	LIB3433-026-P1-K1-G7

Seq. No.	390255
Contig ID	19075_1.R1084
5'-most EST	LIB3433-026-P1-K1-H12
Method	BLASTX
NCBI GI	g4531444
BLAST score	151
E value	2.0e-09
Match length	61
% identity	51
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	390256
Contig ID	19175_1.R1084
5'-most EST	LIB3433-003-Q6-K6-B12

Seq. No.	390257
Contig ID	19177_3.R1084
5'-most EST	uC-osflcyp179b10a1
Method	BLASTX
NCBI GI	g2764802
BLAST score	169
E value	1.0e-11
Match length	38
% identity	79
NCBI Description	(X77795) ras-like gene [Zea mays]

Seq. No.	390258
Contig ID	19180_1.R1084
5'-most EST	uC-osflM202016b12b1
Method	BLASTX
NCBI GI	g3882356
BLAST score	731
E value	2.0e-77
Match length	234
% identity	61
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana]

Seq. No.	390259
Contig ID	19186_1.R1084
5'-most EST	LIB3433-003-Q6-K6-C12
Method	BLASTX
NCBI GI	g5834486
BLAST score	155

E value 3.0e-10
Match length 87
% identity 38
NCBI Description (AB025313) PGP9.5 [Mus musculus]

Seq. No. 390260
Contig ID 19190_1.R1084
5'-most EST g5003498
Method BLASTN
NCBI GI g5922603
BLAST score 38
E value 3.0e-11
Match length 62
% identity 92
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No. 390261
Contig ID 19191_1.R1084
5'-most EST LIB3433-003-Q6-K6-C6

Seq. No. 390262
Contig ID 19210_1.R1084
5'-most EST LIB3433-003-Q6-K6-E3
Method BLASTX
NCBI GI g3522946
BLAST score 311
E value 2.0e-31
Match length 146
% identity 52
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 390263
Contig ID 19213_1.R1084
5'-most EST LIB3433-003-Q6-K6-E6
Method BLASTX
NCBI GI g115840
BLAST score 502
E value 1.0e-53
Match length 147
% identity 73
NCBI Description CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B)

Seq. No. 390264
Contig ID 19224_1.R1084
5'-most EST uC-osrocyp028e08a1

Seq. No. 390265
Contig ID 19235_1.R1084
5'-most EST g2797220

Seq. No. 390266
Contig ID 19237_1.R1084
5'-most EST LIB3433-006-Q6-K6-F2
Method BLASTX
NCBI GI g4567246

BLAST score 545
E value 2.0e-55
Match length 179
% identity 61
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 390267
Contig ID 19238_1.R1084
5'-most EST LIB3433-003-Q6-K6-H1
Method BLASTX
NCBI GI g5802627
BLAST score 614
E value 7.0e-64
Match length 143
% identity 84
NCBI Description (AF176089) COP8 [Arabidopsis thaliana]

Seq. No. 390268
Contig ID 19250_1.R1084
5'-most EST uC-osflcyp169e11b1
Method BLASTX
NCBI GI g2529680
BLAST score 795
E value 5.0e-85
Match length 185
% identity 48
NCBI Description (AC002535) putative protein disulfide-isomerase precursor [Arabidopsis thaliana]

Seq. No. 390269
Contig ID 19252_1.R1084
5'-most EST LIB3433-005-Q6-K1-A3
Method BLASTX
NCBI GI g6094049
BLAST score 557
E value 5.0e-57
Match length 111
% identity 97
NCBI Description 60S RIBOSOMAL PROTEIN L30 >gi_2668750 (AF034949) ribosomal protein L30 [Zea mays]

Seq. No. 390270
Contig ID 19260_1.R1084
5'-most EST g5004858
Method BLASTX
NCBI GI g3193303
BLAST score 334
E value 5.0e-31
Match length 98
% identity 64
NCBI Description (AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No. 390271
Contig ID 19276_1.R1084

5'-most EST	LIB3433-005-Q6-K1-C8
Seq. No.	390272
Contig ID	19278_1.R1084
5'-most EST	LIB3433-005-Q6-K1-D10
Method	BLASTX
NCBI GI	g2462834
BLAST score	246
E value	8.0e-21
Match length	99
% identity	47
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.	390273
Contig ID	19301_1.R1084
5'-most EST	LIB3433-005-Q6-K1-G4
Seq. No.	390274
Contig ID	19303_1.R1084
5'-most EST	LIB3433-005-Q6-K1-G7
Seq. No.	390275
Contig ID	19313_1.R1084
5'-most EST	LIB3433-006-Q6-K6-A2
Seq. No.	390276
Contig ID	19315_1.R1084
5'-most EST	LIB3433-006-Q6-K6-A4
Method	BLASTX
NCBI GI	g4530509
BLAST score	169
E value	2.0e-11
Match length	69
% identity	55
NCBI Description	(AF124748) putative RNA-binding protein [Larix laricina]
Seq. No.	390277
Contig ID	19318_1.R1084
5'-most EST	LIB3433-006-Q6-K6-A7
Method	BLASTX
NCBI GI	g4512685
BLAST score	156
E value	5.0e-10
Match length	72
% identity	43
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]
Seq. No.	390278
Contig ID	19320_1.R1084
5'-most EST	g3764112
Seq. No.	390279
Contig ID	19322_1.R1084
5'-most EST	LIB3434-051-P1-K1-C9

Seq. No.	390280
Contig ID	19323_1.R1084
5'-most EST	LIB3434-058-P1-K1-E7
Method	BLASTX
NCBI GI	g5302796
BLAST score	849
E value	4.0e-91
Match length	228
% identity	70
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390281
Contig ID	19335_1.R1084
5'-most EST	g5803391
Method	BLASTX
NCBI GI	g4544437
BLAST score	186
E value	1.0e-13
Match length	66
% identity	52
NCBI Description	(AC006592) unknown protein [Arabidopsis thaliana]

Seq. No.	390282
Contig ID	19336_1.R1084
5'-most EST	LIB3433-006-Q6-K6-C6
Method	BLASTX
NCBI GI	g4336205
BLAST score	449
E value	3.0e-44
Match length	169
% identity	44
NCBI Description	(AF077372) cytochrome b5 reductase [Zea mays]

Seq. No.	390283
Contig ID	19338_1.R1084
5'-most EST	g2431237
Method	BLASTX
NCBI GI	g82308
BLAST score	260
E value	6.0e-32
Match length	102
% identity	74
NCBI Description	myb protein 308 - garden snapdragon

Seq. No.	390284
Contig ID	19350_1.R1084
5'-most EST	uC-osroM202005c04b1

Seq. No.	390285
Contig ID	19351_1.R1084
5'-most EST	g427584
Method	BLASTX
NCBI GI	g3660467
BLAST score	282
E value	1.0e-32
Match length	93
% identity	83

NCBI Description	(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]

Seq. No.	390286
Contig ID	19375_1.R1084
5'-most EST	LIB3434-011-P1-K1-C2

Seq. No.	390287
Contig ID	19379_1.R1084
5'-most EST	g4716844
Method	BLASTX
NCBI GI	g3461849
BLAST score	225
E value	6.0e-18
Match length	61
% identity	62
NCBI Description	(AC005315) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	390288
Contig ID	19384_1.R1084
5'-most EST	uC-osflcyp002d05b1

Seq. No.	390289
Contig ID	19385_1.R1084
5'-most EST	LIB3434-031-P1-K1-H9
Method	BLASTN
NCBI GI	g5822827
BLAST score	47
E value	3.0e-17
Match length	47
% identity	50
NCBI Description	Oryza sativa d1 gene for alpha-subunit of GTP-binding protein, dwarf mutant, partial sequence

Seq. No.	390290
Contig ID	19386_1.R1084
5'-most EST	uC-osroM202032d03b1

Seq. No.	390291
Contig ID	19468_1.R1084
5'-most EST	uC-osflcyp026g08b1
Method	BLASTX
NCBI GI	g3193203
BLAST score	150
E value	3.0e-09
Match length	133
% identity	32
NCBI Description	(AF067947) similar to triacylgycerol lipases [Caenorhabditis elegans]

Seq. No.	390292
Contig ID	19468_2.R1084
5'-most EST	g3762367
Method	BLASTX
NCBI GI	g443509
BLAST score	263
E value	1.0e-22

Match length	229
% identity	34
NCBI Description	Triacylglycerol Acylhydrolase (E.C.3.1.1.3) Complex With Diethylphosophate

Seq. No.	390293
Contig ID	19476_1.R1084
5'-most EST	uC-osroM202021d04b1

Seq. No.	390294
Contig ID	19489_1.R1084
5'-most EST	LIB3434-004-P1-K1-E5

Seq. No.	390295
Contig ID	19497_1.R1084
5'-most EST	LIB3433-016-Q6-K6-D12
Method	BLASTX
NCBI GI	g678547
BLAST score	432
E value	2.0e-42
Match length	167
% identity	55
NCBI Description	(L13654) peroxidase [Lycopersicon esculentum]

Seq. No.	390296
Contig ID	19498_1.R1084
5'-most EST	LIB3434-003-P1-K1-C1
Method	BLASTX
NCBI GI	g4522009
BLAST score	357
E value	9.0e-47
Match length	226
% identity	49
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	390297
Contig ID	19505_1.R1084
5'-most EST	g3061188
Method	BLASTX
NCBI GI	g5679842
BLAST score	316
E value	1.0e-58
Match length	191
% identity	74
NCBI Description	(AJ243961) l1332.6 [Oryza sativa]

Seq. No.	390298
Contig ID	19507_1.R1084
5'-most EST	g2310207
Method	BLASTX
NCBI GI	g505100
BLAST score	204
E value	2.0e-15
Match length	174
% identity	41
NCBI Description	(D31886) KIAA0066 [Homo sapiens]

Seq. No.	390299
Contig ID	19513_1.R1084
5'-most EST	LIB3433-016-Q6-K6-E8
Method	BLASTX
NCBI GI	g4972089
BLAST score	610
E value	1.0e-63
Match length	139
% identity	80
NCBI Description	(AL078468) acyl-CoA synthetase-like protein [Arabidopsis thaliana]

Seq. No.	390300
Contig ID	19519_1.R1084
5'-most EST	uC-osflcyp153b02b1
Method	BLASTX
NCBI GI	g4103324
BLAST score	1211
E value	1.0e-166
Match length	342
% identity	81
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No.	390301
Contig ID	19520_1.R1084
5'-most EST	uC-osflcyp031h07b1
Method	BLASTX
NCBI GI	g4741931
BLAST score	561
E value	1.0e-57
Match length	139
% identity	78
NCBI Description	(AF130975) plasma membrane intrinsic protein [Zea mays]

Seq. No.	390302
Contig ID	19530_1.R1084
5'-most EST	uC-osrocyp002f04a1

Seq. No.	390303
Contig ID	19531_1.R1084
5'-most EST	g428115

Seq. No.	390304
Contig ID	19532_1.R1084
5'-most EST	LIB3433-016-Q6-K6-G5

Seq. No.	390305
Contig ID	19536_1.R1084
5'-most EST	LIB3433-016-Q6-K6-G9
Method	BLASTX
NCBI GI	g4914331
BLAST score	626
E value	8.0e-68
Match length	201
% identity	70
NCBI Description	(AC005489) F14N23.17 [Arabidopsis thaliana]

Seq. No.	390306
Contig ID	19549_1.R1084
5'-most EST	g571706
Method	BLASTX
NCBI GI	g2668744
BLAST score	804
E value	7.0e-86
Match length	148
% identity	99
NCBI Description	(AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No.	390307
Contig ID	19563_1.R1084
5'-most EST	uC-osflM202086h11a1
Method	BLASTX
NCBI GI	g3643085
BLAST score	603
E value	1.0e-62
Match length	179
% identity	62
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	390308
Contig ID	19573_1.R1084
5'-most EST	LIB3433-017-Q6-K1-C5

Seq. No.	390309
Contig ID	19579_1.R1084
5'-most EST	LIB3433-017-Q6-K1-D11
Method	BLASTX
NCBI GI	g4336205
BLAST score	701
E value	7.0e-74
Match length	148
% identity	87
NCBI Description	(AF077372) cytochrome b5 reductase [Zea mays]

Seq. No.	390310
Contig ID	19583_1.R1084
5'-most EST	LIB3433-017-Q6-K1-D4

Seq. No.	390311
Contig ID	19592_1.R1084
5'-most EST	g5607401

Seq. No.	390312
Contig ID	19595_1.R1084
5'-most EST	g3763240
Method	BLASTX
NCBI GI	g3608481
BLAST score	280
E value	2.0e-49
Match length	136
% identity	64
NCBI Description	(AF088913) ribosomal protein L27a [Petunia x hybrida]

Seq. No.	390313
Contig ID	19595_2.R1084
5'-most EST	LIB3434-026-P1-K1-F9
Method	BLASTX
NCBI GI	g3608481
BLAST score	602
E value	2.0e-62
Match length	136
% identity	82
NCBI Description	(AF088913) ribosomal protein L27a [Petunia x hybrida]

Seq. No.	390314
Contig ID	19595_3.R1084
5'-most EST	g2427970
Method	BLASTX
NCBI GI	g3608481
BLAST score	363
E value	2.0e-34
Match length	103
% identity	66
NCBI Description	(AF088913) ribosomal protein L27a [Petunia x hybrida]

Seq. No.	390315
Contig ID	19604_1.R1084
5'-most EST	LIB3433-017-Q6-K1-F7

Seq. No.	390316
Contig ID	19609_1.R1084
5'-most EST	LIB3434-027-P1-K1-A12
Method	BLASTX
NCBI GI	g3927836
BLAST score	649
E value	9.0e-68
Match length	150
% identity	79
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	390317
Contig ID	19618_1.R1084
5'-most EST	g1632082

Seq. No.	390318
Contig ID	19628_1.R1084
5'-most EST	LIB3433-018-Q6-K6-A11
Method	BLASTX
NCBI GI	g2735017
BLAST score	706
E value	2.0e-74
Match length	205
% identity	65
NCBI Description	(U82481) KI domain interacting kinase 1 [Zea mays]

Seq. No.	390319
Contig ID	19634_1.R1084
5'-most EST	g2799820

Seq. No.	390320
Contig ID	19639_1.R1084
5'-most EST	LIB3474-001-P1-K1-D12
Method	BLASTX
NCBI GI	g5051789
BLAST score	206
E value	5.0e-16
Match length	96
% identity	50
NCBI Description	(AL078637) putative protein [Arabidopsis thaliana]

Seq. No.	390321
Contig ID	19644_1.R1084
5'-most EST	g4716629
Method	BLASTX
NCBI GI	g3776557
BLAST score	209
E value	6.0e-16
Match length	96
% identity	60
NCBI Description	(AC005388) Contains similarity to gi_2924495 hypothetical protein Rv1920 from Mycobacterium tuberculosis genome gb_AL022020. [Arabidopsis thaliana]

Seq. No.	390322
Contig ID	19673_1.R1084
5'-most EST	g3061240
Method	BLASTX
NCBI GI	g5091611
BLAST score	483
E value	3.0e-48
Match length	194
% identity	64
NCBI Description	(AC007858) Similar to gb_U43629 integral membrane protein from Beta vulgaris and is a member of the sugar transporter family PF_00083. ES [Oryza sativa]

Seq. No.	390323
Contig ID	19676_1.R1084
5'-most EST	g3768416
Method	BLASTX
NCBI GI	g3550519
BLAST score	171
E value	3.0e-19
Match length	80
% identity	61
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	390324
Contig ID	19693_1.R1084
5'-most EST	g4714239
Method	BLASTX
NCBI GI	g4309884
BLAST score	326
E value	3.0e-30
Match length	92
% identity	63

NCBI Description	(AC006389) similar to Schizosaccharomyces pombe splicing factor; similar to PID:3395591 [Homo sapiens] >gi_5919157_gb_AAD56232.1_AF182294_1 (AF182294) U6 snRNA-associated Sm-like protein LSm8 [Homo sapiens]

Seq. No.	390325
Contig ID	19694_1.R1084
5'-most EST	g701318
Method	BLASTX
NCBI GI	g3281853
BLAST score	911
E value	2.0e-98
Match length	231
% identity	81
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	390326
Contig ID	19698_1.R1084
5'-most EST	LIB3433-018-Q6-K6-H8
Method	BLASTX
NCBI GI	g2493046
BLAST score	530
E value	6.0e-54
Match length	133
% identity	77
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi_82297_pir__A41740 H+-transporting ATP synthase (EC 3.6.1.34) delta' chain precursor - sweet potato >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase delta subunit [Ipomoea batatas]

Seq. No.	390327
Contig ID	19714_1.R1084
5'-most EST	LIB3433-002-P1-K1-C11
Method	BLASTN
NCBI GI	g5803242
BLAST score	45
E value	7.0e-16
Match length	122
% identity	30
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	390328
Contig ID	19747_1.R1084
5'-most EST	LIB3433-002-P1-K1-G11
Method	BLASTX
NCBI GI	g4406810
BLAST score	521
E value	1.0e-52
Match length	139
% identity	65
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	390329
Contig ID	19789_1.R1084
5'-most EST	uC-osrocyp031b09b1
Method	BLASTX

NCBI GI g2739366
BLAST score 343
E value 4.0e-33
Match length 198
% identity 44
NCBI Description (AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No. 390330
Contig ID 19849_1.R1084
5'-most EST g426916
Method BLASTX
NCBI GI g1732511
BLAST score 351
E value 9.0e-57
Match length 163
% identity 69
NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No. 390331
Contig ID 19867_1.R1084
5'-most EST g4716279

Seq. No. 390332
Contig ID 19873_1.R1084
5'-most EST LIB3434-064-P1-K1-F8
Method BLASTX
NCBI GI g2196466
BLAST score 692
E value 6.0e-73
Match length 205
% identity 64
NCBI Description (Y13673) TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No. 390333
Contig ID 19884_1.R1084
5'-most EST LIB3434-064-P1-K1-H1
Method BLASTX
NCBI GI g4220527
BLAST score 658
E value 7.0e-69
Match length 219
% identity 58
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 390334
Contig ID 19887_1.R1084
5'-most EST LIB3434-064-P1-K1-H2

Seq. No. 390335
Contig ID 19899_1.R1084
5'-most EST g568894

Seq. No. 390336
Contig ID 19919_1.R1084
5'-most EST LIB3434-065-P1-K1-D12

Seq. No.	390337
Contig ID	19926_1.R1084
5'-most EST	g568738
Method	BLASTX
NCBI GI	g1885310
BLAST score	1400
E value	1.0e-155
Match length	269
% identity	94
NCBI Description	(X91659) Endoxyloglucan transferase (EXT) [Hordeum vulgare]

Seq. No.	390338
Contig ID	19933_1.R1084
5'-most EST	uC-osflcyp014e07b1
Method	BLASTX
NCBI GI	g2129740
BLAST score	318
E value	1.0e-28
Match length	75
% identity	79
NCBI Description	small nuclear ribonucleoprotein - Arabidopsis thaliana >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis thaliana >gi_1255711 (M93439) small nuclear ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No.	390339
Contig ID	19937_2.R1084
5'-most EST	LIB3434-065-P1-K1-E8
Method	BLASTX
NCBI GI	g2827544
BLAST score	459
E value	7.0e-46
Match length	123
% identity	72
NCBI Description	(AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No.	390340
Contig ID	19944_1.R1084
5'-most EST	uC-osflcyp127d04a1
Method	BLASTX
NCBI GI	g4835765
BLAST score	254
E value	1.0e-21
Match length	54
% identity	83
NCBI Description	(AC007202) Is a member of the PF_00171 aldehyde dehydrogenase family. ESTs gb_T21534, gb_N65241 and gb_AA395614 come from this gene. [Arabidopsis thaliana]

Seq. No.	390341
Contig ID	19982_1.R1084
5'-most EST	g428445

Seq. No.	390342

Contig ID	19988_1.R1084
5'-most EST	uC-osf1M202080h10b1
Method	BLASTX
NCBI GI	g1839188
BLAST score	576
E value	5.0e-59
Match length	198
% identity	59
NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No.	390343
Contig ID	19990_1.R1084
5'-most EST	LIB3434-047-P1-K1-C1
Method	BLASTX
NCBI GI	g5295968
BLAST score	631
E value	4.0e-67
Match length	141
% identity	97
NCBI Description	(AB026295) ESTs C19441(E10423),C99201(E10423) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	390344
Contig ID	19998_1.R1084
5'-most EST	LIB3434-047-P1-K1-C9

Seq. No.	390345
Contig ID	20000_1.R1084
5'-most EST	LIB3434-047-P1-K1-D10
Method	BLASTX
NCBI GI	g6041807
BLAST score	221
E value	8.0e-18
Match length	58
% identity	69
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]

Seq. No.	390346
Contig ID	20007_1.R1084
5'-most EST	LIB3434-047-P1-K1-D8

Seq. No.	390347
Contig ID	20009_1.R1084
5'-most EST	g2312312
Method	BLASTX
NCBI GI	g135641
BLAST score	372
E value	3.0e-35
Match length	177
% identity	58
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID-1 (TATA-BOX FACTOR 1) (TATA SEQUENCE-BINDING PROTEIN 1) (TBP-1) >gi_283028_pir__S23522 transcription initiation factor IID - wheat >gi_21875_emb_CAA42531_ (X59874) TATA binding protein (TFIID) [Triticum aestivum]

Seq. No.	390348
Contig ID	20015_1.R1084
5'-most EST	LIB3434-047-P1-K1-E6
Method	BLASTX
NCBI GI	g2570505
BLAST score	1085
E value	1.0e-119
Match length	239
% identity	93
NCBI Description	(AF022735) proteasome component [Oryza sativa]

Seq. No.	390349
Contig ID	20016_1.R1084
5'-most EST	g4714071

Seq. No.	390350
Contig ID	20019_1.R1084
5'-most EST	g286597
Method	BLASTX
NCBI GI	g2811026
BLAST score	314
E value	1.0e-28
Match length	80
% identity	76
NCBI Description	TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi_1946375 (U93215) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] >gi_2347204 (AC002338) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]

Seq. No.	390351
Contig ID	20023_1.R1084
5'-most EST	LIB3434-047-P1-K1-F2

Seq. No.	390352
Contig ID	20023_2.R1084
5'-most EST	g2431284
Method	BLASTX
NCBI GI	g2494842
BLAST score	239
E value	4.0e-20
Match length	89
% identity	51
NCBI Description	GLUCOSYLTRANSFERASE ALG6 >gi_2131171_pir__S61985 ALG6 protein - yeast (Saccharomyces cerevisiae) >gi_1150997 (U43491) hypothetical protein UNA544 [Saccharomyces cerevisiae] >gi_1420090_emb_CAA99190_ (Z74910) ORF YOR002w [Saccharomyces cerevisiae]

Seq. No.	390353
Contig ID	20027_1.R1084
5'-most EST	LIB3434-059-P1-K1-F11
Method	BLASTX
NCBI GI	g3153889
BLAST score	755
E value	5.0e-80
Match length	301
% identity	53

NCBI Description (AF065444) root iron transporter protein [Pisum sativum]

Seq. No. 390354
Contig ID 20032_1.R1084
5'-most EST LIB3434-047-P1-K1-G10
Method BLASTX
NCBI GI g2655888
BLAST score 873
E value 1.0e-103
Match length 351
% identity 23
NCBI Description (AL009171) 62D9.a [Drosophila melanogaster]

Seq. No. 390355
Contig ID 20040_1.R1084
5'-most EST g571853

Seq. No. 390356
Contig ID 20049_1.R1084
5'-most EST g3548936
Method BLASTX
NCBI GI g1877279
BLAST score 952
E value 1.0e-107
Match length 388
% identity 53
NCBI Description (Z92770) fadE2 [Mycobacterium tuberculosis]

Seq. No. 390357
Contig ID 20052_1.R1084
5'-most EST uC-osflcyp174b11a1

Seq. No. 390358
Contig ID 20063_1.R1084
5'-most EST uC-osrocyp005e06b1
Method BLASTX
NCBI GI g1352057
BLAST score 223
E value 6.0e-18
Match length 97
% identity 45
NCBI Description AUXIN-INDUCED PROTEIN IAA4 >gi_629633_pir__S39075
auxin-induced protein - garden pea >gi_414181_emb_CAA48297_
(X68215) auxin-induced protein [Pisum sativum]

Seq. No. 390359
Contig ID 20069_1.R1084
5'-most EST uC-osrocyp015f08b1

Seq. No. 390360
Contig ID 20070_1.R1084
5'-most EST g2801149

Seq. No. 390361
Contig ID 20079_1.R1084
5'-most EST LIB3434-048-P1-K1-C7
Method BLASTX

NCBI GI	g4633656
BLAST score	89
E value	2.0e-10
Match length	141
% identity	41
NCBI Description	(AF123263) phenylalanyl tRNA synthetase beta subunit [Mus musculus]

Seq. No.	390362
Contig ID	20084_1.R1084
5'-most EST	uC-osrocyp002d12b1

Seq. No.	390363
Contig ID	20087_1.R1084
5'-most EST	LIB3434-016-P1-K1-E12
Method	BLASTX
NCBI GI	g1402918
BLAST score	223
E value	3.0e-18
Match length	59
% identity	64
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]

Seq. No.	390364
Contig ID	20088_1.R1084
5'-most EST	g2311979
Method	BLASTN
NCBI GI	g6041757
BLAST score	140
E value	3.0e-72
Match length	234
% identity	91
NCBI Description	Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence

Seq. No.	390365
Contig ID	20089_1.R1084
5'-most EST	LIB3434-048-P1-K1-D5

Seq. No.	390366
Contig ID	20091_1.R1084
5'-most EST	LIB3434-048-P1-K1-D7
Method	BLASTX
NCBI GI	g927428
BLAST score	851
E value	2.0e-91
Match length	310
% identity	71
NCBI Description	(X86733) fis1 [Linum usitatissimum]

Seq. No.	390367
Contig ID	20096_1.R1084
5'-most EST	LIB3434-048-P1-K1-E11
Method	BLASTX
NCBI GI	g2853097

BLAST score	178
E value	2.0e-12
Match length	95
% identity	43
NCBI Description	(AL021767) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	390368
Contig ID	20101_1.R1084
5'-most EST	LIB3434-010-P1-K1-D7
Method	BLASTX
NCBI GI	g3080389
BLAST score	428
E value	7.0e-42
Match length	139
% identity	61
NCBI Description	(AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No.	390369
Contig ID	20117_1.R1084
5'-most EST	g2442337

Seq. No.	390370
Contig ID	20118_1.R1084
5'-most EST	g2428524
Method	BLASTX
NCBI GI	g2462834
BLAST score	197
E value	2.0e-19
Match length	135
% identity	41
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390371
Contig ID	20118_2.R1084
5'-most EST	LIB3434-048-P1-K1-G11
Method	BLASTX
NCBI GI	g587566
BLAST score	789
E value	1.0e-146
Match length	376
% identity	69
NCBI Description	(X80237) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	390372
Contig ID	20121_1.R1084
5'-most EST	LIB3434-048-P1-K1-G3
Method	BLASTX
NCBI GI	g1346771
BLAST score	235
E value	2.0e-21
Match length	73
% identity	75
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP] >gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase (PCK1) - Urochloa panicoides >gi_607752 (U09241)

phosphoenolpyruvate carboxykinase [Urochloa panicoides]

Seq. No.	390373
Contig ID	20135_1.R1084
5'-most EST	LIB3434-048-P1-K1-H5

Seq. No.	390374
Contig ID	20139_1.R1084
5'-most EST	LIB3434-048-P1-K1-H9
Method	BLASTX
NCBI GI	g3297823
BLAST score	95
E value	9.0e-09
Match length	43
% identity	70
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	390375
Contig ID	20140_1.R1084
5'-most EST	uC-osrocyp014b09b1
Method	BLASTX
NCBI GI	g4455194
BLAST score	257
E value	6.0e-22
Match length	67
% identity	70
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	390376
Contig ID	20144_1.R1084
5'-most EST	g702387
Method	BLASTX
NCBI GI	g5823556
BLAST score	678
E value	4.0e-71
Match length	286
% identity	43
NCBI Description	(AF181096) ferric leghemoglobin reductase [Vigna unguiculata]

Seq. No.	390377
Contig ID	20149_1.R1084
5'-most EST	g2427242

Seq. No.	390378
Contig ID	20151_1.R1084
5'-most EST	LIB3434-039-P1-K1-D2

Seq. No.	390379
Contig ID	20156_1.R1084
5'-most EST	LIB3434-049-P1-K1-B6
Method	BLASTX
NCBI GI	g4585988
BLAST score	752
E value	5.0e-80
Match length	184
% identity	78

NCBI Description	(AC005287) Similar to phosphoprotein phosphatase 2A regulatory subunit [Arabidopsis thaliana]

Seq. No.	390380
Contig ID	20158_1.R1084
5'-most EST	g701858
Method	BLASTX
NCBI GI	g5091611
BLAST score	1006
E value	1.0e-109
Match length	218
% identity	93
NCBI Description	(AC007858) Similar to gb_U43629 integral membrane protein from Beta vulgaris and is a member of the sugar transporter family PF_00083. ES [Oryza sativa]

Seq. No.	390381
Contig ID	20167_1.R1084
5'-most EST	LIB3434-049-P1-K1-C6
Method	BLASTX
NCBI GI	g5777624
BLAST score	832
E value	7.0e-94
Match length	252
% identity	83
NCBI Description	(AJ245900) CAA303712.1 protein [Oryza sativa]

Seq. No.	390382
Contig ID	20167_2.R1084
5'-most EST	g4878206
Method	BLASTX
NCBI GI	g5777627
BLAST score	820
E value	1.0e-121
Match length	228
% identity	96
NCBI Description	(AJ245900) CAA303715.1 protein [Oryza sativa]

Seq. No.	390383
Contig ID	20167_3.R1084
5'-most EST	g3767945
Method	BLASTX
NCBI GI	g5777625
BLAST score	483
E value	1.0e-48
Match length	136
% identity	79
NCBI Description	(AJ245900) CAA303713.1 protein [Oryza sativa]

Seq. No.	390384
Contig ID	20184_1.R1084
5'-most EST	LIB3434-049-P1-K1-E12
Method	BLASTX
NCBI GI	g6069648
BLAST score	212
E value	6.0e-17
Match length	117

% identity	37
NCBI Description	(AP000616) ESTs AU078644(E0685),C72841(E2351),AU078645(E0685), AU030746(E60179) correspond to a region of the predicted gene.; similar to Arabidopsis thaliana BAC F11O4; similar to Medicago truncatula MtN21 (AF096370) [Oryza

Seq. No.	390385
Contig ID	20200_1.R1084
5'-most EST	g4878207
Method	BLASTX
NCBI GI	g4204304
BLAST score	227
E value	4.0e-34
Match length	159
% identity	54
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	390386
Contig ID	20204_1.R1084
5'-most EST	uC-osflM202046h09b1

Seq. No.	390387
Contig ID	20214_1.R1084
5'-most EST	g2798679

Seq. No.	390388
Contig ID	20214_2.R1084
5'-most EST	g2275989

Seq. No.	390389
Contig ID	20227_1.R1084
5'-most EST	uC-osflcyp081g07b1
Method	BLASTX
NCBI GI	g3894158
BLAST score	239
E value	7.0e-20
Match length	158
% identity	41
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	390390
Contig ID	20228_1.R1084
5'-most EST	uC-osflcyp064a05b1
Method	BLASTX
NCBI GI	g4406775
BLAST score	187
E value	1.0e-13
Match length	178
% identity	33
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	390391
Contig ID	20233_1.R1084
5'-most EST	LIB3434-058-P1-K1-A4

Method	BLASTX
NCBI GI	g3096918
BLAST score	257
E value	4.0e-22
Match length	112
% identity	54
NCBI Description	(AL023094) putative cyclase associated protein CAP [Arabidopsis thaliana] >gi_3169136_dbj_BAA28621_ (AB014759) Atcap1 [Arabidopsis thaliana]

Seq. No.	390392
Contig ID	20235_1.R1084
5'-most EST	LIB3434-058-P1-K1-A6
Method	BLASTX
NCBI GI	g3927836
BLAST score	254
E value	2.0e-21
Match length	64
% identity	73
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	390393
Contig ID	20240_1.R1084
5'-most EST	LIB3434-058-P1-K1-B10
Method	BLASTX
NCBI GI	g4240031
BLAST score	348
E value	2.0e-32
Match length	119
% identity	55
NCBI Description	(AB018422) DNA binding zinc finger protein (Pspzf) [Pisum sativum]

Seq. No.	390394
Contig ID	20241_1.R1084
5'-most EST	g3768853

Seq. No.	390395
Contig ID	20242_1.R1084
5'-most EST	g427815

Seq. No.	390396
Contig ID	20262_1.R1084
5'-most EST	g4714256
Method	BLASTX
NCBI GI	g3402817
BLAST score	222
E value	1.0e-17
Match length	88
% identity	66
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	390397
Contig ID	20266_1.R1084
5'-most EST	LIB3434-058-P1-K1-D4
Method	BLASTX
NCBI GI	g3258570

BLAST score	197
E value	9.0e-17
Match length	94
% identity	73
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]

Seq. No.	390398
Contig ID	20268_1.R1084
5'-most EST	uC-osflcyp121f03b1
Method	BLASTX
NCBI GI	g3548818
BLAST score	664
E value	2.0e-69
Match length	166
% identity	76
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	390399
Contig ID	20270_1.R1084
5'-most EST	LIB3434-052-P1-K1-D1
Method	BLASTX
NCBI GI	g2880048
BLAST score	127
E value	3.0e-09
Match length	49
% identity	55
NCBI Description	(AC002340) unknown protein [Arabidopsis thaliana]

Seq. No.	390400
Contig ID	20276_1.R1084
5'-most EST	g2310998

Seq. No.	390401
Contig ID	20279_1.R1084
5'-most EST	LIB3434-007-P1-K1-A11
Method	BLASTX
NCBI GI	g3935181
BLAST score	1013
E value	1.0e-111
Match length	237
% identity	80
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	390402
Contig ID	20288_1.R1084
5'-most EST	LIB3434-058-P1-K1-F3
Method	BLASTX
NCBI GI	g4588012
BLAST score	281
E value	2.0e-30
Match length	100
% identity	69
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	390403
Contig ID	20297_1.R1084

5'-most EST	LIB3434-058-P1-K1-G11
Seq. No.	390404
Contig ID	20303_1.R1084
5'-most EST	LIB3434-058-P1-K1-G7
Method	BLASTX
NCBI GI	g4585991
BLAST score	261
E value	3.0e-22
Match length	170
% identity	46
NCBI Description	(AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis thaliana]
Seq. No.	390405
Contig ID	20304_1.R1084
5'-most EST	LIB3434-058-P1-K1-G8
Method	BLASTX
NCBI GI	g5731259
BLAST score	624
E value	5.0e-65
Match length	170
% identity	74
NCBI Description	(AF166351) alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis thaliana]
Seq. No.	390406
Contig ID	20310_1.R1084
5'-most EST	uC-osflm202107e10b1
Method	BLASTX
NCBI GI	g3249070
BLAST score	662
E value	3.0e-69
Match length	248
% identity	61
NCBI Description	(AC004473) Contains similarity to siah binding protein 1 (SiahBP1) gb_U51586 from Homo sapiens. ESTs gb_T43314, gb_T43315 and gb_R90521, gb_T75905 [Arabidopsis thaliana]
Seq. No.	390407
Contig ID	20314_1.R1084
5'-most EST	LIB3434-058-P1-K1-H7
Method	BLASTN
NCBI GI	g5091496
BLAST score	175
E value	2.0e-93
Match length	522
% identity	97
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence
Seq. No.	390408
Contig ID	20319_1.R1084
5'-most EST	uC-osflcyp087f11a1
Method	BLASTX
NCBI GI	g2109293
BLAST score	240

E value 5.0e-20
Match length 74
% identity 69
NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 390409
Contig ID 20328_1.R1084
5'-most EST uC-osrocyp033b04b1
Method BLASTX
NCBI GI g4415931
BLAST score 395
E value 8.0e-38
Match length 188
% identity 43
NCBI Description (AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No. 390410
Contig ID 20344_2.R1084
5'-most EST g428691

Seq. No. 390411
Contig ID 20358_1.R1084
5'-most EST uC-osroM202004c12b1

Seq. No. 390412
Contig ID 20359_1.R1084
5'-most EST LIB3434-059-P1-K1-D9
Method BLASTX
NCBI GI g4262236
BLAST score 162
E value 1.0e-14
Match length 83
% identity 59
NCBI Description (AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 390413
Contig ID 20365_1.R1084
5'-most EST LIB3434-052-P1-K1-H4
Method BLASTX
NCBI GI g2281100
BLAST score 327
E value 3.0e-30
Match length 152
% identity 43
NCBI Description (AC002333) LecRK1 protein kinase isolog [Arabidopsis thaliana]

Seq. No. 390414
Contig ID 20366_1.R1084
5'-most EST g4716706
Method BLASTX
NCBI GI g1519680
BLAST score 147

E value 6.0e-09
Match length 62
% identity 37
NCBI Description (U67953) contains similarity to C3HC4-class zinc finger (PS:PS00518) [Caenorhabditis elegans]

Seq. No. 390415
Contig ID 20375_1.R1084
5'-most EST g2310758
Method BLASTX
NCBI GI g131772
BLAST score 567
E value 4.0e-58
Match length 132
% identity 89
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) - maize

Seq. No. 390416
Contig ID 20375_5.R1084
5'-most EST uC-osflcyp125a04b1

Seq. No. 390417
Contig ID 20402_1.R1084
5'-most EST LIB3434-060-P1-K1-A3
Method BLASTX
NCBI GI g4235430
BLAST score 229
E value 7.0e-19
Match length 72
% identity 64
NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No. 390418
Contig ID 20405_1.R1084
5'-most EST LIB3434-060-P1-K1-A6
Method BLASTX
NCBI GI g2384696
BLAST score 144
E value 1.0e-08
Match length 67
% identity 46
NCBI Description (AF013216) acyl-CoA oxidase [Myxococcus xanthus]

Seq. No. 390419
Contig ID 20409_1.R1084
5'-most EST g2428985
Method BLASTX
NCBI GI g2995380
BLAST score 475
E value 3.0e-47
Match length 109
% identity 83
NCBI Description (AJ001903) thioredoxin H [Triticum durum]

Seq. No. 390420

Contig ID	20415_1.R1084
5'-most EST	uC-osflcyp099e11b1
Seq. No.	390421
Contig ID	20430_1.R1084
5'-most EST	LIB3434-060-P1-K1-D10
Method	BLASTX
NCBI GI	g4929751
BLAST score	202
E value	1.0e-15
Match length	98
% identity	42
NCBI Description	(AF151899) CGI-141 protein [Homo sapiens]
Seq. No.	390422
Contig ID	20432_2.R1084
5'-most EST	uC-osflcyp177f12b1
Seq. No.	390423
Contig ID	20435_1.R1084
5'-most EST	uC-osflcyp009f03b1
Seq. No.	390424
Contig ID	20445_1.R1084
5'-most EST	LIB3434-060-P1-K1-E5
Seq. No.	390425
Contig ID	20447_1.R1084
5'-most EST	LIB3477-007-P1-K1-D4
Seq. No.	390426
Contig ID	20447_2.R1084
5'-most EST	g1854277
Method	BLASTN
NCBI GI	g3402815
BLAST score	47
E value	9.0e-17
Match length	60
% identity	93
NCBI Description	Cloning Vector pGreen
Seq. No.	390427
Contig ID	20462_2.R1084
5'-most EST	g701301
Method	BLASTX
NCBI GI	g3298540
BLAST score	367
E value	6.0e-35
Match length	116
% identity	63
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.	390428
Contig ID	20468_1.R1084
5'-most EST	g286662
Seq. No.	390429

Contig ID	20468_2.R1084
5'-most EST	uC-osrocyp025f03a1
Seq. No.	390430
Contig ID	20469_1.R1084
5'-most EST	uC-osflcyp121g11b1
Method	BLASTX
NCBI GI	g4584525
BLAST score	681
E value	9.0e-72
Match length	162
% identity	75
NCBI Description	(AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]
Seq. No.	390431
Contig ID	20474_1.R1084
5'-most EST	LIB3434-060-P1-K1-H10
Method	BLASTX
NCBI GI	g4191789
BLAST score	599
E value	4.0e-62
Match length	162
% identity	77
NCBI Description	(AC005917) putative transmembrane transport protein [Arabidopsis thaliana]
Seq. No.	390432
Contig ID	20480_1.R1084
5'-most EST	uC-osflcyp086d10b1
Seq. No.	390433
Contig ID	20494_1.R1084
5'-most EST	g2310914
Seq. No.	390434
Contig ID	20494_2.R1084
5'-most EST	g568015
Seq. No.	390435
Contig ID	20494_3.R1084
5'-most EST	g2310925
Seq. No.	390436
Contig ID	20494_5.R1084
5'-most EST	g568182
Seq. No.	390437
Contig ID	20494_6.R1084
5'-most EST	g2312843
Seq. No.	390438
Contig ID	20502_1.R1084
5'-most EST	g2797417
Method	BLASTX
NCBI GI	g2493053
BLAST score	299

E value	6.0e-27
Match length	62
% identity	87
NCBI Description	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >gi_639793 (L39120) mitochondrial F1F0 ATP synthase epsilon subunit [Zea mays]

Seq. No.	390439
Contig ID	20503_1.R1084
5'-most EST	uC-osflcyp112b10b1
Method	BLASTX
NCBI GI	g2982458
BLAST score	220
E value	7.0e-23
Match length	105
% identity	55
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	390440
Contig ID	20505_1.R1084
5'-most EST	g701888
Method	BLASTX
NCBI GI	g3327957
BLAST score	160
E value	8.0e-12
Match length	77
% identity	51
NCBI Description	(AF060490) TLS-associated protein TASR-2 [Mus musculus] >gi_3327976 (AF067730) TLS-associated protein TASR-2 [Homo sapiens]

Seq. No.	390441
Contig ID	20519_1.R1084
5'-most EST	uC-osflM202014e05b1
Method	BLASTX
NCBI GI	g1922242
BLAST score	206
E value	4.0e-16
Match length	57
% identity	70
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390442
Contig ID	20524_1.R1084
5'-most EST	LIB3434-062-P1-K1-E10

Seq. No.	390443
Contig ID	20528_1.R1084
5'-most EST	g3107614
Method	BLASTN
NCBI GI	g2280517
BLAST score	70
E value	1.0e-30
Match length	73
% identity	99
NCBI Description	Nicotiana tabacum mRNA for BYJ15, partial cds

Seq. No.	390444
Contig ID	20538_2.R1084
5'-most EST	LIB3475-002-P1-K2-D10
Method	BLASTX
NCBI GI	g3329368
BLAST score	149
E value	2.0e-09
Match length	52
% identity	56
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	390445
Contig ID	20556_1.R1084
5'-most EST	g572429
Method	BLASTX
NCBI GI	g3582339
BLAST score	482
E value	3.0e-48
Match length	118
% identity	76
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	390446
Contig ID	20557_1.R1084
5'-most EST	LIB3434-062-P1-K1-H4
Method	BLASTX
NCBI GI	g1546700
BLAST score	285
E value	2.0e-25
Match length	103
% identity	57
NCBI Description	(X98804) peroxidase ATP18a [Arabidopsis thaliana]

Seq. No.	390447
Contig ID	20560_1.R1084
5'-most EST	uC-osflm202113f06b1

Seq. No.	390448
Contig ID	20561_1.R1084
5'-most EST	g2317560
Method	BLASTX
NCBI GI	g1480078
BLAST score	604
E value	6.0e-63
Match length	124
% identity	89
NCBI Description	(X99696) shaggy-like protein kinase iota [Arabidopsis thaliana] >gi_2444277_gb_AAB71545.1_ (AF019927) GSK3/shaggy-like protein kinase [Arabidopsis thaliana]

Seq. No.	390449
Contig ID	20568_1.R1084
5'-most EST	LIB3434-043-P1-K1-A7
Method	BLASTX
NCBI GI	g5732701
BLAST score	226
E value	3.0e-18

Match length	81
% identity	62
NCBI Description	(AF159386) thioredoxin-like protein [Secale cereale]

Seq. No.	390450
Contig ID	20572_1.R1084
5'-most EST	LIB3434-043-P1-K1-B11
Method	BLASTX
NCBI GI	g4587518
BLAST score	1235
E value	1.0e-136
Match length	346
% identity	73
NCBI Description	(AC007060) Strong similarity to F19I3.8 gi_3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb_AC004238 and is a member of PF_01370 the NAD dependent epimerase/dehydratase family. EST gb_AA59

Seq. No.	390451
Contig ID	20575_1.R1084
5'-most EST	LIB3434-043-P1-K1-B4

Seq. No.	390452
Contig ID	20585_1.R1084
5'-most EST	g2427763
Method	BLASTX
NCBI GI	g295355
BLAST score	235
E value	1.0e-19
Match length	121
% identity	44
NCBI Description	(L13653) peroxidase [Lycopersicon esculentum]

Seq. No.	390453
Contig ID	20586_1.R1084
5'-most EST	LIB3434-043-P1-K1-C4

Seq. No.	390454
Contig ID	20589_1.R1084
5'-most EST	g3760793
Method	BLASTX
NCBI GI	g4490704
BLAST score	411
E value	7.0e-40
Match length	111
% identity	74
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	390455
Contig ID	20594_1.R1084
5'-most EST	LIB3434-043-P1-K1-D2

Seq. No.	390456
Contig ID	20595_1.R1084
5'-most EST	LIB3434-008-P1-K1-E9

Seq. No.	390457

Contig ID	20597_1.R1084
5'-most EST	LIB3434-043-P1-K1-D6
Method	BLASTX
NCBI GI	g6016876
BLAST score	464
E value	6.0e-46
Match length	116
% identity	100
NCBI Description	(AP000570) ESTs C99053(E4383),C99052(E4383) correspond to a region of the predicted gene.; Similar to putative RNA helicase. (AC005309) [Oryza sativa]

Seq. No.	390458
Contig ID	20600_1.R1084
5'-most EST	g2428942

Seq. No.	390459
Contig ID	20602_1.R1084
5'-most EST	LIB3434-043-P1-K1-E10
Method	BLASTX
NCBI GI	g5391446
BLAST score	159
E value	1.0e-10
Match length	59
% identity	32
NCBI Description	(AF031471) pollen allergen [Juniperus oxycedrus]

Seq. No.	390460
Contig ID	20610_1.R1084
5'-most EST	g426104
Method	BLASTX
NCBI GI	g1076316
BLAST score	171
E value	8.0e-12
Match length	85
% identity	38
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	390461
Contig ID	20611_1.R1084
5'-most EST	LIB3434-043-P1-K1-E8

Seq. No.	390462
Contig ID	20612_1.R1084
5'-most EST	LIB3434-043-P1-K1-E9
Method	BLASTX
NCBI GI	g4432855
BLAST score	248
E value	2.0e-24
Match length	114
% identity	59
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	390463
Contig ID	20625_1.R1084

5'-most EST	LIB3434-043-P1-K1-G10
Seq. No.	390464
Contig ID	20626_1.R1084
5'-most EST	uC-osflcyp122d07b1
Method	BLASTX
NCBI GI	g466172
BLAST score	678
E value	4.0e-71
Match length	137
% identity	96
NCBI Description	GTP-BINDING PROTEIN YPTM2 >gi_283056_pir__B38202 ypt family - maize >gi_287835_emb_CAA44919_ (X63278) yptm2 [Zea mays]
Seq. No.	390465
Contig ID	20626_3.R1084
5'-most EST	g427739
Method	BLASTX
NCBI GI	g466172
BLAST score	524
E value	2.0e-62
Match length	128
% identity	98
NCBI Description	GTP-BINDING PROTEIN YPTM2 >gi_283056_pir__B38202 ypt family - maize >gi_287835_emb_CAA44919_ (X63278) yptm2 [Zea mays]
Seq. No.	390466
Contig ID	20626_4.R1084
5'-most EST	g3763506
Method	BLASTX
NCBI GI	g4586580
BLAST score	391
E value	7.0e-38
Match length	76
% identity	100
NCBI Description	(AB024994) rab-type small GTP-binding protein [Cicer arietinum]
Seq. No.	390467
Contig ID	20631_1.R1084
5'-most EST	LIB3434-043-P1-K1-G5
Method	BLASTX
NCBI GI	g4539423
BLAST score	1295
E value	1.0e-152
Match length	366
% identity	74
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]
Seq. No.	390468
Contig ID	20636_1.R1084
5'-most EST	LIB3434-043-P1-K1-H12
Method	BLASTX
NCBI GI	g4337175
BLAST score	230
E value	7.0e-19

Match length	129
% identity	41
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	390469
Contig ID	20639_1.R1084
5'-most EST	LIB3434-043-P1-K1-H7
Method	BLASTN
NCBI GI	g19006
BLAST score	43
E value	1.0e-14
Match length	98
% identity	91
NCBI Description	H.vulgare ids-1 mRNA

Seq. No.	390470
Contig ID	20642_1.R1084
5'-most EST	g1632229
Method	BLASTX
NCBI GI	g5091555
BLAST score	489
E value	6.0e-49
Match length	129
% identity	74
NCBI Description	(AC007067) T10O24.24 [Arabidopsis thaliana]

Seq. No.	390471
Contig ID	20646_1.R1084
5'-most EST	LIB3434-044-P1-K1-A2

Seq. No.	390472
Contig ID	20664_1.R1084
5'-most EST	LIB3434-044-P1-K1-B9
Method	BLASTX
NCBI GI	g4662633
BLAST score	158
E value	2.0e-10
Match length	79
% identity	44
NCBI Description	(AC007267) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390473
Contig ID	20671_1.R1084
5'-most EST	g4715434

Seq. No.	390474
Contig ID	20672_1.R1084
5'-most EST	uC-osflcyp125b06b1

Seq. No.	390475
Contig ID	20678_1.R1084
5'-most EST	g4878938
Method	BLASTX
NCBI GI	g3037045

BLAST score	158
E value	5.0e-10
Match length	121
% identity	30
NCBI Description	(AF052621) hypothetical protein COX4AL [Mus musculus]

Seq. No.	390476
Contig ID	20679_1.R1084
5'-most EST	LIB3434-044-P1-K1-D2
Method	BLASTX
NCBI GI	g4204761
BLAST score	624
E value	7.0e-65
Match length	201
% identity	63
NCBI Description	(U51192) peroxidase precursor [Glycine max]

Seq. No.	390477
Contig ID	20680_1.R1084
5'-most EST	LIB3434-044-P1-K1-D3
Method	BLASTX
NCBI GI	g1854378
BLAST score	620
E value	5.0e-75
Match length	182
% identity	79
NCBI Description	(AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]

Seq. No.	390478
Contig ID	20685_1.R1084
5'-most EST	LIB3434-035-P1-K1-G12
Method	BLASTX
NCBI GI	g4587525
BLAST score	328
E value	3.0e-31
Match length	144
% identity	56
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	390479
Contig ID	20688_1.R1084
5'-most EST	LIB3434-041-P1-K1-E1

Seq. No.	390480
Contig ID	20689_1.R1084
5'-most EST	LIB3434-044-P1-K1-E2

Seq. No.	390481
Contig ID	20702_1.R1084
5'-most EST	LIB3434-044-P1-K1-F3
Method	BLASTX
NCBI GI	g6091742
BLAST score	534

E value	3.0e-54
Match length	159
% identity	69
NCBI Description	(AC010797) putative ribosome recycling factor [Arabidopsis thaliana]

Seq. No.	390482
Contig ID	20710_1.R1084
5'-most EST	g2800230
Method	BLASTX
NCBI GI	g2252863
BLAST score	414
E value	2.0e-40
Match length	190
% identity	34
NCBI Description	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]

Seq. No.	390483
Contig ID	20712_1.R1084
5'-most EST	uC-osroM202019d12b1
Method	BLASTX
NCBI GI	g4490736
BLAST score	592
E value	7.0e-61
Match length	225
% identity	41
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	390484
Contig ID	20714_1.R1084
5'-most EST	g568616
Method	BLASTX
NCBI GI	g3822036
BLAST score	306
E value	1.0e-40
Match length	193
% identity	52
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	390485
Contig ID	20719_1.R1084
5'-most EST	LIB3434-044-P1-K1-G9

Seq. No.	390486
Contig ID	20720_1.R1084
5'-most EST	uC-osflcyp081e04b1
Method	BLASTX
NCBI GI	g2565436
BLAST score	426
E value	8.0e-42
Match length	90
% identity	92
NCBI Description	(AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No.	390487
Contig ID	20721_1.R1084

5'-most EST	LIB3434-044-P1-K1-H10
Method	BLASTX
NCBI GI	g1871194
BLAST score	207
E value	4.0e-16
Match length	136
% identity	43
NCBI Description	(U90439) DNA binding protein isolog [Arabidopsis thaliana] >gi_2335092 (AC002339) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	390488
Contig ID	20723_1.R1084
5'-most EST	LIB3434-010-P1-K1-H3
Method	BLASTN
NCBI GI	g2149018
BLAST score	42
E value	8.0e-14
Match length	54
% identity	94
NCBI Description	Oryza sativa putative ADP-glucose pyrophosphorylase subunit SH2 and putative NADPH-dependent reductase A1 genes, complete cds

Seq. No.	390489
Contig ID	20725_1.R1084
5'-most EST	LIB3434-044-P1-K1-H3
Method	BLASTX
NCBI GI	g2911042
BLAST score	457
E value	2.0e-60
Match length	166
% identity	73
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	390490
Contig ID	20725_2.R1084
5'-most EST	g4879735
Method	BLASTX
NCBI GI	g2911042
BLAST score	397
E value	2.0e-38
Match length	128
% identity	64
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	390491
Contig ID	20725_3.R1084
5'-most EST	uC-osflcyp169a08b1
Method	BLASTX
NCBI GI	g2911042
BLAST score	552
E value	2.0e-62
Match length	174
% identity	78

NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	390492
Contig ID	20729_1.R1084
5'-most EST	LIB3434-044-P1-K1-H7
Method	BLASTX
NCBI GI	g5911167
BLAST score	378
E value	3.0e-36
Match length	124
% identity	52
NCBI Description	(AF136221) putative transposase protein [Zea mays]

Seq. No.	390493
Contig ID	20736_1.R1084
5'-most EST	LIB3434-018-P1-K1-C3

Seq. No.	390494
Contig ID	20751_1.R1084
5'-most EST	LIB3434-045-P1-K1-B6

Seq. No.	390495
Contig ID	20752_1.R1084
5'-most EST	LIB3434-045-P1-K1-B7
Method	BLASTX
NCBI GI	g3047117
BLAST score	385
E value	5.0e-60
Match length	124
% identity	94
NCBI Description	(AF058919) similar to ATP-dependent RNA helicases [Arabidopsis thaliana]

Seq. No.	390496
Contig ID	20754_1.R1084
5'-most EST	LIB3434-045-P1-K1-C10
Method	BLASTX
NCBI GI	g5902407
BLAST score	382
E value	6.0e-74
Match length	232
% identity	68
NCBI Description	(AC008148) Similar to asparaginyl-tRNA synthetases [Arabidopsis thaliana]

Seq. No.	390497
Contig ID	20756_1.R1084
5'-most EST	g5004806

Seq. No.	390498
Contig ID	20758_1.R1084
5'-most EST	LIB3434-045-P1-K1-C4
Method	BLASTX
NCBI GI	g2984225
BLAST score	365
E value	2.0e-34

Match length	154
% identity	50
NCBI Description	(AE000766) enolase-phosphatase E-1 [Aquifex aeolicus]

Seq. No.	390499
Contig ID	20764_1.R1084
5'-most EST	uC-osroM202036g02b1
Method	BLASTX
NCBI GI	g4689108
BLAST score	410
E value	7.0e-40
Match length	187
% identity	43
NCBI Description	(AF077030) hypothetical 43.2 kDa protein [Homo sapiens] >gi_4929577_gb_AAD34049.1_AF151812_1 (AF151812) CGI-54 protein [Homo sapiens]

Seq. No.	390500
Contig ID	20767_1.R1084
5'-most EST	uC-osflcyp155d08b1
Method	BLASTX
NCBI GI	g6041797
BLAST score	387
E value	4.0e-37
Match length	183
% identity	42
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]

Seq. No.	390501
Contig ID	20768_1.R1084
5'-most EST	g428935
Method	BLASTX
NCBI GI	g4469020
BLAST score	207
E value	7.0e-23
Match length	112
% identity	56
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	390502
Contig ID	20773_1.R1084
5'-most EST	g426863
Method	BLASTX
NCBI GI	g4755194
BLAST score	447
E value	2.0e-44
Match length	163
% identity	49
NCBI Description	(AC007018) hypothetical protein [Arabidopsis thaliana] >gi_4755195_gb_AAD29062.1_AC007018_10 (AC007018) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390503
Contig ID	20774_1.R1084
5'-most EST	LIB3475-008-P1-K1-G3
Method	BLASTX

NCBI GI	g1323742
BLAST score	276
E value	6.0e-24
Match length	182
% identity	37
NCBI Description	(U32427) unknown [Triticum aestivum]

Seq. No.	390504
Contig ID	20780_1.R1084
5'-most EST	LIB3434-045-P1-K1-E5
Method	BLASTX
NCBI GI	g3150415
BLAST score	397
E value	2.0e-97
Match length	232
% identity	51
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	390505
Contig ID	20781_1.R1084
5'-most EST	uC-osroM202006d12b1
Method	BLASTX
NCBI GI	g4006902
BLAST score	196
E value	1.0e-14
Match length	125
% identity	34
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	390506
Contig ID	20783_1.R1084
5'-most EST	LIB3475-004-P1-K2-C12

Seq. No.	390507
Contig ID	20783_2.R1084
5'-most EST	uC-osrocyp037h03b1
Method	BLASTX
NCBI GI	g3264767
BLAST score	270
E value	2.0e-23
Match length	56
% identity	88
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	390508
Contig ID	20785_1.R1084
5'-most EST	g568576
Method	BLASTX
NCBI GI	g3341679
BLAST score	449
E value	2.0e-44
Match length	137
% identity	64
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	390509
Contig ID	20785_4.R1084
5'-most EST	LIB3434-045-P1-K1-F10
Method	BLASTX
NCBI GI	g3341679
BLAST score	538
E value	1.0e-57
Match length	196
% identity	59
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	390510
Contig ID	20787_1.R1084
5'-most EST	g3760368
Method	BLASTX
NCBI GI	g4263507
BLAST score	146
E value	1.0e-12
Match length	111
% identity	40
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390511
Contig ID	20795_1.R1084
5'-most EST	uC-osrocyp025g11a1
Method	BLASTX
NCBI GI	g4371292
BLAST score	192
E value	2.0e-14
Match length	57
% identity	61
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	390512
Contig ID	20801_1.R1084
5'-most EST	uC-osflcyp120c01b1
Method	BLASTX
NCBI GI	g2505874
BLAST score	714
E value	1.0e-75
Match length	161
% identity	83
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	390513
Contig ID	20803_1.R1084
5'-most EST	LIB3479-009-Q6-K1-D4

Seq. No.	390514
Contig ID	20805_1.R1084
5'-most EST	g700647

Seq. No.	390515
Contig ID	20805_2.R1084
5'-most EST	LIB3474-002-P1-K1-D1

Seq. No.	390516
Contig ID	20808_1.R1084
5'-most EST	g2798406

Seq. No.	390517
Contig ID	20809_1.R1084
5'-most EST	uC-osf1M202090h12b1
Method	BLASTX
NCBI GI	g4006890
BLAST score	756
E value	3.0e-80
Match length	182
% identity	79
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	390518
Contig ID	20810_1.R1084
5'-most EST	LIB3477-002-P1-K1-C12
Method	BLASTX
NCBI GI	g6056418
BLAST score	220
E value	7.0e-18
Match length	93
% identity	38
NCBI Description	(AC009525) Similar to beta-glucosidases [Arabidopsis thaliana]

Seq. No.	390519
Contig ID	20812_1.R1084
5'-most EST	uC-osf1m202111b12b1
Method	BLASTX
NCBI GI	g3738284
BLAST score	262
E value	3.0e-22
Match length	103
% identity	51
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	390520
Contig ID	20814_1.R1084
5'-most EST	g431827
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36
% identity	59
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	390521
Contig ID	20816_1.R1084
5'-most EST	g5667150
Method	BLASTX
NCBI GI	g2293332
BLAST score	312

E value	4.0e-28
Match length	192
% identity	41
NCBI Description	(AF011338) unknown [Dictyostelium discoideum]

Seq. No.	390522
Contig ID	20819_1.R1084
5'-most EST	LIB3434-046-P1-K1-A4
Method	BLASTX
NCBI GI	g4731167
BLAST score	252
E value	4.0e-21
Match length	137
% identity	36
NCBI Description	(AF108357) c-myc binding protein MM-1 [Mus musculus]

Seq. No.	390523
Contig ID	20826_1.R1084
5'-most EST	LIB3434-041-P1-K1-C7

Seq. No.	390524
Contig ID	20836_1.R1084
5'-most EST	LIB3434-046-P1-K1-C3

Seq. No.	390525
Contig ID	20838_1.R1084
5'-most EST	uC-osflm202107d02b1
Method	BLASTX
NCBI GI	g1168654
BLAST score	798
E value	3.0e-89
Match length	268
% identity	59
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) - garden asparagus >gi_452712_emb_CAA54525_ (X77319) beta-galactosidase [Asparagus officinalis]

Seq. No.	390526
Contig ID	20850_1.R1084
5'-most EST	LIB3434-046-P1-K1-E1
Method	BLASTX
NCBI GI	g3687239
BLAST score	224
E value	3.0e-18
Match length	46
% identity	91
NCBI Description	(AC005169) putative clathrin coat assembly protein [Arabidopsis thaliana]

Seq. No.	390527
Contig ID	20855_1.R1084
5'-most EST	uC-osflM202068g06b1
Method	BLASTX
NCBI GI	g5881779
BLAST score	442
E value	2.0e-43

Match length	128
% identity	60
NCBI Description	(AL117386) putative protein [Arabidopsis thaliana]

Seq. No.	390528
Contig ID	20862_1.R1084
5'-most EST	g5003115
Method	BLASTX
NCBI GI	g5263324
BLAST score	944
E value	1.0e-102
Match length	204
% identity	87
NCBI Description	(AC007727) Identical to gb_Y13173 Arabidopsis thaliana mRNA for proteasome subunit. EST gb_T76747 comes from this gene

Seq. No.	390529
Contig ID	20862_2.R1084
5'-most EST	LIB3434-008-P1-K1-E10
Method	BLASTX
NCBI GI	g2982322
BLAST score	489
E value	2.0e-49
Match length	103
% identity	89
NCBI Description	(AF051246) probable proteasome subunit [Picea mariana]

Seq. No.	390530
Contig ID	20871_1.R1084
5'-most EST	LIB3434-026-P1-K1-A6

Seq. No.	390531
Contig ID	20873_1.R1084
5'-most EST	g3768176
Method	BLASTX
NCBI GI	g2463586
BLAST score	271
E value	1.0e-23
Match length	89
% identity	53
NCBI Description	(D38533) FB22 precursor [Ananas comosus]

Seq. No.	390532
Contig ID	20873_2.R1084
5'-most EST	g3767808
Method	BLASTX
NCBI GI	g2342728
BLAST score	177
E value	1.0e-12
Match length	93
% identity	39
NCBI Description	(AC002341) Cysteine proteinase isolog [Arabidopsis thaliana]

Seq. No.	390533
Contig ID	20874_1.R1084
5'-most EST	uC-osflcyp177e09b1

Seq. No.	390534
Contig ID	20875_1.R1084
5'-most EST	LIB3434-046-P1-K1-G11
Method	BLASTX
NCBI GI	g2618699
BLAST score	250
E value	9.0e-29
Match length	240
% identity	33
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	390535
Contig ID	20878_1.R1084
5'-most EST	g426976
Method	BLASTX
NCBI GI	g1946358
BLAST score	454
E value	4.0e-45
Match length	114
% identity	67
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	390536
Contig ID	20880_1.R1084
5'-most EST	g4879817
Method	BLASTX
NCBI GI	g4731573
BLAST score	160
E value	2.0e-11
Match length	108
% identity	46
NCBI Description	(AF123265) remorin 1 [Lycopersicon esculentum]

Seq. No.	390537
Contig ID	20884_1.R1084
5'-most EST	LIB3434-054-P1-K1-F12
Method	BLASTX
NCBI GI	g4587584
BLAST score	541
E value	1.0e-55
Match length	127
% identity	46
NCBI Description	(AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	390538
Contig ID	20886_2.R1084
5'-most EST	LIB3434-046-P1-K1-H11
Method	BLASTN
NCBI GI	g5257255
BLAST score	58
E value	8.0e-24
Match length	302
% identity	75
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	390539

Contig ID	20896_1.R1084
5'-most EST	g3767080
Method	BLASTX
NCBI GI	g2492519
BLAST score	682
E value	1.0e-71
Match length	133
% identity	98
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No.	390540
Contig ID	20898_1.R1084
5'-most EST	LIB3434-051-P1-K1-A11
Method	BLASTX
NCBI GI	g5734756
BLAST score	359
E value	8.0e-54
Match length	174
% identity	63
NCBI Description	(AC007651) Similar to SOUL Protein [Arabidopsis thaliana]

Seq. No.	390541
Contig ID	20900_1.R1084
5'-most EST	uC-osflM202039b01b1
Method	BLASTX
NCBI GI	g4584343
BLAST score	482
E value	9.0e-48
Match length	317
% identity	44
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis thaliana]

Seq. No.	390542
Contig ID	20902_1.R1084
5'-most EST	g3759659
Method	BLASTX
NCBI GI	g1709925
BLAST score	484
E value	2.0e-48
Match length	140
% identity	69
NCBI Description	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PRECURSOR (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) >gi_945060 (U30895) aminoimidazole ribonucleotide (AIRS) synthetase [Vigna unguiculata]

Seq. No.	390543
Contig ID	20904_1.R1084
5'-most EST	g5038724

Seq. No.	390544
Contig ID	20905_1.R1084
5'-most EST	g431830
Method	BLASTX

NCBI GI g5430769
BLAST score 431
E value 3.0e-42
Match length 196
% identity 48
NCBI Description (AC007504) Similar to somatic embryogenesis receptor-like kinase [Arabidopsis thaliana]

Seq. No. 390545
Contig ID 20912_1.R1084
5'-most EST uC-osflcyp141g05a1
Method BLASTX
NCBI GI g6006848
BLAST score 215
E value 3.0e-17
Match length 47
% identity 87
NCBI Description (AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No. 390546
Contig ID 20916_1.R1084
5'-most EST g428374
Method BLASTX
NCBI GI g6002712
BLAST score 302
E value 7.0e-39
Match length 316
% identity 34
NCBI Description (AF133053) S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase [Clarkia breweri]

Seq. No. 390547
Contig ID 20919_1.R1084
5'-most EST uC-osrocyp026f01a1
Method BLASTX
NCBI GI g6006369
BLAST score 653
E value 7.0e-95
Match length 194
% identity 91
NCBI Description (AP000559) ESTs C99670(E21043),C99671(E21043), AU078262(R10938),AU078261(R10938),D15282(C0402) correspond to a region of the predicted gene.; Similar to arginine decarboxylase (U52851) [Oryza sativa]

Seq. No. 390548
Contig ID 20921_1.R1084
5'-most EST LIB3434-015-P1-K1-F7
Method BLASTX
NCBI GI g3023947
BLAST score 710
E value 6.0e-75
Match length 221
% identity 62
NCBI Description PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi_2665840 (AF035815) putative histone deacetylase RPD3 [Zea mays]

Seq. No.	390549
Contig ID	20922_1.R1084
5'-most EST	g2310385
Method	BLASTX
NCBI GI	g2344871
BLAST score	784
E value	1.0e-83
Match length	203
% identity	69
NCBI Description	(AJ001270) purple acid phosphatase precursor [Phaseolus vulgaris]

Seq. No.	390550
Contig ID	20940_1.R1084
5'-most EST	LIB3434-051-P1-K1-E4
Method	BLASTX
NCBI GI	g4467124
BLAST score	126
E value	9.0e-17
Match length	136
% identity	30
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390551
Contig ID	20945_1.R1084
5'-most EST	g2310387

Seq. No.	390552
Contig ID	20946_1.R1084
5'-most EST	g2310163
Method	BLASTX
NCBI GI	g4826682
BLAST score	518
E value	3.0e-52
Match length	238
% identity	46
NCBI Description	cystinosis, nephropathic >gi_3036840_emb_CAA11021_ (AJ222967) cystinosin [Homo sapiens] >gi_3036851_emb_CAA75882_ (Y15924) cystinosin [Homo sapiens]

Seq. No.	390553
Contig ID	20948_1.R1084
5'-most EST	uC-osrocyp012c12b1

Seq. No.	390554
Contig ID	20962_1.R1084
5'-most EST	LIB3477-010-P1-K1-E2
Method	BLASTX
NCBI GI	g4455328
BLAST score	457
E value	5.0e-45
Match length	209
% identity	54
NCBI Description	(AL035525) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390555
Contig ID	20965_1.R1084
5'-most EST	uC-osflcyp151e10b1

Seq. No.	390556
Contig ID	20973_1.R1084
5'-most EST	LIB3434-051-P1-K1-H9
Method	BLASTX
NCBI GI	g2213597
BLAST score	583
E value	4.0e-60
Match length	202
% identity	54
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No.	390557
Contig ID	20976_1.R1084
5'-most EST	g2797422
Method	BLASTX
NCBI GI	g1262756
BLAST score	164
E value	3.0e-11
Match length	81
% identity	40
NCBI Description	(X97022) lamin [Brassica oleracea]

Seq. No.	390558
Contig ID	20977_1.R1084
5'-most EST	g5003055
Method	BLASTX
NCBI GI	g3522956
BLAST score	1045
E value	1.0e-122
Match length	343
% identity	56
NCBI Description	(AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No.	390559
Contig ID	20978_1.R1084
5'-most EST	g2310317

Seq. No.	390560
Contig ID	20993_1.R1084
5'-most EST	g428791

Seq. No.	390561
Contig ID	20997_1.R1084
5'-most EST	g426257

Seq. No.	390562
Contig ID	20998_1.R1084
5'-most EST	g428731
Method	BLASTX
NCBI GI	g4406781
BLAST score	317
E value	5.0e-29

Match length	127
% identity	55
NCBI Description	(AC006532) putative Na+/H+ antiporter [Arabidopsis thaliana]

Seq. No.	390563
Contig ID	21000_1.R1084
5'-most EST	uC-osf1cyp122b10b1
Method	BLASTX
NCBI GI	g4741844
BLAST score	643
E value	2.0e-67
Match length	141
% identity	90
NCBI Description	(AF112964) small GTP-binding protein [Triticum aestivum]

Seq. No.	390564
Contig ID	21007_1.R1084
5'-most EST	LIB3434-052-P1-K1-D4

Seq. No.	390565
Contig ID	21010_1.R1084
5'-most EST	LIB3434-052-P1-K1-D7

Seq. No.	390566
Contig ID	21015_1.R1084
5'-most EST	uC-osf1M202056b10a1
Method	BLASTX
NCBI GI	g4733891
BLAST score	161
E value	7.0e-11
Match length	58
% identity	59
NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No.	390567
Contig ID	21017_1.R1084
5'-most EST	g4880207
Method	BLASTN
NCBI GI	g6006355
BLAST score	57
E value	2.0e-22
Match length	126
% identity	87
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	390568
Contig ID	21028_1.R1084
5'-most EST	uC-osrocyp009g12b1
Method	BLASTX
NCBI GI	g4680193
BLAST score	607
E value	6.0e-63
Match length	203
% identity	63
NCBI Description	(AF111710) putative farnesyl pyrophosphate synthase [Oryza sativa subsp. indica]

Seq. No.	390569
Contig ID	21031_1.R1084
5'-most EST	LIB3434-052-P1-K1-F6

Seq. No.	390570
Contig ID	21043_1.R1084
5'-most EST	g4878691
Method	BLASTX
NCBI GI	g2760362
BLAST score	416
E value	2.0e-40
Match length	115
% identity	73
NCBI Description	(AF016511) 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana]

Seq. No.	390571
Contig ID	21055_1.R1084
5'-most EST	LIB3479-002-Q6-K1-B9

Seq. No.	390572
Contig ID	21058_1.R1084
5'-most EST	uC-osflcyp064f09b1

Seq. No.	390573
Contig ID	21063_1.R1084
5'-most EST	LIB3434-053-P1-K1-A7
Method	BLASTX
NCBI GI	g3098603
BLAST score	642
E value	4.0e-74
Match length	183
% identity	75
NCBI Description	(AF052191) katanin p60 subunit [Strongylocentrotus purpuratus]

Seq. No.	390574
Contig ID	21070_1.R1084
5'-most EST	LIB3434-053-P1-K1-B4
Method	BLASTX
NCBI GI	g4928460
BLAST score	310
E value	6.0e-28
Match length	124
% identity	48
NCBI Description	(AF133127) thioredoxin h [Hevea brasiliensis]

Seq. No.	390575
Contig ID	21071_1.R1084
5'-most EST	g4969134
Method	BLASTX
NCBI GI	g2065531
BLAST score	1087
E value	1.0e-119
Match length	266
% identity	74

NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	390576
Contig ID	21076_1.R1084
5'-most EST	g3767972

Seq. No.	390577
Contig ID	21082_1.R1084
5'-most EST	g702589
Method	BLASTX
NCBI GI	g3287688
BLAST score	686
E value	5.0e-72
Match length	164
% identity	85
NCBI Description	(AC003979) Contains similarity to ycf37 gene product gb_1001425 from Synechocystis sp. genome gb_D63999. ESTs gb_T43026, gb_R64902, gb_Z18169 and gb_N37374 come from this gene. [Arabidopsis thaliana]

Seq. No.	390578
Contig ID	21085_2.R1084
5'-most EST	LIB3434-053-P1-K1-D1
Method	BLASTX
NCBI GI	g542190
BLAST score	642
E value	6.0e-67
Match length	244
% identity	50
NCBI Description	hypothetical protein 1087 - maize >gi_459269_emb_CAA54960_ (X78029) transcribed sequence 1087 [Zea mays]

Seq. No.	390579
Contig ID	21095_1.R1084
5'-most EST	g4878177

Seq. No.	390580
Contig ID	21097_1.R1084
5'-most EST	LIB3434-053-P1-K1-E1
Method	BLASTX
NCBI GI	g6016690
BLAST score	203
E value	1.0e-15
Match length	128
% identity	34
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	390581
Contig ID	21100_1.R1084
5'-most EST	LIB3434-026-P1-K1-E12
Method	BLASTX
NCBI GI	g4510363
BLAST score	402
E value	4.0e-39
Match length	84
% identity	86
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No.	390582
Contig ID	21101_1.R1084
5'-most EST	LIB3434-053-P1-K1-E2
Method	BLASTX
NCBI GI	g2695711
BLAST score	370
E value	4.0e-35
Match length	136
% identity	51
NCBI Description	(AJ001370) cytochome b5 [Olea europaea]

Seq. No.	390583
Contig ID	21103_1.R1084
5'-most EST	g3107210
Method	BLASTX
NCBI GI	g2598227
BLAST score	439
E value	2.0e-43
Match length	126
% identity	72
NCBI Description	(AJ222585) AT-hook protein 1 [Arabidopsis thaliana]

Seq. No.	390584
Contig ID	21111_1.R1084
5'-most EST	g2800453

Seq. No.	390585
Contig ID	21112_1.R1084
5'-most EST	g1632407

Seq. No.	390586
Contig ID	21121_1.R1084
5'-most EST	LIB3434-053-P1-K1-G11

Seq. No.	390587
Contig ID	21126_1.R1084
5'-most EST	LIB3434-053-P1-K1-G6

Seq. No.	390588
Contig ID	21128_1.R1084
5'-most EST	LIB3434-053-P1-K1-G8
Method	BLASTX
NCBI GI	g3924615
BLAST score	251
E value	3.0e-21
Match length	139
% identity	37
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390589
Contig ID	21132_1.R1084
5'-most EST	g3760752
Method	BLASTX
NCBI GI	g3080740
BLAST score	128

E value	5.0e-10
Match length	139
% identity	38
NCBI Description	(U77366) pasticcino 1-D [Arabidopsis thaliana]

Seq. No.	390590
Contig ID	21137_1.R1084
5'-most EST	LIB3434-053-P1-K1-H6

Seq. No.	390591
Contig ID	21144_1.R1084
5'-most EST	uC-osflcyp128d03a1
Method	BLASTX
NCBI GI	g4093157
BLAST score	217
E value	9.0e-27
Match length	105
% identity	66
NCBI Description	(AF087936) phytochrome-associated protein 2 [Arabidopsis thaliana] >gi_4972054_emb_CAB43922.1_ (AL078470) phytochrome-associated protein PAP2 [Arabidopsis thaliana]

Seq. No.	390592
Contig ID	21145_1.R1084
5'-most EST	LIB3434-054-P1-K1-A4

Seq. No.	390593
Contig ID	21147_1.R1084
5'-most EST	LIB3434-054-P1-K1-A6

Seq. No.	390594
Contig ID	21151_1.R1084
5'-most EST	LIB3475-005-P1-K1-G9
Method	BLASTX
NCBI GI	g6014652
BLAST score	213
E value	1.0e-16
Match length	190
% identity	34
NCBI Description	(AF187961) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]

Seq. No.	390595
Contig ID	21176_1.R1084
5'-most EST	g426554
Method	BLASTX
NCBI GI	g2252871
BLAST score	223
E value	1.0e-19
Match length	178
% identity	42
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	390596
Contig ID	21177_1.R1084
5'-most EST	uC-osflm202111h07b1
Method	BLASTX

NCBI GI	g3252856
BLAST score	1306
E value	0.0e+00
Match length	405
% identity	84
NCBI Description	(AF020425) glutamate decarboxylase isozyme 1 [Nicotiana tabacum]

Seq. No.	390597
Contig ID	21177_2.R1084
5'-most EST	g2427818
Method	BLASTX
NCBI GI	g2494174
BLAST score	444
E value	3.0e-84
Match length	218
% identity	82
NCBI Description	GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034) glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	390598
Contig ID	21177_3.R1084
5'-most EST	uC-osroM202024a04b1
Method	BLASTX
NCBI GI	g4406783
BLAST score	673
E value	2.0e-70
Match length	179
% identity	74
NCBI Description	(AC006532) putative glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	390599
Contig ID	21177_4.R1084
5'-most EST	g2427273
Method	BLASTX
NCBI GI	g1169238
BLAST score	349
E value	4.0e-35
Match length	101
% identity	77
NCBI Description	GLUTAMATE DECARBOXYLASE (GAD) >gi_1076648_pir__A48767 glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia >gi_294112 (L16797) glutamate decarboxylase [Petunia hybrida] >gi_309680 (L16977) glutamate decarboxylase [Petunia hybrida]

Seq. No.	390600
Contig ID	21183_1.R1084
5'-most EST	LIB3434-054-P1-K1-E1

Seq. No.	390601
Contig ID	21186_1.R1084
5'-most EST	LIB3434-054-P1-K1-E12
Method	BLASTX
NCBI GI	g5031275
BLAST score	844

E value	1.0e-90
Match length	202
% identity	78
NCBI Description	(AF139496) unknown [Prunus armeniaca]

Seq. No.	390602
Contig ID	21187_1.R1084
5'-most EST	LIB3434-054-P1-K1-E2

Seq. No.	390603
Contig ID	21191_2.R1084
5'-most EST	LIB3434-054-P1-K1-E7

Seq. No.	390604
Contig ID	21192_1.R1084
5'-most EST	LIB3434-003-P1-K1-E12
Method	BLASTX
NCBI GI	g2462832
BLAST score	378
E value	4.0e-38
Match length	200
% identity	45
NCBI Description	(AF000657) similar to Bacillus CotA [Arabidopsis thaliana]

Seq. No.	390605
Contig ID	21207_1.R1084
5'-most EST	LIB3434-054-P1-K1-G2
Method	BLASTX
NCBI GI	g2369766
BLAST score	320
E value	1.0e-29
Match length	106
% identity	62
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	390606
Contig ID	21217_1.R1084
5'-most EST	LIB3434-055-P1-K1-A10
Method	BLASTX
NCBI GI	g2244709
BLAST score	310
E value	3.0e-28
Match length	142
% identity	52
NCBI Description	(AB005295) HY5 [Arabidopsis thaliana] >gi_2251085_dbj_BAA21327_ (AB005456) HY5 [Arabidopsis thaliana]

Seq. No.	390607
Contig ID	21222_1.R1084
5'-most EST	uC-osrocyp017g05a1
Method	BLASTX
NCBI GI	g4008156
BLAST score	224
E value	4.0e-18
Match length	68
% identity	68

NCBI Description	(AB008845) NADH dependent Glutamate Synthase [Oryza sativa]

Seq. No.	390608
Contig ID	21226_1.R1084
5'-most EST	g4714994
Method	BLASTX
NCBI GI	g6016737
BLAST score	146
E value	1.0e-08
Match length	200
% identity	39
NCBI Description	(AC009325) hypothetical protein [Arabidopsis thaliana] >gi_6091741_gb_AAF03453.1_AC010797_29 (AC010797) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390609
Contig ID	21228_1.R1084
5'-most EST	LIB3434-055-P1-K1-B10

Seq. No.	390610
Contig ID	21236_1.R1084
5'-most EST	g3768447
Method	BLASTX
NCBI GI	g2982303
BLAST score	417
E value	7.0e-43
Match length	127
% identity	75
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	390611
Contig ID	21239_1.R1084
5'-most EST	uC-osflcyp110b08b1
Method	BLASTX
NCBI GI	g3834302
BLAST score	911
E value	1.0e-98
Match length	217
% identity	84
NCBI Description	(AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from this gene. [Arabidopsis thaliana]

Seq. No.	390612
Contig ID	21240_1.R1084
5'-most EST	uC-osrocyp010f04b1
Method	BLASTX
NCBI GI	g2398829
BLAST score	1073
E value	1.0e-117
Match length	269
% identity	75
NCBI Description	(Y11220) mitochondrial uncoupling protein [Solanum tuberosum]

Seq. No.	390613
Contig ID	21247_1.R1084

5'-most EST	g4879688
Method	BLASTX
NCBI GI	g4263714
BLAST score	221
E value	1.0e-17
Match length	162
% identity	33
NCBI Description	(AC006223) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	390614
Contig ID	21253_1.R1084
5'-most EST	LIB3434-055-P1-K1-D12
Method	BLASTN
NCBI GI	g2113846
BLAST score	101
E value	3.0e-49
Match length	173
% identity	90
NCBI Description	Hordeum vulgare mRNA for hypothetical protein, partial, clone WL5

Seq. No.	390615
Contig ID	21255_1.R1084
5'-most EST	LIB3434-055-P1-K1-D4
Method	BLASTX
NCBI GI	g2058284
BLAST score	373
E value	9.0e-36
Match length	131
% identity	55
NCBI Description	(X97378) atranbp1b [Arabidopsis thaliana]

Seq. No.	390616
Contig ID	21259_1.R1084
5'-most EST	g2800803
Method	BLASTN
NCBI GI	g9992
BLAST score	37
E value	4.0e-11
Match length	37
% identity	100
NCBI Description	P.lividus gene for 18S rRNA

Seq. No.	390617
Contig ID	21262_1.R1084
5'-most EST	LIB3477-011-P1-K1-C11

Seq. No.	390618
Contig ID	21272_1.R1084
5'-most EST	LIB3434-055-P1-K1-F11
Method	BLASTX
NCBI GI	g1076670
BLAST score	298
E value	1.0e-50
Match length	105
% identity	97

NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_668985_emb_CAA59062_ (X84319) NADH dehydrogenase [Solanum tuberosum]
Seq. No.	390619
Contig ID	21276_1.R1084
5'-most EST	g286979
Method	BLASTX
NCBI GI	g3421123
BLAST score	842
E value	3.0e-90
Match length	230
% identity	67
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]
Seq. No.	390620
Contig ID	21278_1.R1084
5'-most EST	LIB3475-012-P1-K1-F12
Method	BLASTX
NCBI GI	g1421730
BLAST score	843
E value	2.0e-90
Match length	262
% identity	58
NCBI Description	(U43082) RF2 [Zea mays]
Seq. No.	390621
Contig ID	21284_1.R1084
5'-most EST	uC-osflcyp123c12b1
Method	BLASTX
NCBI GI	g543063
BLAST score	159
E value	7.0e-19
Match length	252
% identity	33
NCBI Description	zinc-finger protein, BR140 - human
Seq. No.	390622
Contig ID	21285_1.R1084
5'-most EST	uC-osroM202038a09b1
Method	BLASTX
NCBI GI	g731718
BLAST score	198
E value	7.0e-15
Match length	206
% identity	30
NCBI Description	HYPOTHETICAL 30.6 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION >gi_626657_pir__S48978 hypothetical protein YHR134w - yeast (Saccharomyces cerevisiae) >gi_500671 (U10398) Yhr134wp [Saccharomyces cerevisiae]
Seq. No.	390623
Contig ID	21286_1.R1084
5'-most EST	LIB3434-004-P1-K1-G8
Method	BLASTX
NCBI GI	g3789948

BLAST score	700
E value	8.0e-74
Match length	161
% identity	84
NCBI Description	(AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No.	390624
Contig ID	21291_1.R1084
5'-most EST	LIB3434-055-P1-K1-H2
Method	BLASTX
NCBI GI	g2702281
BLAST score	670
E value	2.0e-70
Match length	168
% identity	40
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	390625
Contig ID	21295_1.R1084
5'-most EST	LIB3434-055-P1-K1-H7
Method	BLASTX
NCBI GI	g3249039
BLAST score	335
E value	5.0e-31
Match length	194
% identity	42
NCBI Description	(AF071221) N-carbamyl-L-amino acid amidohydrolase [Arthrobacter aurescens]

Seq. No.	390626
Contig ID	21297_1.R1084
5'-most EST	LIB3434-055-P1-K1-H9
Method	BLASTX
NCBI GI	g5729706
BLAST score	227
E value	3.0e-18
Match length	81
% identity	42
NCBI Description	(AC007927) unknown protein [Arabidopsis thaliana]

Seq. No.	390627
Contig ID	21304_1.R1084
5'-most EST	LIB3434-056-P1-K1-A5

Seq. No.	390628
Contig ID	21305_1.R1084
5'-most EST	g4878599
Method	BLASTX
NCBI GI	g2160163
BLAST score	279
E value	8.0e-25
Match length	76
% identity	71
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	390629

Contig ID	21315_1.R1084
5'-most EST	g426274
Method	BLASTX
NCBI GI	g2832683
BLAST score	943
E value	1.0e-102
Match length	237
% identity	71
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	390630
Contig ID	21326_1.R1084
5'-most EST	g4716060

Seq. No.	390631
Contig ID	21335_1.R1084
5'-most EST	g2317402
Method	BLASTX
NCBI GI	g1314712
BLAST score	409
E value	4.0e-69
Match length	189
% identity	75
NCBI Description	(U54615) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	390632
Contig ID	21345_1.R1084
5'-most EST	LIB3434-056-P1-K1-E4
Method	BLASTX
NCBI GI	g4874290
BLAST score	406
E value	2.0e-39
Match length	163
% identity	50
NCBI Description	(AC007212) putative purple acid phosphatase [Arabidopsis thaliana]

Seq. No.	390633
Contig ID	21346_1.R1084
5'-most EST	LIB3434-056-P1-K1-E5

Seq. No.	390634
Contig ID	21348_1.R1084
5'-most EST	LIB3434-056-P1-K1-E7
Method	BLASTX
NCBI GI	g6069648
BLAST score	204
E value	1.0e-15
Match length	48
% identity	85
NCBI Description	(AP000616) ESTs AU078644(E0685),C72841(E2351),AU078645(E0685), AU030746(E60179) correspond to a region of the predicted gene.; similar to Arabidopsis thaliana BAC F11O4; similar to Medicago truncatula MtN21 (AF096370) [Oryza

Seq. No.	390635
Contig ID	21349_1.R1084
5'-most EST	uC-osflcyp153h10b1
Method	BLASTX
NCBI GI	g3212868
BLAST score	259
E value	3.0e-23
Match length	117
% identity	54
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	390636
Contig ID	21353_1.R1084
5'-most EST	uC-osrocyp013g11b1

Seq. No.	390637
Contig ID	21356_1.R1084
5'-most EST	LIB3434-056-P1-K1-F5
Method	BLASTX
NCBI GI	g2497539
BLAST score	556
E value	2.0e-58
Match length	166
% identity	72
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	390638
Contig ID	21358_1.R1084
5'-most EST	LIB3434-026-P1-K1-H4
Method	BLASTX
NCBI GI	g1208496
BLAST score	245
E value	1.0e-20
Match length	104
% identity	53
NCBI Description	(D38124) EREBP-3 [Nicotiana tabacum]

Seq. No.	390639
Contig ID	21362_1.R1084
5'-most EST	LIB3434-056-P1-K1-G12
Method	BLASTN
NCBI GI	g5042437
BLAST score	485
E value	0.0e+00
Match length	524
% identity	99
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	390640
Contig ID	21363_1.R1084
5'-most EST	LIB3434-056-P1-K1-G2
Method	BLASTX
NCBI GI	g4566505
BLAST score	636
E value	1.0e-110
Match length	238

% identity	83
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	390641
Contig ID	21363_2.R1084
5'-most EST	g4878705
Method	BLASTX
NCBI GI	g4731111
BLAST score	486
E value	4.0e-49
Match length	122
% identity	75
NCBI Description	(AF064707) exhydrolase II [Zea mays]

Seq. No.	390642
Contig ID	21367_1.R1084
5'-most EST	g428543
Method	BLASTX
NCBI GI	g571484
BLAST score	396
E value	2.0e-38
Match length	106
% identity	69
NCBI Description	(U16727) peroxidase precursor [Medicago truncatula]

Seq. No.	390643
Contig ID	21372_1.R1084
5'-most EST	g568475
Method	BLASTX
NCBI GI	g4506233
BLAST score	380
E value	6.0e-36
Match length	257
% identity	36
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 >gi_1346766_sp_P48556_PSD8_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 (P31) >gi_1362741_pir__S56108 multicatalytic endopeptidase complex (EC 3.4.99.46) regulatory chain 31 - human >gi_1037164_dbj_BAA07237_ (D38047) 26S proteasome subunit p31 [Homo sapiens] >gi_3702282 (AC005789) PP31_HUMAN [Homo sapiens]

Seq. No.	390644
Contig ID	21376_1.R1084
5'-most EST	LIB3434-056-P1-K1-H4
Method	BLASTX
NCBI GI	g3063442
BLAST score	162
E value	4.0e-11
Match length	97
% identity	45
NCBI Description	(AC003981) F22O13.6 [Arabidopsis thaliana]

Seq. No.	390645
Contig ID	21380_1.R1084
5'-most EST	g5003835

Method	BLASTX
NCBI GI	g1170767
BLAST score	667
E value	7.0e-70
Match length	183
% identity	72
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN) >gi_626074_pir__S45176 transcription factor SUG1 homolog - fission yeast (Schizosaccharomyces pombe) >gi_406051 (U02280) Let1 [Schizosaccharomyces pombe] >gi_4106689_emb_CAA22628.1_ (AL035065) 26s protease regulatory subunit 8 homolog [Schizosaccharomyces pombe]

Seq. No.	390646
Contig ID	21396_1.R1084
5'-most EST	LIB3434-057-P1-K1-B5
Method	BLASTX
NCBI GI	g1352186
BLAST score	465
E value	2.0e-46
Match length	140
% identity	61
NCBI Description	ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74A) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No.	390647
Contig ID	21403_1.R1084
5'-most EST	LIB3434-057-P1-K1-C2
Method	BLASTX
NCBI GI	g1351989
BLAST score	292
E value	3.0e-30
Match length	75
% identity	87
NCBI Description	ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_984262_emb_CAA58052_ (X82849) asparragine synthetase [Zea mays]

Seq. No.	390648
Contig ID	21405_1.R1084
5'-most EST	LIB3434-057-P1-K1-C5

Seq. No.	390649
Contig ID	21407_1.R1084
5'-most EST	g4715097
Method	BLASTX
NCBI GI	g2370312
BLAST score	473
E value	3.0e-47
Match length	149
% identity	64
NCBI Description	(AJ000995) DnaJ-like protein [Medicago sativa] >gi_3202020_gb_AAC19391.1_ (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]

Seq. No.	390650
Contig ID	21408_1.R1084
5'-most EST	g2317353
Method	BLASTX
NCBI GI	g4512705
BLAST score	224
E value	1.0e-36
Match length	196
% identity	41
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	390651
Contig ID	21411_1.R1084
5'-most EST	g2431411
Method	BLASTX
NCBI GI	g6016736
BLAST score	168
E value	2.0e-11
Match length	81
% identity	44
NCBI Description	(AC009325) unknown protein [Arabidopsis thaliana]

Seq. No.	390652
Contig ID	21413_1.R1084
5'-most EST	LIB3475-007-P1-K1-G9
Method	BLASTX
NCBI GI	g4680207
BLAST score	244
E value	4.0e-20
Match length	178
% identity	34
NCBI Description	(AF114171) disease resistance protein RPM1 homolog [Sorghum bicolor]

Seq. No.	390653
Contig ID	21414_1.R1084
5'-most EST	uC-osf1M202085b03a1

Seq. No.	390654
Contig ID	21416_1.R1084
5'-most EST	g426641
Method	BLASTX
NCBI GI	g2739168
BLAST score	284
E value	1.0e-35
Match length	156
% identity	47
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	390655
Contig ID	21421_1.R1084
5'-most EST	LIB3434-057-P1-K1-E11

Seq. No.	390656
Contig ID	21423_1.R1084

5'-most EST	g702009
Method	BLASTX
NCBI GI	g3256770
BLAST score	151
E value	1.0e-09
Match length	128
% identity	35
NCBI Description	(AP000002) 318aa long hypothetical UDP-glucose 4-epimerase [Pyrococcus horikoshii]

Seq. No.	390657
Contig ID	21427_1.R1084
5'-most EST	g568161
Method	BLASTX
NCBI GI	g3168840
BLAST score	312
E value	2.0e-28
Match length	78
% identity	79
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	390658
Contig ID	21429_1.R1084
5'-most EST	uC-osroM202032c03b1

Seq. No.	390659
Contig ID	21434_1.R1084
5'-most EST	LIB3434-057-P1-K1-F3
Method	BLASTX
NCBI GI	g4680675
BLAST score	184
E value	2.0e-13
Match length	159
% identity	32
NCBI Description	(AF132952) CGI-18 protein [Homo sapiens]

Seq. No.	390660
Contig ID	21437_1.R1084
5'-most EST	g701755
Method	BLASTX
NCBI GI	g4093155
BLAST score	381
E value	1.0e-36
Match length	110
% identity	70
NCBI Description	(AF088281) phytochrome-associated protein 1 [Arabidopsis thaliana]

Seq. No.	390661
Contig ID	21438_1.R1084
5'-most EST	uC-osflcyp012g03b1
Method	BLASTX
NCBI GI	g4406819
BLAST score	430
E value	5.0e-42
Match length	146
% identity	58

NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 390662
Contig ID 21439_1.R1084
5'-most EST LIB3434-057-P1-K1-F8
Method BLASTX
NCBI GI g4572669
BLAST score 190
E value 5.0e-14
Match length 83
% identity 45
NCBI Description (AC006954) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No. 390663
Contig ID 21448_1.R1084
5'-most EST LIB3434-057-P1-K1-G6
Method BLASTX
NCBI GI g4467156
BLAST score 415
E value 1.0e-40
Match length 123
% identity 61
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 390664
Contig ID 21456_1.R1084
5'-most EST LIB3434-057-P1-K1-H2

Seq. No. 390665
Contig ID 21459_1.R1084
5'-most EST g4714419
Method BLASTX
NCBI GI g4512653
BLAST score 857
E value 1.0e-100
Match length 237
% identity 78
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 390666
Contig ID 21459_2.R1084
5'-most EST LIB3434-057-P1-K1-H5
Method BLASTX
NCBI GI g4512653
BLAST score 235
E value 5.0e-30
Match length 101
% identity 69
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 390667
Contig ID 21463_1.R1084
5'-most EST LIB3434-003-P1-K1-A1
Method BLASTX
NCBI GI g401238
BLAST score 465

E value	3.0e-46
Match length	216
% identity	43
NCBI Description	UBIQUITIN-ACTIVATING ENZYME E1 3 >gi_170686 (M90664) ubiquitin activating enzyme [Triticum aestivum]

Seq. No.	390668
Contig ID	21466_1.R1084
5'-most EST	LIB3434-003-P1-K1-A12
Method	BLASTN
NCBI GI	g6006355
BLAST score	461
E value	0.0e+00
Match length	528
% identity	97
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	390669
Contig ID	21468_1.R1084
5'-most EST	LIB3434-003-P1-K1-A3
Method	BLASTX
NCBI GI	g3757529
BLAST score	265
E value	5.0e-23
Match length	98
% identity	49
NCBI Description	(AC005167) tetracycline transporter-like protein [Arabidopsis thaliana]

Seq. No.	390670
Contig ID	21471_1.R1084
5'-most EST	g3762543
Method	BLASTX
NCBI GI	g3041758
BLAST score	166
E value	3.0e-11
Match length	112
% identity	33
NCBI Description	(D85081) unnamed protein product [Escherichia coli]

Seq. No.	390671
Contig ID	21474_1.R1084
5'-most EST	LIB3434-017-P1-K1-B1
Method	BLASTX
NCBI GI	g3894159
BLAST score	143
E value	2.0e-10
Match length	92
% identity	46
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390672
Contig ID	21479_1.R1084
5'-most EST	uC-osf1M202020c01b1
Method	BLASTX
NCBI GI	g4204295
BLAST score	210

E value	3.0e-16
Match length	138
% identity	35
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	390673
Contig ID	21480_1.R1084
5'-most EST	g2800427
Method	BLASTX
NCBI GI	g3746059
BLAST score	175
E value	3.0e-12
Match length	66
% identity	55
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	390674
Contig ID	21480_2.R1084
5'-most EST	LIB3434-003-P1-K1-B3
Method	BLASTX
NCBI GI	g3746059
BLAST score	186
E value	2.0e-13
Match length	150
% identity	37
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	390675
Contig ID	21488_1.R1084
5'-most EST	LIB3434-003-P1-K1-C10
Method	BLASTX
NCBI GI	g5453379
BLAST score	493
E value	2.0e-49
Match length	140
% identity	66
NCBI Description	(AF155124) bacterial-induced peroxidase precursor [Gossypium hirsutum]

Seq. No.	390676
Contig ID	21490_1.R1084
5'-most EST	uC-osrocyp027c12b1
Method	BLASTX
NCBI GI	g4580398
BLAST score	702
E value	8.0e-74
Match length	232
% identity	62
NCBI Description	(AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No.	390677

Contig ID	21496_1.R1084
5'-most EST	uC-osroM202032g10b1
Method	BLASTX
NCBI GI	g4406759
BLAST score	205
E value	1.0e-15
Match length	202
% identity	40
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390678
Contig ID	21504_1.R1084
5'-most EST	uC-osflcyp176f04b1

Seq. No.	390679
Contig ID	21511_1.R1084
5'-most EST	g2312022
Method	BLASTX
NCBI GI	g3850999
BLAST score	683
E value	7.0e-91
Match length	187
% identity	93
NCBI Description	(AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1 [Zea mays]

Seq. No.	390680
Contig ID	21523_1.R1084
5'-most EST	uC-osrocyp010c10b1

Seq. No.	390681
Contig ID	21528_1.R1084
5'-most EST	g3759151

Seq. No.	390682
Contig ID	21531_1.R1084
5'-most EST	uC-osrocyp029e11b1
Method	BLASTX
NCBI GI	g2641619
BLAST score	732
E value	2.0e-77
Match length	148
% identity	89
NCBI Description	(AF032468) ubiquitin-conjugating enzyme protein E2 [Zea mays]

Seq. No.	390683
Contig ID	21539_1.R1084
5'-most EST	g2800930

Seq. No.	390684
Contig ID	21540_1.R1084
5'-most EST	g2427208
Method	BLASTX
NCBI GI	g4835237
BLAST score	364
E value	2.0e-34

Match length	96
% identity	65
NCBI Description	(AL049862) putative clathrin coat assembly protein [Arabidopsis thaliana]

Seq. No.	390685
Contig ID	21546_1.R1084
5'-most EST	LIB3434-003-P1-K1-H2
Method	BLASTX
NCBI GI	g3236253
BLAST score	904
E value	9.0e-98
Match length	221
% identity	76
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	390686
Contig ID	21546_2.R1084
5'-most EST	uC-osrocyp007h03b1
Method	BLASTX
NCBI GI	g3236253
BLAST score	288
E value	6.0e-55
Match length	145
% identity	74
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	390687
Contig ID	21547_1.R1084
5'-most EST	LIB3434-003-P1-K1-H3
Method	BLASTX
NCBI GI	g3309269
BLAST score	955
E value	1.0e-104
Match length	214
% identity	86
NCBI Description	(AF074940) ferric leghemoglobin reductase-2 precursor [Glycine max]

Seq. No.	390688
Contig ID	21549_1.R1084
5'-most EST	LIB3434-003-P1-K1-H5
Method	BLASTX
NCBI GI	g3929647
BLAST score	241
E value	4.0e-20
Match length	104
% identity	48
NCBI Description	(AJ004881) Immutans protein [Arabidopsis thaliana]

Seq. No.	390689
Contig ID	21564_1.R1084
5'-most EST	LIB3434-004-P1-K1-A8

Seq. No. 390690

Contig ID	21567_1.R1084
5'-most EST	uC-osf1M202090g04b1
Method	BLASTX
NCBI GI	g2911076
BLAST score	784
E value	1.0e-83
Match length	211
% identity	68
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	390691
Contig ID	21572_1.R1084
5'-most EST	g700805
Method	BLASTX
NCBI GI	g1314742
BLAST score	150
E value	2.0e-09
Match length	131
% identity	33
NCBI Description	(U54767) caffeic acid O-methyltransferase [Hordeum vulgare]

Seq. No.	390692
Contig ID	21576_1.R1084
5'-most EST	LIB3475-002-P1-K2-B3
Method	BLASTX
NCBI GI	g2104908
BLAST score	947
E value	1.0e-102
Match length	270
% identity	69
NCBI Description	(Y07632) potassium channel [Zea mays]

Seq. No.	390693
Contig ID	21583_1.R1084
5'-most EST	LIB3475-008-P1-K1-F12

Seq. No.	390694
Contig ID	21588_1.R1084
5'-most EST	LIB3434-004-P1-K1-D10

Seq. No.	390695
Contig ID	21593_1.R1084
5'-most EST	LIB3434-042-P1-K1-E11

Seq. No.	390696
Contig ID	21597_1.R1084
5'-most EST	LIB3434-004-P1-K1-D9

Seq. No.	390697
Contig ID	21604_1.R1084
5'-most EST	LIB3434-004-P1-K1-E4

Seq. No.	390698
Contig ID	21611_1.R1084
5'-most EST	LIB3434-004-P1-K1-F10

Seq. No.	390699

Contig ID 21617_1.R1084
5'-most EST uC-osroM202010g04a1

Seq. No. 390700
Contig ID 21631_1.R1084
5'-most EST LIB3434-004-P1-K1-G7

Seq. No. 390701
Contig ID 21639_1.R1084
5'-most EST uC-osflcyp112f04b1
Method BLASTX
NCBI GI g2997589
BLAST score 863
E value 1.0e-103
Match length 201
% identity 96
NCBI Description (AF020813) glucose-6-phosphate/phosphate-translocator precursor [Zea mays]

Seq. No. 390702
Contig ID 21644_1.R1084
5'-most EST LIB3434-004-P1-K1-H9

Seq. No. 390703
Contig ID 21650_1.R1084
5'-most EST LIB3475-002-P1-K2-A7
Method BLASTN
NCBI GI g4689381
BLAST score 36
E value 2.0e-10
Match length 100
% identity 84
NCBI Description Vigna radiata chlorophyll a/b binding protein CP29 (CipCp29) mRNA, complete cds, chloroplast gene for chloroplast product

Seq. No. 390704
Contig ID 21651_1.R1084
5'-most EST uC-osflcyp027h12b1
Method BLASTX
NCBI GI g6017110
BLAST score 663
E value 1.0e-69
Match length 170
% identity 74
NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]

Seq. No. 390705
Contig ID 21654_1.R1084
5'-most EST LIB3479-001-Q6-K1-G3

Seq. No. 390706
Contig ID 21668_1.R1084
5'-most EST uC-osflM202055b12b1
Method BLASTX
NCBI GI g3641837
BLAST score 526

E value	1.0e-105
Match length	324
% identity	70
NCBI Description	(AL023094) Nonclathrin coat protein gamma-like protein [Arabidopsis thaliana]

Seq. No.	390707
Contig ID	21671_1.R1084
5'-most EST	LIB3434-005-P1-K1-C4

Seq. No.	390708
Contig ID	21672_1.R1084
5'-most EST	LIB3434-005-P1-K1-C5

Seq. No.	390709
Contig ID	21674_1.R1084
5'-most EST	LIB3434-005-P1-K1-C7
Method	BLASTX
NCBI GI	g4836876
BLAST score	311
E value	6.0e-60
Match length	164
% identity	76
NCBI Description	(AC007260) Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana]

Seq. No.	390710
Contig ID	21679_1.R1084
5'-most EST	uC-osflm202107e04b1

Seq. No.	390711
Contig ID	21681_1.R1084
5'-most EST	LIB3434-005-P1-K1-D4
Method	BLASTX
NCBI GI	g2191150
BLAST score	163
E value	8.0e-11
Match length	85
% identity	14
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No.	390712
Contig ID	21687_1.R1084
5'-most EST	LIB3434-005-P1-K1-E10
Method	BLASTX
NCBI GI	g4160347
BLAST score	393
E value	2.0e-51
Match length	172
% identity	64
NCBI Description	(AL035216) component of chaperonin-containing T-complex (zeta subunit) [Schizosaccharomyces pombe]

Seq. No.	390713
Contig ID	21694_1.R1084
5'-most EST	LIB3434-005-P1-K1-E6

Seq. No.	390714
Contig ID	21707_1.R1084
5'-most EST	LIB3434-005-P1-K1-F7
Method	BLASTX
NCBI GI	g4220479
BLAST score	515
E value	7.0e-52
Match length	210
% identity	58
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	390715
Contig ID	21716_1.R1084
5'-most EST	LIB3434-005-P1-K1-G4
Method	BLASTX
NCBI GI	g4490293
BLAST score	593
E value	1.0e-61
Match length	129
% identity	42
NCBI Description	(AL035678) WD-repeat protein-like protein [Arabidopsis thaliana]

Seq. No.	390716
Contig ID	21719_1.R1084
5'-most EST	LIB3434-005-P1-K1-G8
Method	BLASTX
NCBI GI	g4836773
BLAST score	277
E value	2.0e-24
Match length	105
% identity	51
NCBI Description	(AF136580) iron-regulated transporter 2 [Lycopersicon esculentum]

Seq. No.	390717
Contig ID	21728_1.R1084
5'-most EST	uC-osflM202097h04b1
Method	BLASTX
NCBI GI	g6015106
BLAST score	193
E value	2.0e-14
Match length	190
% identity	31
NCBI Description	C-14 STEROL REDUCTASE (STEROL C14-REDUCTASE) >gi_1805625_emb_CAA71650_ (Y10624) sterol C-14 reductase [Ascobolus immersus]

Seq. No.	390718
Contig ID	21736_1.R1084
5'-most EST	g2443147
Method	BLASTX
NCBI GI	g1170088
BLAST score	191
E value	3.0e-14
Match length	81

% identity	48
NCBI Description	GLUTATHIONE S-TRANSFERASE APIC (GST CLASS-PHI) >gi_676880_dbj_BAA06150_ (D29680) The expression is induced by aluminium treatment and Pi starvation. [Nicotiana tabacum] >gi_1094818_prf__2106387B Al-induced protein [Nicotiana tabacum]

Seq. No.	390719
Contig ID	21749_1.R1084
5'-most EST	LIB3434-007-P1-K1-B3
Method	BLASTX
NCBI GI	g1086252
BLAST score	175
E value	1.0e-14
Match length	111
% identity	44
NCBI Description	sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	390720
Contig ID	21758_1.R1084
5'-most EST	g3548945
Method	BLASTX
NCBI GI	g4220474
BLAST score	344
E value	9.0e-46
Match length	209
% identity	57
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	390721
Contig ID	21771_1.R1084
5'-most EST	LIB3434-007-P1-K1-D12
Method	BLASTX
NCBI GI	g4454472
BLAST score	302
E value	4.0e-27
Match length	114
% identity	54
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	390722
Contig ID	21775_1.R1084
5'-most EST	g3762442
Method	BLASTX
NCBI GI	g4107276
BLAST score	543
E value	3.0e-55
Match length	194
% identity	65
NCBI Description	(X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No.	390723
Contig ID	21775_2.R1084

09950-74-09950-74-09950-74-

5'-most EST	LIB3479-012-Q6-K1-C6
Method	BLASTX
NCBI GI	g4107276
BLAST score	1575
E value	0.0e+00
Match length	380
% identity	82
NCBI Description	(X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No.	390724
Contig ID	21781_1.R1084
5'-most EST	LIB3434-007-P1-K1-E10
Method	BLASTX
NCBI GI	g2088650
BLAST score	363
E value	1.0e-34
Match length	117
% identity	62
NCBI Description	(AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]

Seq. No.	390725
Contig ID	21784_1.R1084
5'-most EST	uC-osflcyp057g09b1
Method	BLASTX
NCBI GI	g3128209
BLAST score	271
E value	2.0e-23
Match length	106
% identity	33
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]

Seq. No.	390726
Contig ID	21785_1.R1084
5'-most EST	g427738
Method	BLASTX
NCBI GI	g2285792
BLAST score	288
E value	9.0e-26
Match length	69
% identity	78
NCBI Description	(AB004568) cyanase [Arabidopsis thaliana] >gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis thaliana]

Seq. No.	390727
Contig ID	21789_1.R1084
5'-most EST	g2312630

Seq. No.	390728
Contig ID	21798_1.R1084
5'-most EST	LIB3434-007-P1-K1-F4

Seq. No.	390729
Contig ID	21824_1.R1084
5'-most EST	LIB3434-007-P1-K1-H9
Method	BLASTX

NCBI GI	g4850386
BLAST score	253
E value	3.0e-21
Match length	162
% identity	40
NCBI Description	(AC007357) F3F19.5 [Arabidopsis thaliana]

Seq. No.	390730
Contig ID	21836_1.R1084
5'-most EST	LIB3434-035-P1-K1-F12
Method	BLASTX
NCBI GI	g4538939
BLAST score	632
E value	5.0e-66
Match length	157
% identity	76
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	390731
Contig ID	21839_1.R1084
5'-most EST	LIB3434-008-P1-K1-B11
Method	BLASTX
NCBI GI	g4406759
BLAST score	349
E value	9.0e-33
Match length	163
% identity	48
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390732
Contig ID	21844_1.R1084
5'-most EST	LIB3434-008-P1-K1-B6
Method	BLASTX
NCBI GI	g1943751
BLAST score	356
E value	2.0e-33
Match length	112
% identity	69
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	390733
Contig ID	21847_1.R1084
5'-most EST	LIB3434-008-P1-K1-B9

Seq. No.	390734
Contig ID	21850_1.R1084
5'-most EST	LIB3434-008-P1-K1-C12

Seq. No.	390735
Contig ID	21860_2.R1084
5'-most EST	uC-osrocyp011d07b1
Method	BLASTX
NCBI GI	g5734462
BLAST score	161

E value	1.0e-10
Match length	128
% identity	34
NCBI Description	(AL109832) hypothetical protein [Schizosaccharomyces pombe] >gi_5912375_emb_CAB55874.1_ (Z66568) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	390736
Contig ID	21864_1.R1084
5'-most EST	g2428213
Method	BLASTX
NCBI GI	g3047114
BLAST score	559
E value	5.0e-57
Match length	255
% identity	48
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	390737
Contig ID	21868_1.R1084
5'-most EST	LIB3434-008-P1-K1-D9
Method	BLASTX
NCBI GI	g2225982
BLAST score	179
E value	9.0e-13
Match length	127
% identity	35
NCBI Description	(Z97193) glnA3 [Mycobacterium tuberculosis]

Seq. No.	390738
Contig ID	21871_1.R1084
5'-most EST	LIB3434-008-P1-K1-E11

Seq. No.	390739
Contig ID	21874_1.R1084
5'-most EST	uC-osflcyp156c03b1
Method	BLASTX
NCBI GI	g1915960
BLAST score	517
E value	5.0e-73
Match length	223
% identity	38
NCBI Description	(Y07636) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	390740
Contig ID	21877_1.R1084
5'-most EST	LIB3434-008-P1-K1-E7

Seq. No.	390741
Contig ID	21886_1.R1084
5'-most EST	g2310257
Method	BLASTX
NCBI GI	g1001478
BLAST score	196
E value	6.0e-15
Match length	123
% identity	38

NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]

Seq. No.	390742
Contig ID	21891_1.R1084
5'-most EST	LIB3434-008-P1-K1-G10

Seq. No.	390743
Contig ID	21895_1.R1084
5'-most EST	LIB3434-008-P1-K1-G4
Method	BLASTX
NCBI GI	g3790569
BLAST score	164
E value	3.0e-11
Match length	56
% identity	50
NCBI Description	(AF078822) RING-H2 finger protein RHA2a [Arabidopsis thaliana] >gi_5103808_gb_AAD39638.1_AC007591_3 (AC007591) Identical to gb_AF078822 RING-H2 finger RHA2a protein from Arabidopsis thaliana. ESTs gb_N37587, gb_T04684, gb_AA394318, gb_Z35014 and gb_AA713343 come from this gene

Seq. No.	390744
Contig ID	21907_1.R1084
5'-most EST	LIB3434-009-P1-K1-A11
Method	BLASTX
NCBI GI	g1171866
BLAST score	468
E value	1.0e-46
Match length	104
% identity	83
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No.	390745
Contig ID	21910_1.R1084
5'-most EST	g2796273
Method	BLASTX
NCBI GI	g6017110
BLAST score	247
E value	7.0e-21
Match length	53
% identity	81
NCBI Description	(AC009895) unknown protein [Arabidopsis thaliana]

Seq. No.	390746
Contig ID	21915_1.R1084
5'-most EST	g426833
Method	BLASTX
NCBI GI	g2583108
BLAST score	462
E value	1.0e-92
Match length	301
% identity	60
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	390747
Contig ID	21921_1.R1084
5'-most EST	LIB3434-009-P1-K1-B4

Seq. No.	390748
Contig ID	21922_1.R1084
5'-most EST	LIB3434-009-P1-K1-B6

Seq. No.	390749
Contig ID	21927_1.R1084
5'-most EST	LIB3434-009-P1-K1-C10
Method	BLASTX
NCBI GI	g4503363
BLAST score	385
E value	4.0e-44
Match length	131
% identity	71
NCBI Description	dolichyl-phosphate mannosyltransferase polypeptide 1 >gi_3062806_dbj_BAA25646_ (D86198) dolichol-phosphate-mannose synthase [Homo sapiens] >gi_5817251_emb_CAB53749.1_ (AL034553) dJ914P20.1 (dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit) [Homo sapiens]

Seq. No.	390750
Contig ID	21928_1.R1084
5'-most EST	uC-osf1cyp154a06a1
Method	BLASTX
NCBI GI	g4507711
BLAST score	144
E value	7.0e-09
Match length	48
% identity	60
NCBI Description	tetratricopeptide repeat domain 1 >gi_1688074 (U46570) tetratricopeptide repeat protein [Homo sapiens]

Seq. No.	390751
Contig ID	21929_1.R1084
5'-most EST	LIB3434-033-P1-K1-C4
Method	BLASTX
NCBI GI	g2832660
BLAST score	539
E value	6.0e-55
Match length	212
% identity	51
NCBI Description	(AL021710) lipase-like protein [Arabidopsis thaliana]

Seq. No.	390752
Contig ID	21932_1.R1084
5'-most EST	LIB3434-009-P1-K1-E8

Seq. No.	390753
Contig ID	21938_1.R1084
5'-most EST	g5003603
Method	BLASTX
NCBI GI	g5596468

BLAST score	637
E value	4.0e-66
Match length	215
% identity	55
NCBI Description	(AL096882) putative protein [Arabidopsis thaliana]

Seq. No.	390754
Contig ID	21941_1.R1084
5'-most EST	LIB3434-009-P1-K1-D2

Seq. No.	390755
Contig ID	21947_1.R1084
5'-most EST	LIB3434-040-P1-K1-D3
Method	BLASTN
NCBI GI	g3805839
BLAST score	53
E value	1.0e-20
Match length	203
% identity	29
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSA project)

Seq. No.	390756
Contig ID	21951_1.R1084
5'-most EST	LIB3434-009-P1-K1-E3
Method	BLASTX
NCBI GI	g4325345
BLAST score	712
E value	2.0e-80
Match length	220
% identity	26
NCBI Description	(AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]

Seq. No.	390757
Contig ID	21953_1.R1084
5'-most EST	LIB3434-009-P1-K1-E5
Method	BLASTX
NCBI GI	g1169782
BLAST score	201
E value	2.0e-22
Match length	78
% identity	71
NCBI Description	FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No.	390758
Contig ID	21958_1.R1084
5'-most EST	LIB3434-009-P1-K1-F1

Seq. No.	390759
Contig ID	21960_1.R1084
5'-most EST	LIB3434-009-P1-K1-F11

Seq. No.	390760

Contig ID	21975_1.R1084
5'-most EST	uC-osflcyp005a07b1
Seq. No.	390761
Contig ID	21978_1.R1084
5'-most EST	LIB3434-016-P1-K1-B6
Seq. No.	390762
Contig ID	21982_1.R1084
5'-most EST	LIB3434-009-P1-K1-H11
Seq. No.	390763
Contig ID	21990_1.R1084
5'-most EST	uC-osflm202100e12b1
Method	BLASTX
NCBI GI	g3142301
BLAST score	292
E value	3.0e-26
Match length	140
% identity	52
NCBI Description	(AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb_M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101, gb_H3630
Seq. No.	390764
Contig ID	21994_1.R1084
5'-most EST	LIB3434-042-P1-K1-G1
Method	BLASTN
NCBI GI	g1245938
BLAST score	36
E value	2.0e-10
Match length	36
% identity	62
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]
Seq. No.	390765
Contig ID	22002_1.R1084
5'-most EST	uC-osflcyp051a07b1
Method	BLASTX
NCBI GI	g4587570
BLAST score	260
E value	3.0e-22
Match length	186
% identity	35
NCBI Description	(AC006550) Strong similarity to gi_2244833 centromere protein homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from this gene
Seq. No.	390766
Contig ID	22005_1.R1084
5'-most EST	LIB3434-010-P1-K1-B3
Method	BLASTX
NCBI GI	g124036

BLAST score 181
E value 2.0e-13
Match length 63
% identity 26
NCBI Description BOWMAN-BIRK TYPE BRAN TRYPSIN INHIBITOR (RBTI) >gi_476550_pir__TIRZBR trypsin inhibitor (Bowman-Birk) - rice >gi_359095_prf__1310273A trypsin inhibitor [Oryza sativa]

Seq. No. 390767
Contig ID 22006_1.R1084
5'-most EST LIB3434-010-P1-K1-B4
Method BLASTX
NCBI GI g2935529
BLAST score 865
E value 4.0e-93
Match length 194
% identity 78
NCBI Description (AF049069) No definition line found [Pinus radiata]

Seq. No. 390768
Contig ID 22024_1.R1084
5'-most EST g4715029
Method BLASTX
NCBI GI g3540195
BLAST score 824
E value 5.0e-88
Match length 343
% identity 20
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 390769
Contig ID 22025_1.R1084
5'-most EST g428451

Seq. No. 390770
Contig ID 22028_1.R1084
5'-most EST LIB3434-010-P1-K1-D6
Method BLASTX
NCBI GI g5923675
BLAST score 597
E value 6.0e-65
Match length 242
% identity 55
NCBI Description (AC009326) putative mRNA capping enzyme, RNA guanylyltransferase [Arabidopsis thaliana]

Seq. No. 390771
Contig ID 22040_1.R1084
5'-most EST uC-osrocyp010c05a1

Seq. No. 390772
Contig ID 22044_1.R1084
5'-most EST uC-osf1cyp022e03b1

Seq. No. 390773
Contig ID 22045_1.R1084

5'-most EST	LIB3434-010-P1-K1-F11
Seq. No.	390774
Contig ID	22048_1.R1084
5'-most EST	uC-osflcyp143a07b1
Method	BLASTX
NCBI GI	g4567247
BLAST score	345
E value	2.0e-32
Match length	110
% identity	62
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.	390775
Contig ID	22049_1.R1084
5'-most EST	LIB3434-010-P1-K1-F4
Seq. No.	390776
Contig ID	22051_1.R1084
5'-most EST	LIB3434-010-P1-K1-F6
Method	BLASTX
NCBI GI	g5679842
BLAST score	737
E value	4.0e-78
Match length	139
% identity	99
NCBI Description	(AJ243961) l1332.6 [Oryza sativa]
Seq. No.	390777
Contig ID	22058_1.R1084
5'-most EST	LIB3434-010-P1-K1-G2
Seq. No.	390778
Contig ID	22066_1.R1084
5'-most EST	LIB3434-010-P1-K1-H10
Method	BLASTX
NCBI GI	g2244787
BLAST score	453
E value	1.0e-44
Match length	149
% identity	58
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.	390779
Contig ID	22071_1.R1084
5'-most EST	g2796411
Seq. No.	390780
Contig ID	22080_1.R1084
5'-most EST	LIB3434-011-P1-K1-A4
Method	BLASTX
NCBI GI	g2129578
BLAST score	999
E value	1.0e-108
Match length	217
% identity	86
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis

thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	390781
Contig ID	22081_1.R1084
5'-most EST	LIB3434-011-P1-K1-A5

Seq. No.	390782
Contig ID	22082_1.R1084
5'-most EST	g428271
Method	BLASTX
NCBI GI	g5734786
BLAST score	517
E value	1.0e-58
Match length	150
% identity	76
NCBI Description	(AC007980) Similar to oligopeptidases [Arabidopsis thaliana]

Seq. No.	390783
Contig ID	22083_1.R1084
5'-most EST	LIB3434-034-P1-K1-G7

Seq. No.	390784
Contig ID	22084_1.R1084
5'-most EST	LIB3434-011-P1-K1-A8
Method	BLASTX
NCBI GI	g5051781
BLAST score	567
E value	4.0e-58
Match length	196
% identity	61
NCBI Description	(AL078637) transport inhibitor response-like protein [Arabidopsis thaliana]

Seq. No.	390785
Contig ID	22086_1.R1084
5'-most EST	LIB3434-011-P1-K1-B1
Method	BLASTX
NCBI GI	g2506139
BLAST score	1414
E value	1.0e-157
Match length	369
% identity	74
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	390786
Contig ID	22092_1.R1084
5'-most EST	g568422

Seq. No.	390787
Contig ID	22098_2.R1084
5'-most EST	LIB3434-035-P1-K1-G8

Seq. No.	390788
Contig ID	22100_1.R1084
5'-most EST	LIB3434-011-P1-K1-C3
Method	BLASTX
NCBI GI	g2511715
BLAST score	383
E value	1.0e-36
Match length	111
% identity	68
NCBI Description	(AF019380) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]

Seq. No.	390789
Contig ID	22108_1.R1084
5'-most EST	g3762034

Seq. No.	390790
Contig ID	22112_1.R1084
5'-most EST	g2310391
Method	BLASTX
NCBI GI	g3355471
BLAST score	288
E value	1.0e-25
Match length	92
% identity	55
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	390791
Contig ID	22117_1.R1084
5'-most EST	uC-osf1cyp120a09b1
Method	BLASTX
NCBI GI	g4027891
BLAST score	503
E value	6.0e-51
Match length	137
% identity	66
NCBI Description	(AF049350) alpha-expansin precursor [Nicotiana tabacum]

Seq. No.	390792
Contig ID	22130_1.R1084
5'-most EST	g5700019
Method	BLASTX
NCBI GI	g4490309
BLAST score	338
E value	2.0e-31
Match length	125
% identity	51
NCBI Description	(AL035678) peroxidase ATP17a-like protein [Arabidopsis thaliana]

Seq. No.	390793
Contig ID	22132_1.R1084
5'-most EST	LIB3434-011-P1-K1-F4

Seq. No.	390794

Contig ID	22141_1.R1084
5'-most EST	g2427752
Method	BLASTX
NCBI GI	g5803167
BLAST score	353
E value	4.0e-36
Match length	245
% identity	36
NCBI Description	pre-mRNA splicing factor SF3a (60kD), similar to S. cerevisiae PRP9 (spliceosome-associated protein 61) >gi_1082798_pir__A55749 spliceosome-associated protein SAP 61 - human >gi_508723 (U08815) SAP 61 [Homo sapiens]

Seq. No.	390795
Contig ID	22146_1.R1084
5'-most EST	LIB3434-011-P1-K1-G7
Method	BLASTX
NCBI GI	g4929689
BLAST score	314
E value	6.0e-31
Match length	100
% identity	63
NCBI Description	(AF151868) CGI-110 protein [Homo sapiens]

Seq. No.	390796
Contig ID	22156_1.R1084
5'-most EST	uC-osflcyp109h07b1
Method	BLASTX
NCBI GI	g4850408
BLAST score	317
E value	3.0e-51
Match length	229
% identity	47
NCBI Description	(AC007357) Contains PF_00097 Zinc finger (C3HC4) ring finger motif. [Arabidopsis thaliana]

Seq. No.	390797
Contig ID	22163_1.R1084
5'-most EST	LIB3434-012-P1-K1-A3
Method	BLASTX
NCBI GI	g5922606
BLAST score	372
E value	6.0e-46
Match length	106
% identity	86
NCBI Description	(AP000492) EST AU031699(R0618) corresponds to a region of the predicted gene.; similar to pollen specific like protein. (AL021710) [Oryza sativa]

Seq. No.	390798
Contig ID	22164_1.R1084
5'-most EST	g2275799
Method	BLASTX
NCBI GI	g4679028
BLAST score	394
E value	7.0e-38
Match length	174

% identity	45
NCBI Description	(AF077207) HSPC021 [Homo sapiens] >gi_5106781_gb_AAD39841.1_ (AF083243) HSPC025 [Homo sapiens]
Seq. No.	390799
Contig ID	22170_1.R1084
5'-most EST	g3767725
Seq. No.	390800
Contig ID	22176_1.R1084
5'-most EST	LIB3434-012-P1-K1-B6
Method	BLASTX
NCBI GI	g4581162
BLAST score	523
E value	5.0e-53
Match length	118
% identity	86
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]
Seq. No.	390801
Contig ID	22181_1.R1084
5'-most EST	g428689
Method	BLASTX
NCBI GI	g2425066
BLAST score	130
E value	1.0e-12
Match length	131
% identity	37
NCBI Description	(AF019147) cysteine proteinase Mir3 [Zea mays]
Seq. No.	390802
Contig ID	22187_1.R1084
5'-most EST	LIB3434-012-P1-K1-C7
Seq. No.	390803
Contig ID	22189_1.R1084
5'-most EST	g702803
Seq. No.	390804
Contig ID	22207_1.R1084
5'-most EST	g571559
Method	BLASTX
NCBI GI	g5106785
BLAST score	150
E value	5.0e-13
Match length	170
% identity	30
NCBI Description	(AF083245) HSPC027 [Homo sapiens]
Seq. No.	390805
Contig ID	22217_1.R1084
5'-most EST	LIB3434-012-P1-K1-F3
Seq. No.	390806
Contig ID	22218_1.R1084

5'-most EST	LIB3434-012-P1-K1-F4
Seq. No.	390807
Contig ID	22228_1.R1084
5'-most EST	g2312416
Method	BLASTX
NCBI GI	g3128180
BLAST score	1690
E value	0.0e+00
Match length	409
% identity	78
NCBI Description	(AC004521) citrate synthetase [Arabidopsis thaliana]
Seq. No.	390808
Contig ID	22230_1.R1084
5'-most EST	uC-osroM202035h04b1
Method	BLASTX
NCBI GI	g1351270
BLAST score	896
E value	1.0e-105
Match length	237
% identity	81
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]
Seq. No.	390809
Contig ID	22231_1.R1084
5'-most EST	LIB3434-042-P1-K1-F6
Method	BLASTX
NCBI GI	g5729706
BLAST score	222
E value	1.0e-17
Match length	79
% identity	43
NCBI Description	(AC007927) unknown protein [Arabidopsis thaliana]
Seq. No.	390810
Contig ID	22234_1.R1084
5'-most EST	uC-osflcyp109b09b1
Method	BLASTX
NCBI GI	g1620896
BLAST score	872
E value	8.0e-94
Match length	259
% identity	67
NCBI Description	(D87956) protein involved in sexual development [Schizosaccharomyces pombe] >gi_2408048_emb_CAB16251_ (Z99164) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	390811
Contig ID	22235_1.R1084
5'-most EST	uC-osrocyp017e01b1
Method	BLASTX
NCBI GI	g5815235
BLAST score	478

E value	7.0e-71
Match length	188
% identity	71
NCBI Description	(AF173640) splicing factor SR1 [Arabidopsis thaliana]

Seq. No.	390812
Contig ID	22248_1.R1084
5'-most EST	uC-osflcyp033h03b1
Method	BLASTX
NCBI GI	g5262777
BLAST score	423
E value	2.0e-41
Match length	123
% identity	63
NCBI Description	(AL080282) fatty acid hydroxylase-like protein [Arabidopsis thaliana]

Seq. No.	390813
Contig ID	22256_1.R1084
5'-most EST	uC-osflM202082b09b1
Method	BLASTX
NCBI GI	g4982509
BLAST score	169
E value	1.0e-11
Match length	35
% identity	89
NCBI Description	(AC000107) F17F8.15 [Arabidopsis thaliana]

Seq. No.	390814
Contig ID	22267_1.R1084
5'-most EST	g700320
Method	BLASTX
NCBI GI	g3924611
BLAST score	691
E value	1.0e-72
Match length	211
% identity	63
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390815
Contig ID	22272_1.R1084
5'-most EST	g2312801
Method	BLASTX
NCBI GI	g2244834
BLAST score	499
E value	4.0e-50
Match length	292
% identity	42
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390816
Contig ID	22287_1.R1084
5'-most EST	LIB3434-013-P1-K1-E3

Seq. No.	390817
Contig ID	22292_1.R1084
5'-most EST	uC-osrocyp036a11b1

Seq. No.	390818
Contig ID	22294_1.R1084
5'-most EST	LIB3434-013-P1-K1-E9

Seq. No.	390819
Contig ID	22300_1.R1084
5'-most EST	g427816
Method	BLASTX
NCBI GI	g5051773
BLAST score	238
E value	8.0e-22
Match length	160
% identity	42
NCBI Description	(AL078637) putative protein [Arabidopsis thaliana]

Seq. No.	390820
Contig ID	22313_1.R1084
5'-most EST	g571810

Seq. No.	390821
Contig ID	22314_1.R1084
5'-most EST	g3768012

Seq. No.	390822
Contig ID	22314_2.R1084
5'-most EST	g3763356

Seq. No.	390823
Contig ID	22315_1.R1084
5'-most EST	uC-osrocyp026e03a1

Seq. No.	390824
Contig ID	22321_1.R1084
5'-most EST	uC-osflcyp109h05b1
Method	BLASTX
NCBI GI	g123549
BLAST score	470
E value	1.0e-46
Match length	143
% identity	68
NCBI Description	17.5 KD CLASS II HEAT SHOCK PROTEIN >gi_100885_pir__S14998 heat shock protein, 18K - maize >gi_22339_emb_CAA38013_ (X54076) 18kDa heat shock protein [Zea mays]

Seq. No.	390825
Contig ID	22323_1.R1084
5'-most EST	LIB3434-013-P1-K1-H4

Seq. No.	390826
Contig ID	22342_1.R1084
5'-most EST	g5667337
Method	BLASTX
NCBI GI	g5714737
BLAST score	199
E value	1.0e-14
Match length	280

% identity	25
NCBI Description	(AF171060) RING finger protein AO7 [Mus musculus]

Seq. No.	390827
Contig ID	22347_1.R1084
5'-most EST	LIB3434-014-P1-K1-B9
Method	BLASTX
NCBI GI	g5596470
BLAST score	408
E value	8.0e-40
Match length	90
% identity	84
NCBI Description	(AL096882) protein phosphatase type 1 PP1BG [Arabidopsis thaliana]

Seq. No.	390828
Contig ID	22361_2.R1084
5'-most EST	g426314

Seq. No.	390829
Contig ID	22365_1.R1084
5'-most EST	g699764

Seq. No.	390830
Contig ID	22365_2.R1084
5'-most EST	LIB3434-016-P1-K1-H3

Seq. No.	390831
Contig ID	22365_3.R1084
5'-most EST	g701842

Seq. No.	390832
Contig ID	22370_1.R1084
5'-most EST	uC-osflcyp078a10b1
Method	BLASTX
NCBI GI	g2499005
BLAST score	304
E value	3.0e-27
Match length	212
% identity	41
NCBI Description	4-METHYL-5(B-HYDROXYETHYL)-THIAZOLE MONOPHOSPHATE BIOSYNTHESIS ENZYME >gi_1100872 (U34923) ThiJ [Escherichia coli] >gi_1773108 (U82664) 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein [Escherichia coli] >gi_1786626 (AE000148) 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis [Escherichia coli]

Seq. No.	390833
Contig ID	22373_1.R1084
5'-most EST	LIB3434-014-P1-K1-E11

Seq. No.	390834
Contig ID	22374_1.R1084
5'-most EST	LIB3434-014-P1-K1-E12
Method	BLASTX
NCBI GI	g4008156

BLAST score 619
E value 3.0e-64
Match length 235
% identity 54
NCBI Description (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]

Seq. No. 390835
Contig ID 22376_1.R1084
5'-most EST g4880877
Method BLASTX
NCBI GI g1619300
BLAST score 808
E value 3.0e-86
Match length 190
% identity 79
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 390836
Contig ID 22382_1.R1084
5'-most EST LIB3479-010-Q6-K1-G9
Method BLASTX
NCBI GI g4559368
BLAST score 460
E value 1.0e-45
Match length 165
% identity 59
NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No. 390837
Contig ID 22385_1.R1084
5'-most EST LIB3434-014-P1-K1-F12

Seq. No. 390838
Contig ID 22386_1.R1084
5'-most EST uC-osflM202097h11b1
Method BLASTX
NCBI GI g544184
BLAST score 682
E value 6.0e-92
Match length 241
% identity 68
NCBI Description 4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME) >gi_322785_pir__A45049 4-alpha-glucanotransferase (EC 2.4.1.25) - potato >gi_296692_emb_CAA48630_ (X68664) 4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No. 390839
Contig ID 22388_1.R1084
5'-most EST LIB3434-014-P1-K1-F4
Method BLASTX
NCBI GI g3894168
BLAST score 190
E value 2.0e-14
Match length 114
% identity 40
NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No.	390840
Contig ID	22391_1.R1084
5'-most EST	g5056118
Method	BLASTX
NCBI GI	g4102839
BLAST score	161
E value	2.0e-16
Match length	149
% identity	38
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	390841
Contig ID	22393_1.R1084
5'-most EST	LIB3434-014-P1-K1-F9

Seq. No.	390842
Contig ID	22395_1.R1084
5'-most EST	g3767204

Seq. No.	390843
Contig ID	22397_1.R1084
5'-most EST	LIB3434-014-P1-K1-G12
Method	BLASTX
NCBI GI	g4511988
BLAST score	323
E value	8.0e-30
Match length	151
% identity	48
NCBI Description	(AF088896) ubiquinone methyltransferase [Zymomonas mobilis]

Seq. No.	390844
Contig ID	22399_1.R1084
5'-most EST	g2275792
Method	BLASTX
NCBI GI	g130709
BLAST score	519
E value	3.0e-64
Match length	132
% identity	93
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 >gi_322875_pir__S29317 phosphoprotein phosphatase (EC 3.1.3.16) 1 - maize >gi_168723 (M60215) protein phosphatase-1 [Zea mays] >gi_445586_prf__1909338A protein phosphatase 1 [Zea mays]

Seq. No.	390845
Contig ID	22399_2.R1084
5'-most EST	uC-osflcyp007c06b1
Method	BLASTX
NCBI GI	g130709
BLAST score	115
E value	1.0e-13
Match length	51
% identity	78
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1

>gi_322875_pir__S29317 phosphoprotein phosphatase (EC 3.1.3.16) 1 - maize >gi_168723 (M60215) protein phosphatase-1 [Zea mays] >gi_445586_prf__1909338A protein phosphatase 1 [Zea mays]

Seq. No.	390846
Contig ID	22403_1.R1084
5'-most EST	LIB3434-014-P1-K1-G9

Seq. No.	390847
Contig ID	22406_1.R1084
5'-most EST	LIB3434-014-P1-K1-H11
Method	BLASTX
NCBI GI	g2231312
BLAST score	893
E value	3.0e-96
Match length	197
% identity	87
NCBI Description	(U75603) AtRab18 [Arabidopsis thaliana]

Seq. No.	390848
Contig ID	22429_1.R1084
5'-most EST	g4716544

Seq. No.	390849
Contig ID	22442_1.R1084
5'-most EST	uC-osflcyp141e04b1
Method	BLASTX
NCBI GI	g3600033
BLAST score	862
E value	1.0e-92
Match length	287
% identity	60
NCBI Description	(AF080119) contains similarity to the N terminal domain of the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis thaliana]

Seq. No.	390850
Contig ID	22450_1.R1084
5'-most EST	LIB3475-012-P1-K1-A1

Seq. No.	390851
Contig ID	22470_1.R1084
5'-most EST	LIB3434-015-P1-K1-F3
Method	BLASTX
NCBI GI	g1778147
BLAST score	468
E value	1.0e-46
Match length	96
% identity	97
NCBI Description	(U66403) phosphate/phosphoenolpyruvate translocator precursor [Zea mays]

Seq. No.	390852
Contig ID	22474_1.R1084
5'-most EST	g5004605
Method	BLASTX

NCBI GI	g629772
BLAST score	1091
E value	1.0e-119
Match length	239
% identity	88
NCBI Description	beta-ketoacyl-ACP synthase - barley >gi_498740_emb_CAA84022_ (Z34268) beta-ketoacyl-ACP synthase [Hordeum vulgare]

Seq. No.	390853
Contig ID	22479_1.R1084
5'-most EST	g4879132
Method	BLASTN
NCBI GI	g6063530
BLAST score	91
E value	2.0e-43
Match length	163
% identity	93
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	390854
Contig ID	22493_1.R1084
5'-most EST	g2442227
Method	BLASTX
NCBI GI	g1532171
BLAST score	280
E value	1.0e-25
Match length	97
% identity	61
NCBI Description	(U63815) AT.I.24-9 gene product [Arabidopsis thaliana]

Seq. No.	390855
Contig ID	22494_1.R1084
5'-most EST	LIB3434-015-P1-K1-H6

Seq. No.	390856
Contig ID	22504_2.R1084
5'-most EST	g427169

Seq. No.	390857
Contig ID	22513_1.R1084
5'-most EST	LIB3434-016-P1-K1-B2
Method	BLASTX
NCBI GI	g3377794
BLAST score	240
E value	3.0e-20
Match length	77
% identity	64
NCBI Description	(AF034572) proteasome IOTA subunit [Glycine max]

Seq. No.	390858
Contig ID	22528_1.R1084
5'-most EST	g2310715
Method	BLASTX
NCBI GI	g1174162
BLAST score	406
E value	1.0e-39

Match length	88
% identity	80
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	390859
Contig ID	22533_1.R1084
5'-most EST	uC-osflcyp021h09b1
Method	BLASTX
NCBI GI	g5931761
BLAST score	633
E value	8.0e-74
Match length	208
% identity	55
NCBI Description	(AJ234901) acetolactate synthase small subunit [Nicotiana plumbaginifolia]

Seq. No.	390860
Contig ID	22540_1.R1084
5'-most EST	LIB3434-016-P1-K1-D7
Method	BLASTX
NCBI GI	g2224812
BLAST score	260
E value	2.0e-22
Match length	127
% identity	46
NCBI Description	(Z97023) cysteine endopeptidase EP-A [Hordeum vulgare]

Seq. No.	390861
Contig ID	22543_1.R1084
5'-most EST	LIB3474-006-P1-K1-H3
Method	BLASTX
NCBI GI	g300265
BLAST score	795
E value	4.0e-85
Match length	174
% identity	92
NCBI Description	HSP68=68 kda heat-stress DnaK homolog [Lycopersicon peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No.	390862
Contig ID	22547_1.R1084
5'-most EST	LIB3434-016-P1-K1-E2
Method	BLASTX
NCBI GI	g1710424
BLAST score	265
E value	8.0e-28
Match length	103
% identity	67
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	390863
Contig ID	22551_1.R1084

5'-most EST	LIB3474-005-P1-K1-E12
Method	BLASTX
NCBI GI	g5734502
BLAST score	821
E value	4.0e-88
Match length	174
% identity	89
NCBI Description	(AJ010712) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]

Seq. No.	390864
Contig ID	22566_1.R1084
5'-most EST	uC-osroM202016a05b1
Method	BLASTX
NCBI GI	g2493646
BLAST score	647
E value	1.0e-67
Match length	230
% identity	51
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi_309559 (L21008) chaperonin 60 [Zea mays] >gi_309561 (L21006) mitochondrial chaperonin 60 [Zea mays]

Seq. No.	390865
Contig ID	22567_1.R1084
5'-most EST	LIB3434-016-P1-K1-G1
Method	BLASTX
NCBI GI	g5689994
BLAST score	164
E value	6.0e-11
Match length	105
% identity	29
NCBI Description	(AL109731) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	390866
Contig ID	22570_1.R1084
5'-most EST	LIB3434-016-P1-K1-G3
Method	BLASTX
NCBI GI	g2271477
BLAST score	468
E value	1.0e-46
Match length	94
% identity	91
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	390867
Contig ID	22586_1.R1084
5'-most EST	LIB3434-016-P1-K1-H8
Method	BLASTX
NCBI GI	g2204077
BLAST score	170
E value	1.0e-15
Match length	91
% identity	52
NCBI Description	(D85623) extracellular insoluble cystatin [Daucus carota]

Seq. No.	390868

Contig ID 22592_1.R1084
5'-most EST LIB3434-017-P1-K1-A3

Seq. No. 390869
Contig ID 22594_1.R1084
5'-most EST g5667497

Seq. No. 390870
Contig ID 22598_1.R1084
5'-most EST uC-osf1M2020117a11a1
Method BLASTX
NCBI GI g5051775
BLAST score 448
E value 4.0e-44
Match length 138
% identity 62
NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 390871
Contig ID 22598_2.R1084
5'-most EST uC-osroM202032a05b1

Seq. No. 390872
Contig ID 22601_1.R1084
5'-most EST LIB3434-017-P1-K1-B11

Seq. No. 390873
Contig ID 22604_1.R1084
5'-most EST LIB3434-017-P1-K1-B3
Method BLASTX
NCBI GI g3551257
BLAST score 255
E value 6.0e-22
Match length 92
% identity 22
NCBI Description (AB012708) 98b [Daucus carota]

Seq. No. 390874
Contig ID 22607_1.R1084
5'-most EST LIB3434-019-P1-K1-E8

Seq. No. 390875
Contig ID 22608_2.R1084
5'-most EST uC-osf1cyp012b10b1
Method BLASTX
NCBI GI g4884932
BLAST score 485
E value 9.0e-49
Match length 117
% identity 72
NCBI Description (AF141659) AtHVA22a [Arabidopsis thaliana]
>gi_4884944_gb_AAD31885.1_AF141977_1 (AF141977) AtHVA22a
[Arabidopsis thaliana]

Seq. No. 390876
Contig ID 22611_1.R1084
5'-most EST g568331

Method	BLASTX
NCBI GI	g2773404
BLAST score	346
E value	2.0e-32
Match length	165
% identity	47
NCBI Description	(AF041255) pyridoxal kinase [Sus scrofa]

Seq. No.	390877
Contig ID	22615_1.R1084
5'-most EST	LIB3434-017-P1-K1-C2
Method	BLASTX
NCBI GI	g399028
BLAST score	174
E value	3.0e-12
Match length	62
% identity	52
NCBI Description	ALLIIN LYASE PRECURSOR (ALLIINASE) (CYSTEINE SULPHOXIDE LYASE) >gi_419808_pir__S29302 alliin lyase (EC 4.4.1.4) precursor - garlic >gi_16109_emb_CAA78268_ (Z12622) precursor alliinase [Allium sativum]

Seq. No.	390878
Contig ID	22619_1.R1084
5'-most EST	LIB3434-017-P1-K1-C6
Method	BLASTX
NCBI GI	g2982458
BLAST score	757
E value	2.0e-80
Match length	207
% identity	72
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	390879
Contig ID	22631_1.R1084
5'-most EST	g427438

Seq. No.	390880
Contig ID	22632_1.R1084
5'-most EST	LIB3434-017-P1-K1-E1

Seq. No.	390881
Contig ID	22637_1.R1084
5'-most EST	g1631446
Method	BLASTX
NCBI GI	g5903103
BLAST score	249
E value	7.0e-21
Match length	148
% identity	36
NCBI Description	(AC008017) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	390882
Contig ID	22640_1.R1084
5'-most EST	LIB3434-017-P1-K1-E6

Seq. No.	390883

Contig ID	22645_1.R1084
5'-most EST	uC-osf1cyp157f02b1
Method	BLASTX
NCBI GI	g4530611
BLAST score	540
E value	1.0e-66
Match length	129
% identity	98
NCBI Description	(AF134552) serine/threonine protein phosphatase PP2A-2 catalytic subunit [Oryza sativa subsp. indica]

Seq. No.	390884
Contig ID	22646_1.R1084
5'-most EST	LIB3599-001-P1-K6-C4
Method	BLASTX
NCBI GI	g5042424
BLAST score	442
E value	2.0e-43
Match length	152
% identity	54
NCBI Description	(AC006193) Hypothetical Protein [Arabidopsis thaliana]

Seq. No.	390885
Contig ID	22663_1.R1084
5'-most EST	LIB3434-017-P1-K1-G6
Method	BLASTX
NCBI GI	g5725430
BLAST score	162
E value	7.0e-11
Match length	47
% identity	64
NCBI Description	(AL109787) stress responsive protein homolog [Arabidopsis thaliana]

Seq. No.	390886
Contig ID	22664_1.R1084
5'-most EST	g2428693

Seq. No.	390887
Contig ID	22669_1.R1084
5'-most EST	LIB3434-017-P1-K1-H4
Method	BLASTX
NCBI GI	g285636
BLAST score	210
E value	2.0e-21
Match length	66
% identity	82
NCBI Description	(D14161) ORF [Hordeum vulgare]

Seq. No.	390888
Contig ID	22676_1.R1084
5'-most EST	LIB3434-018-P1-K1-A12
Method	BLASTX
NCBI GI	g3152568
BLAST score	483
E value	2.0e-48
Match length	162

% identity	59
NCBI Description	(AC002986) Similar to hypothetical protein product gb_Z97337 from A. thaliana. EST gb_H76597 comes from this gene. [Arabidopsis thaliana]

Seq. No.	390889
Contig ID	22697_1.R1084
5'-most EST	LIB3434-018-P1-K1-C1
Method	BLASTX
NCBI GI	g2982432
BLAST score	294
E value	3.0e-26
Match length	102
% identity	59
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	390890
Contig ID	22706_1.R1084
5'-most EST	LIB3434-018-P1-K1-C8

Seq. No.	390891
Contig ID	22707_1.R1084
5'-most EST	LIB3434-018-P1-K1-D1
Method	BLASTX
NCBI GI	g3142303
BLAST score	761
E value	5.0e-81
Match length	175
% identity	43
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	390892
Contig ID	22709_1.R1084
5'-most EST	LIB3434-018-P1-K1-D11
Method	BLASTN
NCBI GI	g6063530
BLAST score	437
E value	0.0e+00
Match length	875
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	390893
Contig ID	22714_1.R1084
5'-most EST	g2442695

Seq. No.	390894
Contig ID	22717_1.R1084
5'-most EST	LIB3434-018-P1-K1-D9

Seq. No.	390895
Contig ID	22731_1.R1084
5'-most EST	g2310426
Method	BLASTX

NCBI GI	g2132293
BLAST score	200
E value	5.0e-15
Match length	286
% identity	25
NCBI Description	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae) >gi_1066487 (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325) [Saccharomyces cerevisiae]

Seq. No.	390896
Contig ID	22738_1.R1084
5'-most EST	LIB3434-018-P1-K1-F6

Seq. No.	390897
Contig ID	22743_1.R1084
5'-most EST	uC-osf1M202048g03b1
Method	BLASTX
NCBI GI	g3157928
BLAST score	628
E value	6.0e-69
Match length	220
% identity	58
NCBI Description	(AC002131) Similar to fumarylacetoacetate hydrolase, gb_L41670 from Emericella nidulans. [Arabidopsis thaliana]

Seq. No.	390898
Contig ID	22746_1.R1084
5'-most EST	LIB3434-018-P1-K1-G2
Method	BLASTX
NCBI GI	g3337361
BLAST score	443
E value	1.0e-43
Match length	188
% identity	26
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	390899
Contig ID	22752_1.R1084
5'-most EST	LIB3475-008-P1-K1-F4
Method	BLASTX
NCBI GI	g4850408
BLAST score	213
E value	7.0e-17
Match length	95
% identity	41
NCBI Description	(AC007357) Contains PF_00097 Zinc finger (C3HC4) ring finger motif. [Arabidopsis thaliana]

Seq. No.	390900
Contig ID	22762_1.R1084
5'-most EST	LIB3479-012-Q6-K1-F2
Method	BLASTX
NCBI GI	g2384696
BLAST score	311
E value	3.0e-28

Match length	230
% identity	38
NCBI Description	(AF013216) acyl-CoA oxidase [Myxococcus xanthus]

Seq. No.	390901
Contig ID	22764_1.R1084
5'-most EST	g3760785
Method	BLASTN
NCBI GI	g2522426
BLAST score	46
E value	2.0e-16
Match length	125
% identity	82
NCBI Description	Cloning vector pWSK29, complete sequence

Seq. No.	390902
Contig ID	22766_1.R1084
5'-most EST	g4716370
Method	BLASTX
NCBI GI	g2852449
BLAST score	318
E value	5.0e-29
Match length	119
% identity	57
NCBI Description	(D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No.	390903
Contig ID	22772_1.R1084
5'-most EST	LIB3434-019-P1-K1-A6
Method	BLASTX
NCBI GI	g2262115
BLAST score	338
E value	2.0e-31
Match length	197
% identity	36
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.	390904
Contig ID	22777_1.R1084
5'-most EST	uC-osroM202029f10b1
Method	BLASTX
NCBI GI	g3980396
BLAST score	599
E value	5.0e-62
Match length	157
% identity	67
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	390905
Contig ID	22778_1.R1084
5'-most EST	uC-osflcyp153b07b1
Method	BLASTX
NCBI GI	g2131751
BLAST score	212
E value	2.0e-16

Match length	131
% identity	35
NCBI Description	hypothetical protein YLR019w - yeast (Saccharomyces cerevisiae) >gi_1360322_emb_CAA97541_ (Z73191) ORF YLR019w [Saccharomyces cerevisiae]

Seq. No.	390906
Contig ID	22784_1.R1084
5'-most EST	LIB3434-019-P1-K1-B7
Method	BLASTX
NCBI GI	g5091610
BLAST score	357
E value	1.0e-37
Match length	160
% identity	57
NCBI Description	(AC007858) 10A19I.15 [Oryza sativa]

Seq. No.	390907
Contig ID	22786_1.R1084
5'-most EST	LIB3434-019-P1-K1-B9

Seq. No.	390908
Contig ID	22820_1.R1084
5'-most EST	uC-osf1cyp156a08b1
Method	BLASTX
NCBI GI	g4337178
BLAST score	336
E value	1.0e-50
Match length	130
% identity	78
NCBI Description	(AC006416) T31J12.5 [Arabidopsis thaliana]

Seq. No.	390909
Contig ID	22826_1.R1084
5'-most EST	g3760201
Method	BLASTX
NCBI GI	g4678262
BLAST score	1122
E value	1.0e-123
Match length	327
% identity	64
NCBI Description	(AL049657) argininosuccinate synthase-like protein [Arabidopsis thaliana]

Seq. No.	390910
Contig ID	22827_1.R1084
5'-most EST	LIB3434-019-P1-K1-F2
Method	BLASTX
NCBI GI	g5882749
BLAST score	301
E value	7.0e-27
Match length	154
% identity	47
NCBI Description	(AC008263) Contains 2 PF_00612 IQ calmodulin-binding motif domains. [Arabidopsis thaliana]

Seq. No.	390911

Contig ID	22840_1.R1084
5'-most EST	LIB3434-025-P1-K1-D2

Seq. No.	390912
Contig ID	22850_1.R1084
5'-most EST	LIB3434-019-P1-K1-H4

Seq. No.	390913
Contig ID	22860_1.R1084
5'-most EST	g2312556
Method	BLASTX
NCBI GI	g5002526
BLAST score	186
E value	1.0e-13
Match length	84
% identity	30
NCBI Description	(AL078606) putative protein [Arabidopsis thaliana]

Seq. No.	390914
Contig ID	22868_1.R1084
5'-most EST	LIB3434-021-P1-K1-B5
Method	BLASTX
NCBI GI	g4467111
BLAST score	222
E value	8.0e-18
Match length	103
% identity	42
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	390915
Contig ID	22870_1.R1084
5'-most EST	g427220
Method	BLASTX
NCBI GI	g416922
BLAST score	355
E value	2.0e-33
Match length	90
% identity	78
NCBI Description	DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE) (DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir__JQ1599 dUTP pyrophosphatase (EC 3.6.1.23) - tomato >gi_251897_bbs_109276 (S40549) deoxyuridine triphosphatase, dUTPase, P18 {EC 3.6.1.23} [tomatoes, Tint Tim cultivar LA154, Peptide, 169 aa] [Lycopersicon esculentum]

Seq. No.	390916
Contig ID	22877_1.R1084
5'-most EST	LIB3434-021-P1-K1-C2

Seq. No.	390917
Contig ID	22881_1.R1084
5'-most EST	g2312205
Method	BLASTX
NCBI GI	g3924598
BLAST score	95
E value	2.0e-09
Match length	145

% identity	35
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	390918
Contig ID	22888_1.R1084
5'-most EST	LIB3434-021-P1-K1-D3
Method	BLASTX
NCBI GI	g6056374
BLAST score	277
E value	3.0e-24
Match length	109
% identity	47
NCBI Description	(AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	390919
Contig ID	22892_1.R1084
5'-most EST	g568695
Method	BLASTX
NCBI GI	g2270994
BLAST score	321
E value	3.0e-29
Match length	124
% identity	53
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	390920
Contig ID	22892_2.R1084
5'-most EST	LIB3434-021-P1-K1-D7
Method	BLASTX
NCBI GI	g2270994
BLAST score	187
E value	9.0e-14
Match length	84
% identity	49
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	390921
Contig ID	22895_1.R1084
5'-most EST	g702531
Method	BLASTX
NCBI GI	g6016479
BLAST score	564
E value	3.0e-61
Match length	156
% identity	77
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	390922
Contig ID	22896_1.R1084
5'-most EST	g2280587

Seq. No.	390923
Contig ID	22904_1.R1084
5'-most EST	g2800524

Seq. No.	390924
Contig ID	22908_1.R1084
5'-most EST	g2797877

Seq. No.	390925
Contig ID	22910_1.R1084
5'-most EST	uC-osf1cyp162e12b1
Method	BLASTX
NCBI GI	g1408222
BLAST score	489
E value	6.0e-49
Match length	160
% identity	71
NCBI Description	(U60764) pathogenesis-related protein [Sorghum bicolor]

Seq. No.	390926
Contig ID	22911_1.R1084
5'-most EST	LIB3434-021-P1-K1-F6

Seq. No.	390927
Contig ID	22925_1.R1084
5'-most EST	LIB3434-021-P1-K1-G9
Method	BLASTX
NCBI GI	g1168217
BLAST score	346
E value	3.0e-32
Match length	178
% identity	38
NCBI Description	DNA-3-METHYLADENINE GLYCOSYLASE (3-METHYLADENINE-DNA GLYCOSIDASE) (TAG) >gi_1074039_pir__G64084 DNA-3-methyladenine glycosidase I (tagI) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1573653 (U32748) DNA-3-methyladenine glycosidase I (tagI) [Haemophilus influenzae Rd]

Seq. No.	390928
Contig ID	22926_1.R1084
5'-most EST	g5667446
Method	BLASTX
NCBI GI	g3096939
BLAST score	368
E value	6.0e-35
Match length	104
% identity	68
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	390929
Contig ID	22932_1.R1084
5'-most EST	LIB3434-021-P1-K1-H9
Method	BLASTX
NCBI GI	g3193292
BLAST score	640
E value	7.0e-67
Match length	179
% identity	76
NCBI Description	(AF069298) similar to ATPases associated with various

cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	390930
Contig ID	22935_1.R1084
5'-most EST	g702878
Method	BLASTX
NCBI GI	g5729706
BLAST score	274
E value	4.0e-24
Match length	84
% identity	52
NCBI Description	(AC007927) unknown protein [Arabidopsis thaliana]

Seq. No.	390931
Contig ID	22938_1.R1084
5'-most EST	LIB3434-023-P1-K1-A6

Seq. No.	390932
Contig ID	22951_1.R1084
5'-most EST	LIB3434-023-P1-K1-C3

Seq. No.	390933
Contig ID	22956_1.R1084
5'-most EST	g428715
Method	BLASTX
NCBI GI	g4803960
BLAST score	213
E value	4.0e-17
Match length	78
% identity	50
NCBI Description	(AC006202) putative carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	390934
Contig ID	22957_1.R1084
5'-most EST	g2428009
Method	BLASTX
NCBI GI	g4803952
BLAST score	435
E value	1.0e-42
Match length	115
% identity	72
NCBI Description	(AC006202) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390935
Contig ID	22975_1.R1084
5'-most EST	g569620
Method	BLASTX
NCBI GI	g4455349
BLAST score	206
E value	5.0e-16
Match length	89
% identity	46
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	390936

Contig ID	22987_1.R1084
5'-most EST	uC-osroM202031h08b1
Method	BLASTX
NCBI GI	g4490733
BLAST score	399
E value	2.0e-38
Match length	186
% identity	45
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	390937
Contig ID	22991_1.R1084
5'-most EST	LIB3434-024-P1-K1-B1

Seq. No.	390938
Contig ID	23001_1.R1084
5'-most EST	LIB3434-024-P1-K1-B9
Method	BLASTX
NCBI GI	g4586449
BLAST score	324
E value	6.0e-30
Match length	78
% identity	68
NCBI Description	(AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]

Seq. No.	390939
Contig ID	23004_1.R1084
5'-most EST	g571681
Method	BLASTN
NCBI GI	g5777612
BLAST score	458
E value	0.0e+00
Match length	599
% identity	98
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	390940
Contig ID	23005_1.R1084
5'-most EST	g571627
Method	BLASTX
NCBI GI	g3201541
BLAST score	1123
E value	1.0e-123
Match length	283
% identity	75
NCBI Description	(AJ005077) TCTR2 protein [Lycopersicon esculentum]

Seq. No.	390941
Contig ID	23006_1.R1084
5'-most EST	uC-osflcyp174a02a1
Method	BLASTX
NCBI GI	g1236961
BLAST score	408
E value	9.0e-40
Match length	110
% identity	65
NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No.	390942
Contig ID	23010_1.R1084
5'-most EST	g3767667
Method	BLASTX
NCBI GI	g5777631
BLAST score	364
E value	2.0e-34
Match length	145
% identity	62
NCBI Description	(AJ245900) CAA303719.1 protein [Oryza sativa]

Seq. No.	390943
Contig ID	23011_1.R1084
5'-most EST	uC-osrocyp010d04b1
Method	BLASTX
NCBI GI	g3063710
BLAST score	706
E value	3.0e-74
Match length	184
% identity	70
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	390944
Contig ID	23020_1.R1084
5'-most EST	LIB3434-024-P1-K1-D5
Method	BLASTX
NCBI GI	g3367522
BLAST score	303
E value	2.0e-27
Match length	105
% identity	52
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	390945
Contig ID	23038_1.R1084
5'-most EST	LIB3434-024-P1-K1-F12

Seq. No.	390946
Contig ID	23048_1.R1084
5'-most EST	g2311116
Method	BLASTX
NCBI GI	g4191778
BLAST score	926
E value	1.0e-100
Match length	271
% identity	66
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	390947
Contig ID	23074_1.R1084
5'-most EST	g5004340

Seq. No.	390948
Contig ID	23078_1.R1084

5'-most EST	g2310217
Method	BLASTX
NCBI GI	g4587615
BLAST score	1024
E value	1.0e-111
Match length	267
% identity	71
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	390949
Contig ID	23079_1.R1084
5'-most EST	g4716458

Seq. No.	390950
Contig ID	23082_1.R1084
5'-most EST	g2442664
Method	BLASTX
NCBI GI	g2129854
BLAST score	257
E value	2.0e-43
Match length	217
% identity	47
NCBI Description	early nodulin 8 precursor - alfalfa >gi_304037 (L18899) early nodulin [Medicago sativa]

Seq. No.	390951
Contig ID	23083_1.R1084
5'-most EST	LIB3434-025-P1-K1-B8
Method	BLASTX
NCBI GI	g4309698
BLAST score	494
E value	2.0e-49
Match length	246
% identity	66
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	390952
Contig ID	23085_1.R1084
5'-most EST	uC-osflcyp065c03b1
Method	BLASTX
NCBI GI	g2352492
BLAST score	274
E value	1.0e-23
Match length	98
% identity	56
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	390953
Contig ID	23091_1.R1084
5'-most EST	g5005361
Method	BLASTX
NCBI GI	g4454006

BLAST score	185
E value	2.0e-13
Match length	87
% identity	47
NCBI Description	(AL035396) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390954
Contig ID	23097_1.R1084
5'-most EST	LIB3479-002-Q6-K2-E3

Seq. No.	390955
Contig ID	23097_2.R1084
5'-most EST	LIB3434-025-P1-K1-D10

Seq. No.	390956
Contig ID	23106_1.R1084
5'-most EST	uC-osflcyp022d12b1
Method	BLASTX
NCBI GI	g729442
BLAST score	677
E value	6.0e-71
Match length	186
% identity	48
NCBI Description	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR >gi_166380 (M80235) glucose-regulated endoplasmic reticular protein precursor [Medicago sativa]

Seq. No.	390957
Contig ID	23107_1.R1084
5'-most EST	LIB3434-025-P1-K1-E1
Method	BLASTX
NCBI GI	g5295970
BLAST score	527
E value	8.0e-54
Match length	134
% identity	83
NCBI Description	(AB026295) ESTs D22477(C11179),AU075323(C11179) corresponds to a region of the predicted gene.; Similar to Rabbit multifunctional thyroid hormone binding protein mRNA, complete cds.(J05602) [Oryza sativa]

Seq. No.	390958
Contig ID	23112_1.R1084
5'-most EST	uC-osrocyp015e08a1
Method	BLASTX
NCBI GI	g4514635
BLAST score	266
E value	3.0e-23
Match length	68
% identity	75
NCBI Description	(AB021175) root cap protein 1 [Zea mays]

Seq. No.	390959
Contig ID	23131_1.R1084
5'-most EST	g428784
Method	BLASTX
NCBI GI	g2088652

BLAST score	532
E value	9.0e-95
Match length	268
% identity	69
NCBI Description	(AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

Seq. No.	390960
Contig ID	23134_1.R1084
5'-most EST	uC-osf1cyp170a04b1

Seq. No.	390961
Contig ID	23151_1.R1084
5'-most EST	LIB3434-026-P1-K1-A12
Method	BLASTX
NCBI GI	g5777621
BLAST score	782
E value	2.0e-83
Match length	155
% identity	99
NCBI Description	(AJ245900) CAA30379.1 protein [Oryza sativa]

Seq. No.	390962
Contig ID	23154_1.R1084
5'-most EST	uC-osf1m202100c11b1

Seq. No.	390963
Contig ID	23156_1.R1084
5'-most EST	g5038790
Method	BLASTX
NCBI GI	g3335359
BLAST score	472
E value	3.0e-47
Match length	136
% identity	65
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	390964
Contig ID	23158_1.R1084
5'-most EST	g2442486
Method	BLASTX
NCBI GI	g3688174
BLAST score	332
E value	8.0e-31
Match length	109
% identity	58
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	390965
Contig ID	23159_1.R1084
5'-most EST	g3760326
Method	BLASTX
NCBI GI	g4406815
BLAST score	590
E value	7.0e-61

Match length	161
% identity	67
NCBI Description	(AC006201) putative peptide methionine sulfoxide reductase [Arabidopsis thaliana]

Seq. No.	390966
Contig ID	23173_1.R1084
5'-most EST	LIB3434-026-P1-K1-C3

Seq. No.	390967
Contig ID	23174_1.R1084
5'-most EST	g700092
Method	BLASTX
NCBI GI	g3249086
BLAST score	611
E value	3.0e-63
Match length	170
% identity	72
NCBI Description	(AC004473) Contains similarity to 21 KD subunit of the Arp2/3 protein complex (ARC21) gb_AF006086 from Homo sapiens. EST gb_Z37222 comes [Arabidopsis thaliana]

Seq. No.	390968
Contig ID	23175_1.R1084
5'-most EST	LIB3434-032-P1-K1-E10
Method	BLASTX
NCBI GI	g2224808
BLAST score	165
E value	1.0e-18
Match length	152
% identity	45
NCBI Description	(Z97021) cysteine endopeptidase EP-A [Hordeum vulgare]

Seq. No.	390969
Contig ID	23176_1.R1084
5'-most EST	LIB3434-026-P1-K1-C6
Method	BLASTX
NCBI GI	g2342728
BLAST score	409
E value	1.0e-39
Match length	147
% identity	53
NCBI Description	(AC002341) Cysteine proteinase isolog [Arabidopsis thaliana]

Seq. No.	390970
Contig ID	23179_1.R1084
5'-most EST	LIB3434-026-P1-K1-D1

Seq. No.	390971
Contig ID	23182_1.R1084
5'-most EST	LIB3434-026-P1-K1-D2
Method	BLASTX
NCBI GI	g2194132
BLAST score	805
E value	4.0e-86
Match length	251

% identity	64
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	390972
Contig ID	23187_1.R1084
5'-most EST	LIB3434-026-P1-K1-D9
Method	BLASTX
NCBI GI	g3402675
BLAST score	217
E value	5.0e-17
Match length	118
% identity	40
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	390973
Contig ID	23188_1.R1084
5'-most EST	LIB3434-029-P1-K1-F6
Method	BLASTX
NCBI GI	g3170525
BLAST score	363
E value	4.0e-34
Match length	148
% identity	49
NCBI Description	(AF054615) cellulase [Fragaria x ananassa]

Seq. No.	390974
Contig ID	23204_1.R1084
5'-most EST	uC-osrocyp015b10b1
Method	BLASTX
NCBI GI	g623586
BLAST score	527
E value	2.0e-53
Match length	117
% identity	92
NCBI Description	(L29273) putative [Nicotiana tabacum]

Seq. No.	390975
Contig ID	23206_1.R1084
5'-most EST	g2428860
Method	BLASTX
NCBI GI	g2826882
BLAST score	470
E value	9.0e-47
Match length	106
% identity	86
NCBI Description	(AJ223634) transcription factor IIA small subunit [Arabidopsis thaliana] >gi_5051786_emb_CAB45079.1_ (AL078637) transcription factor IIA small subunit [Arabidopsis thaliana]

Seq. No.	390976
Contig ID	23206_2.R1084
5'-most EST	g569277
Method	BLASTX
NCBI GI	g2833374
BLAST score	259
E value	2.0e-26

Match length	81
% identity	73
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIA GAMMA CHAIN (TFIIA-GAMMA) >gi_1429228_emb_CAA67369_ (X98862) putative small subunit [Arabidopsis thaliana]

Seq. No.	390977
Contig ID	23208_1.R1084
5'-most EST	g700359

Seq. No.	390978
Contig ID	23232_1.R1084
5'-most EST	LIB3434-026-P1-K1-H8

Seq. No.	390979
Contig ID	23235_1.R1084
5'-most EST	LIB3434-027-P1-K1-A10
Method	BLASTX
NCBI GI	g3702317
BLAST score	155
E value	4.0e-10
Match length	37
% identity	84
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana] >gi_4559376_gb_AAD23036.1_AC006526_1 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	390980
Contig ID	23244_1.R1084
5'-most EST	g2312754

Seq. No.	390981
Contig ID	23253_1.R1084
5'-most EST	g701276
Method	BLASTN
NCBI GI	g2624212
BLAST score	42
E value	3.0e-14
Match length	80
% identity	88
NCBI Description	M.acuminata mRNA; clone pBAN UU130 >gi_4774586_emb_A70171.1_A70171 Sequence 32 from Patent WO9811228

Seq. No.	390982
Contig ID	23266_1.R1084
5'-most EST	g428163
Method	BLASTX
NCBI GI	g1575752
BLAST score	272
E value	1.0e-46
Match length	213
% identity	45
NCBI Description	(U70672) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	390983
Contig ID	23269_1.R1084

5'-most EST	LIB3434-027-P1-K1-D6
Method	BLASTX
NCBI GI	g3643610
BLAST score	515
E value	2.0e-52
Match length	110
% identity	87
NCBI Description	(AC005395) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	390984
Contig ID	23273_1.R1084
5'-most EST	uC-osflM202014a04b1
Method	BLASTX
NCBI GI	g4887010
BLAST score	328
E value	1.0e-30
Match length	93
% identity	72
NCBI Description	(AF123503) Nt-gh3 deduced protein [Nicotiana tabacum]

Seq. No.	390985
Contig ID	23301_1.R1084
5'-most EST	uC-osflcyp019h10b1
Method	BLASTX
NCBI GI	g6069504
BLAST score	260
E value	3.0e-22
Match length	129
% identity	51
NCBI Description	(AB022076) S-locus protein 8 [Brassica rapa]

Seq. No.	390986
Contig ID	23304_1.R1084
5'-most EST	g4878289
Method	BLASTX
NCBI GI	g3461848
BLAST score	1060
E value	1.0e-116
Match length	259
% identity	85
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	390987
Contig ID	23307_1.R1084
5'-most EST	LIB3479-011-Q6-K1-A11
Method	BLASTX
NCBI GI	g1777312
BLAST score	527
E value	3.0e-67
Match length	169
% identity	76
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	390988
Contig ID	23314_1.R1084

5'-most EST	g702372
Seq. No.	390989
Contig ID	23317_1.R1084
5'-most EST	LIB3434-028-P1-K1-A5
Method	BLASTX
NCBI GI	g4582436
BLAST score	605
E value	9.0e-63
Match length	176
% identity	69
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.	390990
Contig ID	23320_1.R1084
5'-most EST	LIB3434-028-P1-K1-A8
Method	BLASTX
NCBI GI	g1399303
BLAST score	313
E value	2.0e-28
Match length	92
% identity	63
NCBI Description	(U41473) phosphoinositide-specific phospholipase C P12 [Glycine max]
Seq. No.	390991
Contig ID	23325_1.R1084
5'-most EST	LIB3434-028-P1-K1-B4
Seq. No.	390992
Contig ID	23342_1.R1084
5'-most EST	uC-osf1cyp083b07a1
Seq. No.	390993
Contig ID	23345_1.R1084
5'-most EST	LIB3477-006-P1-K1-D11
Method	BLASTX
NCBI GI	g5817279
BLAST score	239
E value	1.0e-36
Match length	284
% identity	34
NCBI Description	(AL110295) conserved hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	390994
Contig ID	23354_1.R1084
5'-most EST	LIB3434-028-P1-K1-E4
Method	BLASTX
NCBI GI	g4102600
BLAST score	145
E value	8.0e-09
Match length	75
% identity	43
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.	390995

Contig ID	23368_1.R1084
5'-most EST	uC-osf1M202063e03a1
Seq. No.	390996
Contig ID	23372_1.R1084
5'-most EST	g426951
Seq. No.	390997
Contig ID	23376_1.R1084
5'-most EST	uC-osf1M202095f08b1
Method	BLASTX
NCBI GI	g5669650
BLAST score	374
E value	9.0e-36
Match length	114
% identity	63
NCBI Description	(AF096260) ER66 protein [Lycopersicon esculentum]
Seq. No.	390998
Contig ID	23384_1.R1084
5'-most EST	g700275
Seq. No.	390999
Contig ID	23385_1.R1084
5'-most EST	g3766789
Method	BLASTX
NCBI GI	g5051789
BLAST score	207
E value	1.0e-25
Match length	137
% identity	48
NCBI Description	(AL078637) putative protein [Arabidopsis thaliana]
Seq. No.	391000
Contig ID	23386_1.R1084
5'-most EST	g5005166
Seq. No.	391001
Contig ID	23392_1.R1084
5'-most EST	LIB3434-029-P1-K1-A10
Seq. No.	391002
Contig ID	23395_1.R1084
5'-most EST	LIB3434-029-P1-K1-A2
Method	BLASTX
NCBI GI	g2914710
BLAST score	317
E value	7.0e-56
Match length	182
% identity	59
NCBI Description	(AC003974) putative beta-D-galactosidase [Arabidopsis thaliana]
Seq. No.	391003
Contig ID	23399_1.R1084
5'-most EST	uC-osf1M202016g03b1

Seq. No.	391004
Contig ID	23411_1.R1084
5'-most EST	g5455369
Method	BLASTX
NCBI GI	g4314378
BLAST score	165
E value	4.0e-14
Match length	94
% identity	44
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana] >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative lipase [Arabidopsis thaliana]

Seq. No.	391005
Contig ID	23415_1.R1084
5'-most EST	g2312399
Method	BLASTX
NCBI GI	g2809385
BLAST score	1472
E value	1.0e-164
Match length	367
% identity	75
NCBI Description	(AF024634) NADPH cytochrome P450 reductase [Petroselinum crispum]

Seq. No.	391006
Contig ID	23423_1.R1084
5'-most EST	LIB3434-029-P1-K1-C9
Method	BLASTX
NCBI GI	g1841468
BLAST score	369
E value	5.0e-35
Match length	117
% identity	56
NCBI Description	(Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]

Seq. No.	391007
Contig ID	23425_1.R1084
5'-most EST	uC-osroM202028g04a1
Method	BLASTX
NCBI GI	g3757522
BLAST score	180
E value	4.0e-13
Match length	48
% identity	67
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	391008
Contig ID	23441_1.R1084
5'-most EST	LIB3434-029-P1-K1-E5
Method	BLASTX
NCBI GI	g5734704
BLAST score	683
E value	9.0e-72
Match length	249
% identity	51
NCBI Description	(AC008075) Contains similarity to gb_AF114753 polytropic

murine leukamia virus receptor SYG1 from Mus musculus. EST gb_N96331 comes from this gene. [Arabidopsis thaliana]

Seq. No.	391009
Contig ID	23445_1.R1084
5'-most EST	uC-osflcyp009e12b1
Method	BLASTX
NCBI GI	g2464901
BLAST score	282
E value	1.0e-24
Match length	133
% identity	40
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	391010
Contig ID	23448_1.R1084
5'-most EST	uC-osflcyp061a04b1
Method	BLASTX
NCBI GI	g464981
BLAST score	778
E value	6.0e-83
Match length	148
% identity	96
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	391011
Contig ID	23451_1.R1084
5'-most EST	g5003575
Method	BLASTX
NCBI GI	g3894158
BLAST score	240
E value	2.0e-26
Match length	134
% identity	47
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	391012
Contig ID	23452_1.R1084
5'-most EST	LIB3434-029-P1-K1-F5
Method	BLASTX
NCBI GI	g4249382
BLAST score	1268
E value	1.0e-144
Match length	347
% identity	68
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	391013
Contig ID	23455_1.R1084
5'-most EST	LIB3434-029-P1-K1-F9
Method	BLASTX
NCBI GI	g1431622

BLAST score	1035
E value	1.0e-113
Match length	214
% identity	89
NCBI Description	(X99100) protein kinase [Trifolium repens]

Seq. No.	391014
Contig ID	23461_1.R1084
5'-most EST	LIB3434-029-P1-K1-G3
Method	BLASTX
NCBI GI	g3881836
BLAST score	1187
E value	1.0e-130
Match length	295
% identity	75
NCBI Description	(Z78019) Similarity to Yeast LPG22P protein (TR:G1151240); cDNA EST EMBL:T00686 comes from this gene; cDNA EST EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728 comes from this gene; cDNA EST EMBL:C10626 comes from this

Seq. No.	391015
Contig ID	23462_1.R1084
5'-most EST	g1944249
Method	BLASTX
NCBI GI	g481815
BLAST score	551
E value	5.0e-56
Match length	278
% identity	43
NCBI Description	vegetative storage protein - western balsam poplar x cottonwood >gi_309839 (L20233) vegetative storage protein [Populus trichocarpa x Populus deltoides]

Seq. No.	391016
Contig ID	23464_1.R1084
5'-most EST	LIB3434-029-P1-K1-G6
Method	BLASTX
NCBI GI	g4165510
BLAST score	274
E value	7.0e-24
Match length	106
% identity	49
NCBI Description	(AL034356) predicted using hexExon; L7610.8, DNAJ-like protein, len:232 aa; Similarity to prokaryotic DNAJ proteins and eukarytoic DNAJ-like chaperones. E.coli DNAJ (SW:DNAJ_ECOLI) BLAST score: 405 P: 5.3e-38, 37% identity in

Seq. No.	391017
Contig ID	23470_1.R1084
5'-most EST	LIB3434-029-P1-K1-H11

Seq. No.	391018
Contig ID	23471_1.R1084
5'-most EST	uC-osf1M202069f01a1

Seq. No.	391019

Contig ID	23473_1.R1084
5'-most EST	LIB3434-029-P1-K1-H3

Seq. No.	391020
Contig ID	23478_1.R1084
5'-most EST	LIB3434-029-P1-K1-H8

Seq. No.	391021
Contig ID	23488_1.R1084
5'-most EST	uC-osflM202048g12b1
Method	BLASTX
NCBI GI	g4914371
BLAST score	271
E value	2.0e-23
Match length	166
% identity	31
NCBI Description	(AC007584) unknown protein [Arabidopsis thaliana]

Seq. No.	391022
Contig ID	23490_1.R1084
5'-most EST	g701231
Method	BLASTX
NCBI GI	g3927806
BLAST score	246
E value	2.0e-51
Match length	144
% identity	76
NCBI Description	(U96439) aminoalcoholphosphotransferase [Pimpinella brachycarpa]

Seq. No.	391023
Contig ID	23495_1.R1084
5'-most EST	LIB3434-030-P1-K1-B4
Method	BLASTX
NCBI GI	g3377820
BLAST score	458
E value	3.0e-45
Match length	123
% identity	72
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	391024
Contig ID	23516_1.R1084
5'-most EST	uC-osflcyp126c11b1
Method	BLASTX
NCBI GI	g2995370
BLAST score	279
E value	2.0e-24
Match length	138
% identity	37
NCBI Description	(AL022245) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	391025
Contig ID	23528_1.R1084
5'-most EST	uC-osroM202016a11b1

Seq. No.	391026
Contig ID	23542_1.R1084
5'-most EST	uC-osflcyp176d09b1
Method	BLASTX
NCBI GI	g1449179
BLAST score	791
E value	3.0e-84
Match length	225
% identity	69
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	391027
Contig ID	23550_1.R1084
5'-most EST	LIB3434-030-P1-K1-G7

Seq. No.	391028
Contig ID	23551_1.R1084
5'-most EST	LIB3434-030-P1-K1-G8

Seq. No.	391029
Contig ID	23552_1.R1084
5'-most EST	LIB3434-030-P1-K1-H1
Method	BLASTX
NCBI GI	g4006913
BLAST score	324
E value	5.0e-30
Match length	132
% identity	56
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391030
Contig ID	23553_1.R1084
5'-most EST	g3760363
Method	BLASTN
NCBI GI	g5295936
BLAST score	39
E value	5.0e-12
Match length	55
% identity	95
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	391031
Contig ID	23554_1.R1084
5'-most EST	LIB3434-030-P1-K1-H11
Method	BLASTX
NCBI GI	g4995890
BLAST score	1102
E value	1.0e-121
Match length	269
% identity	78
NCBI Description	(AJ242659) serine palmitoyltransferase [Solanum tuberosum]

Seq. No.	391032
Contig ID	23560_1.R1084
5'-most EST	LIB3434-030-P1-K1-H8

Method	BLASTX
NCBI GI	g465602
BLAST score	269
E value	2.0e-23
Match length	115
% identity	49
NCBI Description	HYPOTHETICAL 32.9 KD PROTEIN IN NFO-FRUA INTERGENIC REGION >gi_405885 (U00007) yeiN [Escherichia coli] >gi_1788490 (AE000306) orf, hypothetical protein [Escherichia coli] >gi_744200_prf__2014253BL yeiN gene [Escherichia coli]

Seq. No.	391033
Contig ID	23563_1.R1084
5'-most EST	uC-osflcyp027a09b1
Method	BLASTX
NCBI GI	g5103807
BLAST score	219
E value	2.0e-17
Match length	70
% identity	61
NCBI Description	(AC007591) Contains similarity to gb_AF014403 type-2 phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo sapiens. ESTs gb_T88254 and gb_AA394650 come from this gene. [Arabidopsis thaliana]

Seq. No.	391034
Contig ID	23571_1.R1084
5'-most EST	g4878890
Method	BLASTX
NCBI GI	g2980773
BLAST score	294
E value	3.0e-26
Match length	72
% identity	79
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	391035
Contig ID	23582_1.R1084
5'-most EST	LIB3434-031-P1-K1-C4
Method	BLASTX
NCBI GI	g5734713
BLAST score	195
E value	1.0e-14
Match length	66
% identity	62
NCBI Description	(AC008075) Is a member of PF_01169 Uncharacterized (transmembrane domain) protein family. [Arabidopsis thaliana]

Seq. No.	391036
Contig ID	23588_1.R1084
5'-most EST	g2312223
Method	BLASTX
NCBI GI	g4468796
BLAST score	509
E value	2.0e-51
Match length	155

% identity	70
NCBI Description	(AJ010439) GST6 protein [Zea mays]

Seq. No.	391037
Contig ID	23598_1.R1084
5'-most EST	g701758
Method	BLASTX
NCBI GI	g3695023
BLAST score	194
E value	1.0e-14
Match length	119
% identity	34
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	391038
Contig ID	23603_1.R1084
5'-most EST	g2442968
Method	BLASTX
NCBI GI	g3738285
BLAST score	239
E value	9.0e-20
Match length	159
% identity	37
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	391039
Contig ID	23604_1.R1084
5'-most EST	g4715037
Method	BLASTX
NCBI GI	g3004565
BLAST score	328
E value	3.0e-37
Match length	102
% identity	28
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	391040
Contig ID	23604_2.R1084
5'-most EST	LIB3434-031-P1-K1-E7
Method	BLASTX
NCBI GI	g3004565
BLAST score	255
E value	5.0e-22
Match length	56
% identity	28
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	391041
Contig ID	23606_1.R1084
5'-most EST	uC-osroM202017d09a1
Method	BLASTX
NCBI GI	g4406812
BLAST score	196
E value	7.0e-15
Match length	69
% identity	58
NCBI Description	(AC006201) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No.	391042
Contig ID	23609_1.R1084
5'-most EST	LIB3434-031-P1-K1-F12

Seq. No.	391043
Contig ID	23613_1.R1084
5'-most EST	LIB3475-010-P1-K1-H2
Method	BLASTX
NCBI GI	g4884966
BLAST score	677
E value	3.0e-71
Match length	143
% identity	94
NCBI Description	(AF145478) calcium ATPase [Mesembryanthemum crystallinum]

Seq. No.	391044
Contig ID	23622_1.R1084
5'-most EST	g701363
Method	BLASTX
NCBI GI	g4455190
BLAST score	299
E value	4.0e-28
Match length	120
% identity	57
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	391045
Contig ID	23631_1.R1084
5'-most EST	g2427796
Method	BLASTX
NCBI GI	g584893
BLAST score	1678
E value	0.0e+00
Match length	316
% identity	99
NCBI Description	SERINE CARBOXYPEPTIDASE III PRECURSOR >gi_283002_pir__S22530 carboxypeptidase III (EC 3.4.16.-) - rice >gi_218153_dbj_BAA01757_ (D10985) serine carboxypeptidase III [Oryza sativa]

Seq. No.	391046
Contig ID	23634_1.R1084
5'-most EST	g2428630
Method	BLASTX
NCBI GI	g5123942
BLAST score	340
E value	1.0e-31
Match length	122
% identity	56
NCBI Description	(AL079349) putative protein [Arabidopsis thaliana]

Seq. No.	391047
Contig ID	23641_1.R1084
5'-most EST	LIB3434-032-P1-K1-B12
Method	BLASTX

NCBI GI	g1778147
BLAST score	379
E value	3.0e-36
Match length	81
% identity	94
NCBI Description	(U66403) phosphate/phosphoenolpyruvate translocator precursor [Zea mays]

Seq. No.	391048
Contig ID	23645_1.R1084
5'-most EST	LIB3434-032-P1-K1-B5
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	40
% identity	61
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	391049
Contig ID	23647_1.R1084
5'-most EST	LIB3434-032-P1-K1-B8

Seq. No.	391050
Contig ID	23649_1.R1084
5'-most EST	uC-osflcyp120d09b1
Method	BLASTX
NCBI GI	g2493650
BLAST score	766
E value	1.0e-81
Match length	173
% identity	88
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale cereale]

Seq. No.	391051
Contig ID	23651_1.R1084
5'-most EST	LIB3434-032-P1-K1-C11
Method	BLASTX
NCBI GI	g2982445
BLAST score	149
E value	2.0e-09
Match length	31
% identity	81
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	391052
Contig ID	23661_1.R1084
5'-most EST	LIB3434-041-P1-K1-E6
Method	BLASTX
NCBI GI	g4454032
BLAST score	471
E value	5.0e-47
Match length	183
% identity	48

NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	391053
Contig ID	23663_2.R1084
5'-most EST	uC-osflm202106c01b1
Method	BLASTX
NCBI GI	g3882356
BLAST score	1132
E value	1.0e-124
Match length	263
% identity	79
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana]

Seq. No.	391054
Contig ID	23663_3.R1084
5'-most EST	uC-osflM202066b04b1
Method	BLASTX
NCBI GI	g4894182
BLAST score	474
E value	1.0e-75
Match length	172
% identity	80
NCBI Description	(AJ242551) 12-oxophytodienoate reductase [Lycopersicon esculentum]

Seq. No.	391055
Contig ID	23665_1.R1084
5'-most EST	LIB3434-035-P1-K1-G11
Method	BLASTX
NCBI GI	g4581162
BLAST score	544
E value	2.0e-55
Match length	119
% identity	88
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	391056
Contig ID	23683_1.R1084
5'-most EST	LIB3434-032-P1-K1-F1
Method	BLASTX
NCBI GI	g4538961
BLAST score	314
E value	2.0e-56
Match length	230
% identity	57
NCBI Description	(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis thaliana]

Seq. No.	391057
Contig ID	23685_1.R1084
5'-most EST	g2312394

Seq. No.	391058
Contig ID	23688_1.R1084
5'-most EST	uC-osroM202007g09b1

Seq. No.	391059
Contig ID	23689_1.R1084
5'-most EST	uC-osflcyp159e12b1
Method	BLASTX
NCBI GI	g2911044
BLAST score	288
E value	2.0e-30
Match length	219
% identity	41
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	391060
Contig ID	23689_2.R1084
5'-most EST	uC-osflcyp172f09b1

Seq. No.	391061
Contig ID	23692_1.R1084
5'-most EST	uC-osflcyp151g10b1

Seq. No.	391062
Contig ID	23698_1.R1084
5'-most EST	LIB3434-032-P1-K1-G3

Seq. No.	391063
Contig ID	23700_1.R1084
5'-most EST	g568338
Method	BLASTX
NCBI GI	g3360289
BLAST score	484
E value	1.0e-48
Match length	202
% identity	71
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	391064
Contig ID	23710_1.R1084
5'-most EST	LIB3434-032-P1-K1-H3
Method	BLASTX
NCBI GI	g3894197
BLAST score	922
E value	1.0e-99
Match length	229
% identity	71
NCBI Description	(AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391065
Contig ID	23711_1.R1084
5'-most EST	g286913
Method	BLASTX
NCBI GI	g1362152
BLAST score	839
E value	4.0e-90
Match length	235
% identity	74
NCBI Description	ribosomal protein S6 kinase homolog (clone Aspk11) - oat

>gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa]

Seq. No.	391066
Contig ID	23717_1.R1084
5'-most EST	g2798281
Method	BLASTX
NCBI GI	g4678323
BLAST score	417
E value	2.0e-40
Match length	265
% identity	37
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	391067
Contig ID	23721_1.R1084
5'-most EST	g5455519
Method	BLASTN
NCBI GI	g1732362
BLAST score	40
E value	8.0e-13
Match length	78
% identity	95
NCBI Description	Malus domestica pAFD103 mRNA, partial cds

Seq. No.	391068
Contig ID	23724_1.R1084
5'-most EST	LIB3434-033-P1-K1-A8
Method	BLASTX
NCBI GI	g1351359
BLAST score	241
E value	5.0e-20
Match length	69
% identity	67
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein - potato >gi_488712_emb_CAA55860_ (X79273) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	391069
Contig ID	23733_1.R1084
5'-most EST	LIB3434-033-P1-K1-B7
Method	BLASTX
NCBI GI	g3367537
BLAST score	158
E value	1.0e-10
Match length	70
% identity	41
NCBI Description	(AC004392) Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375. [Arabid

Seq. No.	391070
Contig ID	23746_1.R1084

5'-most EST	uC-osflm202104d08b1
Method	BLASTX
NCBI GI	g557474
BLAST score	218
E value	6.0e-18
Match length	209
% identity	31
NCBI Description	(U15179) ORF1 [Bacteroides ovatus]

Seq. No.	391071
Contig ID	23751_1.R1084
5'-most EST	g3767999

Seq. No.	391072
Contig ID	23753_1.R1084
5'-most EST	g572442
Method	BLASTN
NCBI GI	g2462784
BLAST score	42
E value	4.0e-14
Match length	155
% identity	35
NCBI Description	Streptococcus equi M-like protein (szPSe) gene, complete cds

Seq. No.	391073
Contig ID	23760_1.R1084
5'-most EST	g2431220

Seq. No.	391074
Contig ID	23760_2.R1084
5'-most EST	g3762291

Seq. No.	391075
Contig ID	23764_1.R1084
5'-most EST	g3761122

Seq. No.	391076
Contig ID	23771_1.R1084
5'-most EST	uC-osflcyp169f04b1
Method	BLASTX
NCBI GI	g1903021
BLAST score	1042
E value	1.0e-113
Match length	235
% identity	85
NCBI Description	(Y10216) hypothetical 3-isopropylmalate dehydrogenase [Arabidopsis thaliana]

Seq. No.	391077
Contig ID	23772_1.R1084
5'-most EST	LIB3434-033-P1-K1-F6
Method	BLASTX
NCBI GI	g4056494
BLAST score	429
E value	3.0e-42
Match length	120

% identity	66
NCBI Description	(AC005896) putative protein translocase [Arabidopsis thaliana]

Seq. No.	391078
Contig ID	23776_1.R1084
5'-most EST	LIB3434-033-P1-K1-G10
Method	BLASTX
NCBI GI	g3242705
BLAST score	517
E value	4.0e-52
Match length	216
% identity	71
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	391079
Contig ID	23790_1.R1084
5'-most EST	uC-osflM202016c09b1
Method	BLASTX
NCBI GI	g4336436
BLAST score	340
E value	1.0e-31
Match length	104
% identity	61
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	391080
Contig ID	23792_1.R1084
5'-most EST	g5038896
Method	BLASTX
NCBI GI	g2746086
BLAST score	176
E value	7.0e-21
Match length	67
% identity	84
NCBI Description	(AF025292) putative high-affinity potassium transporter [Hordeum vulgare]

Seq. No.	391081
Contig ID	23802_1.R1084
5'-most EST	g286310
Method	BLASTX
NCBI GI	g4587567
BLAST score	157
E value	6.0e-10
Match length	85
% identity	38
NCBI Description	(AC006550) F10O3.7 [Arabidopsis thaliana]

Seq. No.	391082
Contig ID	23808_1.R1084
5'-most EST	g5056116
Method	BLASTN
NCBI GI	g5410347
BLAST score	125
E value	3.0e-63

Match length	419
% identity	91
NCBI Description	Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No.	391083
Contig ID	23809_1.R1084
5'-most EST	LIB3434-034-P1-K1-B11

Seq. No.	391084
Contig ID	23812_1.R1084
5'-most EST	LIB3434-034-P1-K1-B3

Seq. No.	391085
Contig ID	23815_1.R1084
5'-most EST	uC-osroM202025b07b1
Method	BLASTX
NCBI GI	g1076821
BLAST score	1053
E value	1.0e-115
Match length	239
% identity	85
NCBI Description	probable 1-acyl-glycerol-3-phosphate acyltransferase - maize >gi_575960_emb_CAA82638_ (Z29518) 1-acyl-glycerol-3-phosphate acyltransferase (putative) [Zea mays]

Seq. No.	391086
Contig ID	23821_1.R1084
5'-most EST	LIB3434-034-P1-K1-C11

Seq. No.	391087
Contig ID	23825_1.R1084
5'-most EST	uC-osroM202020c12b1
Method	BLASTX
NCBI GI	g6056199
BLAST score	324
E value	7.0e-30
Match length	123
% identity	52
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	391088
Contig ID	23828_1.R1084
5'-most EST	LIB3434-034-P1-K1-C7

Seq. No.	391089
Contig ID	23829_1.R1084
5'-most EST	g426147
Method	BLASTX
NCBI GI	g4467359
BLAST score	550
E value	1.0e-90
Match length	188
% identity	84
NCBI Description	(AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

Seq. No.	391090
Contig ID	23830_1.R1084
5'-most EST	uC-osf1cyp162d08b1
Method	BLASTX
NCBI GI	g3513727
BLAST score	632
E value	6.0e-66
Match length	181
% identity	29
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	391091
Contig ID	23842_1.R1084
5'-most EST	LIB3434-034-P1-K1-E1
Method	BLASTX
NCBI GI	g4455250
BLAST score	364
E value	1.0e-34
Match length	153
% identity	40
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	391092
Contig ID	23850_1.R1084
5'-most EST	g2311744
Method	BLASTX
NCBI GI	g3927827
BLAST score	360
E value	4.0e-34
Match length	88
% identity	69
NCBI Description	(AC005727) osmotin-like protein precursor [Arabidopsis thaliana]

Seq. No.	391093
Contig ID	23854_4.R1084
5'-most EST	uC-osf1M202049e05b1

Seq. No.	391094
Contig ID	23858_1.R1084
5'-most EST	LIB3434-034-P1-K1-F2
Method	BLASTX
NCBI GI	g2811226
BLAST score	1081
E value	1.0e-118
Match length	281
% identity	37
NCBI Description	(AF042669) fimbrin 2 [Arabidopsis thaliana] >gi_2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]

Seq. No.	391095
Contig ID	23859_1.R1084
5'-most EST	uC-osroM202031b01b1

Method	BLASTX
NCBI GI	g5734756
BLAST score	326
E value	5.0e-30
Match length	164
% identity	42
NCBI Description	(AC007651) Similar to SOUL Protein [Arabidopsis thaliana]

Seq. No.	391096
Contig ID	23869_1.R1084
5'-most EST	LIB3475-008-P1-K1-B5
Method	BLASTX
NCBI GI	g1737492
BLAST score	682
E value	2.0e-74
Match length	195
% identity	29
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	391097
Contig ID	23880_1.R1084
5'-most EST	LIB3475-009-P1-K1-C7
Method	BLASTN
NCBI GI	g5777612
BLAST score	366
E value	0.0e+00
Match length	557
% identity	88
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	391098
Contig ID	23880_2.R1084
5'-most EST	LIB3477-001-P1-K1-A10
Method	BLASTN
NCBI GI	g4680189
BLAST score	39
E value	3.0e-12
Match length	67
% identity	91
NCBI Description	Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds

Seq. No.	391099
Contig ID	23880_3.R1084
5'-most EST	g3061018
Method	BLASTN
NCBI GI	g5777612
BLAST score	451
E value	0.0e+00
Match length	507
% identity	90
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	391100
Contig ID	23880_4.R1084

5'-most EST	g4879055
Method	BLASTN
NCBI GI	g5777612
BLAST score	179
E value	7.0e-96
Match length	315
% identity	84
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	391101
Contig ID	23880_5.R1084
5'-most EST	g3061024
Method	BLASTN
NCBI GI	g4680189
BLAST score	61
E value	1.0e-25
Match length	136
% identity	93
NCBI Description	Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds

Seq. No.	391102
Contig ID	23881_1.R1084
5'-most EST	uC-osflcyp175c12b1
Method	BLASTX
NCBI GI	g2493132
BLAST score	839
E value	5.0e-90
Match length	166
% identity	97
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B SUBUNIT) >gi_167110 (L11873) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No.	391103
Contig ID	23885_1.R1084
5'-most EST	LIB3434-034-P1-K1-H6
Method	BLASTX
NCBI GI	g2384717
BLAST score	207
E value	6.0e-16
Match length	133
% identity	33
NCBI Description	(AF015308) nucleolar protein [Homo sapiens]

Seq. No.	391104
Contig ID	23887_1.R1084
5'-most EST	LIB3434-034-P1-K1-H8
Method	BLASTX
NCBI GI	g3128218
BLAST score	546
E value	1.0e-63
Match length	181
% identity	72
NCBI Description	(AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No.	391105
Contig ID	23891_1.R1084
5'-most EST	g1944222
Method	BLASTX
NCBI GI	g1531541
BLAST score	462
E value	4.0e-46
Match length	159
% identity	52
NCBI Description	(D83391) uroporphyrinogen III methyltransferase [Zea mays]

Seq. No.	391106
Contig ID	23897_1.R1084
5'-most EST	g3760328
Method	BLASTN
NCBI GI	g5441876
BLAST score	116
E value	5.0e-58
Match length	152
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	391107
Contig ID	23903_1.R1084
5'-most EST	g2309678

Seq. No.	391108
Contig ID	23906_1.R1084
5'-most EST	uC-osf1cyp179f08b1
Method	BLASTX
NCBI GI	g2281085
BLAST score	308
E value	1.0e-30
Match length	136
% identity	55
NCBI Description	(AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]

Seq. No.	391109
Contig ID	23924_1.R1084
5'-most EST	g3761419
Method	BLASTX
NCBI GI	g5734732
BLAST score	218
E value	1.0e-19
Match length	67
% identity	70
NCBI Description	(AC007259) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	391110
Contig ID	23929_1.R1084
5'-most EST	LIB3434-035-P1-K1-D4
Method	BLASTX
NCBI GI	g2624417
BLAST score	770

E value	9.0e-82
Match length	146
% identity	96
NCBI Description	(AJ002959) Ubiquitin carrier protein [Zea mays]

Seq. No.	391111
Contig ID	23932_1.R1084
5'-most EST	LIB3434-035-P1-K1-D7

Seq. No.	391112
Contig ID	23935_1.R1084
5'-most EST	LIB3475-007-P1-K1-E7
Method	BLASTX
NCBI GI	g4584520
BLAST score	432
E value	2.0e-42
Match length	203
% identity	43
NCBI Description	(AL049607) enoyl-CoA hydratase-like protein [Arabidopsis thaliana]

Seq. No.	391113
Contig ID	23945_1.R1084
5'-most EST	LIB3434-035-P1-K1-E9
Method	BLASTX
NCBI GI	g6069666
BLAST score	221
E value	1.0e-22
Match length	109
% identity	56
NCBI Description	(AP000616) ESTs AU070998(R10588),D46106(S10554) correspond to a region of the predicted gene.; similar to Arabidopsis thaliana chromosome II BAC T6A23; unknown protein (AC005499) [Oryza sativa]

Seq. No.	391114
Contig ID	23953_1.R1084
5'-most EST	uC-osroM202029h05b1
Method	BLASTX
NCBI GI	g2832660
BLAST score	460
E value	9.0e-46
Match length	163
% identity	55
NCBI Description	(AL021710) lipase-like protein [Arabidopsis thaliana]

Seq. No.	391115
Contig ID	23955_1.R1084
5'-most EST	LIB3434-035-P1-K1-F7
Method	BLASTX
NCBI GI	g3695388
BLAST score	157
E value	3.0e-10
Match length	88
% identity	38
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	391116
Contig ID	23956_1.R1084
5'-most EST	LIB3434-035-P1-K1-F8

Seq. No.	391117
Contig ID	23958_1.R1084
5'-most EST	LIB3434-035-P1-K1-G10

Seq. No.	391118
Contig ID	23978_1.R1084
5'-most EST	LIB3434-035-P1-K1-H7
Method	BLASTN
NCBI GI	g2062705
BLAST score	36
E value	3.0e-10
Match length	36
% identity	38
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	391119
Contig ID	23986_1.R1084
5'-most EST	g572384
Method	BLASTX
NCBI GI	g5734636
BLAST score	290
E value	6.0e-51
Match length	193
% identity	53
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No.	391120
Contig ID	23992_1.R1084
5'-most EST	LIB3434-037-P1-K1-B7
Method	BLASTX
NCBI GI	g2213583
BLAST score	195
E value	9.0e-15
Match length	90
% identity	47
NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No.	391121
Contig ID	23994_1.R1084
5'-most EST	LIB3474-006-P1-K1-A12
Method	BLASTX
NCBI GI	g6017108
BLAST score	191
E value	3.0e-14
Match length	53
% identity	72
NCBI Description	(AC009895) unknown protein [Arabidopsis thaliana]

Seq. No.	391122
Contig ID	23995_1.R1084
5'-most EST	uC-osflm202109f11b1
Method	BLASTX

NCBI GI	g4415936
BLAST score	148
E value	9.0e-09
Match length	141
% identity	28
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana]

Seq. No.	391123
Contig ID	23997_1.R1084
5'-most EST	g1631617
Method	BLASTX
NCBI GI	g2894599
BLAST score	248
E value	4.0e-21
Match length	126
% identity	48
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	391124
Contig ID	23998_1.R1084
5'-most EST	g426215

Seq. No.	391125
Contig ID	24000_1.R1084
5'-most EST	g428941

Seq. No.	391126
Contig ID	24003_1.R1084
5'-most EST	uC-osrocyp002c06b1
Method	BLASTX
NCBI GI	g2668492
BLAST score	489
E value	4.0e-49
Match length	199
% identity	55
NCBI Description	(D89981) metal-transporting P-type ATPase [Arabidopsis thaliana]

Seq. No.	391127
Contig ID	24005_1.R1084
5'-most EST	uC-osf1M202040d09b1
Method	BLASTX
NCBI GI	g3892051
BLAST score	698
E value	1.0e-73
Match length	156
% identity	79
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]

Seq. No.	391128
Contig ID	24014_1.R1084
5'-most EST	LIB3479-004-Q6-K1-G12
Method	BLASTX
NCBI GI	g4104060
BLAST score	552
E value	3.0e-99

Match length	283
% identity	52
NCBI Description	(AF031231) S222 [Triticum aestivum]

Seq. No.	391129
Contig ID	24021_1.R1084
5'-most EST	uC-osflcyp106a10b1

Seq. No.	391130
Contig ID	24036_1.R1084
5'-most EST	LIB3434-037-P1-K1-G6

Seq. No.	391131
Contig ID	24037_1.R1084
5'-most EST	LIB3434-037-P1-K1-H1
Method	BLASTX
NCBI GI	g3702338
BLAST score	396
E value	1.0e-38
Match length	104
% identity	72
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	391132
Contig ID	24039_1.R1084
5'-most EST	g3766700
Method	BLASTX
NCBI GI	g5911685
BLAST score	286
E value	3.0e-25
Match length	77
% identity	66
NCBI Description	(Y11996) PRT1 protein [Nicotiana tabacum]

Seq. No.	391133
Contig ID	24039_2.R1084
5'-most EST	LIB3434-037-P1-K1-H10
Method	BLASTX
NCBI GI	g5911685
BLAST score	528
E value	7.0e-59
Match length	145
% identity	71
NCBI Description	(Y11996) PRT1 protein [Nicotiana tabacum]

Seq. No.	391134
Contig ID	24040_1.R1084
5'-most EST	g2442241

Seq. No.	391135
Contig ID	24043_1.R1084
5'-most EST	uC-osflcyp012a10b1
Method	BLASTN
NCBI GI	g5381221
BLAST score	86
E value	3.0e-40
Match length	90

% identity	99
NCBI Description	Oryza sativa rwc3 gene for water channel protein, 3'-terminal genomic region

Seq. No.	391136
Contig ID	24045_1.R1084
5'-most EST	LIB3434-037-P1-K1-H7

Seq. No.	391137
Contig ID	24051_1.R1084
5'-most EST	g3763283
Method	BLASTX
NCBI GI	g3402817
BLAST score	317
E value	7.0e-29
Match length	68
% identity	91
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	391138
Contig ID	24051_2.R1084
5'-most EST	g3763318
Method	BLASTX
NCBI GI	g2739219
BLAST score	245
E value	2.0e-20
Match length	51
% identity	98
NCBI Description	(AJ001161) rpS28 [Hordeum vulgare]

Seq. No.	391139
Contig ID	24055_1.R1084
5'-most EST	g2800817
Method	BLASTX
NCBI GI	g3746431
BLAST score	267
E value	3.0e-27
Match length	81
% identity	84
NCBI Description	(AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1 [Zea mays]

Seq. No.	391140
Contig ID	24055_2.R1084
5'-most EST	LIB3434-038-P1-K1-B1
Method	BLASTX
NCBI GI	g3746431
BLAST score	634
E value	4.0e-66
Match length	127
% identity	97
NCBI Description	(AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1 [Zea mays]

Seq. No.	391141
Contig ID	24058_1.R1084
5'-most EST	g2309901

Method	BLASTX
NCBI GI	g2245125
BLAST score	150
E value	4.0e-09
Match length	43
% identity	53
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391142
Contig ID	24060_1.R1084
5'-most EST	g2309671
Method	BLASTX
NCBI GI	g5103818
BLAST score	501
E value	2.0e-54
Match length	216
% identity	50
NCBI Description	(AC007591) Strong similarity to gi_4734005 F3L12.7 hypothetical protein from Arabidopsis thaliana BAC gb_AC007178

Seq. No.	391143
Contig ID	24081_1.R1084
5'-most EST	LIB3479-012-Q6-K1-A6

Seq. No.	391144
Contig ID	24094_1.R1084
5'-most EST	LIB3434-038-P1-K1-E6
Method	BLASTX
NCBI GI	g3335359
BLAST score	581
E value	4.0e-64
Match length	200
% identity	63
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	391145
Contig ID	24094_2.R1084
5'-most EST	g2428629
Method	BLASTX
NCBI GI	g3335359
BLAST score	327
E value	2.0e-30
Match length	112
% identity	55
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	391146
Contig ID	24095_1.R1084
5'-most EST	uC-osf1cyp013d02b1

Seq. No.	391147
Contig ID	24105_1.R1084
5'-most EST	g286437

Seq. No.	391148
Contig ID	24113_1.R1084

5'-most EST	uC-osrocyp034h02a1
Seq. No.	391149
Contig ID	24124_1.R1084
5'-most EST	uC-osflcyp179g02b1
Method	BLASTX
NCBI GI	g1076486
BLAST score	371
E value	2.0e-35
Match length	116
% identity	65
NCBI Description	cim1 protein - soybean >gi_555616 (U03860) cytokinin induced message [Glycine max]
Seq. No.	391150
Contig ID	24125_1.R1084
5'-most EST	uC-osflcyp026a10b1
Method	BLASTX
NCBI GI	g4914429
BLAST score	1083
E value	1.0e-118
Match length	284
% identity	71
NCBI Description	(AL050351) SEC14-like protein [Arabidopsis thaliana]
Seq. No.	391151
Contig ID	24131_1.R1084
5'-most EST	LIB3434-039-P1-K1-A12
Method	BLASTX
NCBI GI	g2281090
BLAST score	564
E value	6.0e-58
Match length	196
% identity	62
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]
Seq. No.	391152
Contig ID	24132_1.R1084
5'-most EST	g3760411
Seq. No.	391153
Contig ID	24136_1.R1084
5'-most EST	uC-osroM202038d03b1
Method	BLASTX
NCBI GI	g2641211
BLAST score	287
E value	3.0e-25
Match length	68
% identity	81
NCBI Description	(AF031547) histone-like protein [Fritillaria agrestis]
Seq. No.	391154
Contig ID	24144_1.R1084
5'-most EST	uC-osroM202021e05b1
Method	BLASTX
NCBI GI	g3641836
BLAST score	150

E value	2.0e-19
Match length	165
% identity	34
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	391155
Contig ID	24160_1.R1084
5'-most EST	g3719462
Method	BLASTX
NCBI GI	g3860277
BLAST score	707
E value	8.0e-90
Match length	217
% identity	78
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	391156
Contig ID	24160_2.R1084
5'-most EST	g2442273
Method	BLASTX
NCBI GI	g3860277
BLAST score	407
E value	1.0e-78
Match length	215
% identity	69
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	391157
Contig ID	24164_1.R1084
5'-most EST	LIB3434-039-P1-K1-D5
Method	BLASTX
NCBI GI	g2842486
BLAST score	458
E value	3.0e-45
Match length	132
% identity	70
NCBI Description	(AL021749) putative protein [Arabidopsis thaliana]

Seq. No.	391158
Contig ID	24179_1.R1084
5'-most EST	g3760675
Method	BLASTX
NCBI GI	g1173350
BLAST score	174
E value	3.0e-12
Match length	76
% identity	53
NCBI Description	DNA BINDING PROTEIN S1FA

Seq. No.	391159
Contig ID	24179_2.R1084
5'-most EST	g2428000

Method	BLASTN
NCBI GI	g4680189
BLAST score	58
E value	1.0e-23
Match length	83
% identity	93
NCBI Description	Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds

Seq. No.	391160
Contig ID	24181_1.R1084
5'-most EST	g5005503

Seq. No.	391161
Contig ID	24184_1.R1084
5'-most EST	LIB3434-039-P1-K1-F5

Seq. No.	391162
Contig ID	24193_1.R1084
5'-most EST	LIB3434-039-P1-K1-G2
Method	BLASTX
NCBI GI	g4914331
BLAST score	599
E value	4.0e-62
Match length	174
% identity	73
NCBI Description	(AC005489) F14N23.17 [Arabidopsis thaliana]

Seq. No.	391163
Contig ID	24194_1.R1084
5'-most EST	g2798697

Seq. No.	391164
Contig ID	24200_1.R1084
5'-most EST	uC-osrocyp004g06a1
Method	BLASTX
NCBI GI	g4115377
BLAST score	194
E value	1.0e-14
Match length	48
% identity	77
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	391165
Contig ID	24208_1.R1084
5'-most EST	g2427501
Method	BLASTX
NCBI GI	g5051781
BLAST score	276
E value	7.0e-40
Match length	194
% identity	48
NCBI Description	(AL078637) transport inhibitor response-like protein [Arabidopsis thaliana]

Seq. No.	391166
Contig ID	24217_1.R1084
5'-most EST	LIB3434-040-P1-K1-A7

Seq. No.	391167
Contig ID	24218_1.R1084
5'-most EST	LIB3434-040-P1-K1-A8
Method	BLASTX
NCBI GI	g5381253
BLAST score	653
E value	3.0e-68
Match length	173
% identity	73
NCBI Description	(AB027752) peroxidase [Nicotiana tabacum]

Seq. No.	391168
Contig ID	24221_1.R1084
5'-most EST	uC-osflcyp013f03b1
Method	BLASTX
NCBI GI	g6006879
BLAST score	992
E value	1.0e-108
Match length	261
% identity	74
NCBI Description	(AC008153) putative eukaryotic translation initiation factor 3 subunit [Arabidopsis thaliana]

Seq. No.	391169
Contig ID	24240_1.R1084
5'-most EST	LIB3434-040-P1-K1-C6
Method	BLASTX
NCBI GI	g2347098
BLAST score	880
E value	7.0e-95
Match length	254
% identity	66
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No.	391170
Contig ID	24245_1.R1084
5'-most EST	g3763303
Method	BLASTX
NCBI GI	g3402817
BLAST score	214
E value	1.0e-16
Match length	50
% identity	86
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	391171
Contig ID	24248_1.R1084
5'-most EST	uC-osflcyp085b02b1
Method	BLASTX
NCBI GI	g4589961
BLAST score	477

E value	3.0e-51
Match length	200
% identity	58
NCBI Description	(AC007169) unknown protein [Arabidopsis thaliana]

Seq. No.	391172
Contig ID	24251_1.R1084
5'-most EST	LIB3434-040-P1-K1-D5
Method	BLASTX
NCBI GI	g5262759
BLAST score	1144
E value	1.0e-126
Match length	260
% identity	82
NCBI Description	(AL080283) putative protein [Arabidopsis thaliana]

Seq. No.	391173
Contig ID	24263_1.R1084
5'-most EST	LIB3434-040-P1-K1-E6
Method	BLASTX
NCBI GI	g3702317
BLAST score	172
E value	5.0e-12
Match length	38
% identity	87
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana] >gi_4559376_gb_AAD23036.1_AC006526_1 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	391174
Contig ID	24271_1.R1084
5'-most EST	LIB3434-040-P1-K1-F3

Seq. No.	391175
Contig ID	24279_1.R1084
5'-most EST	g2442668
Method	BLASTX
NCBI GI	g1723231
BLAST score	131
E value	7.0e-13
Match length	128
% identity	36
NCBI Description	HYPOTHETICAL 27.1 KD PROTEIN C1D4.09C IN CHROMOSOME I >gi_1177342_emb_CAA93218.1_ (Z69239) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	391176
Contig ID	24283_1.R1084
5'-most EST	g5056092
Method	BLASTX
NCBI GI	g4938501
BLAST score	215
E value	7.0e-17
Match length	95
% identity	45
NCBI Description	(AL078465) putative protein [Arabidopsis thaliana]

Seq. No.	391177
Contig ID	24303_1.R1084
5'-most EST	LIB3434-041-P1-K1-A3
Method	BLASTX
NCBI GI	g4567314
BLAST score	170
E value	5.0e-18
Match length	71
% identity	69
NCBI Description	(AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391178
Contig ID	24304_1.R1084
5'-most EST	g5667315
Method	BLASTX
NCBI GI	g729704
BLAST score	192
E value	4.0e-14
Match length	79
% identity	8
NCBI Description	DNA-BINDING PROTEIN HEXBP (HEXAMER-BINDING PROTEIN) >gi_1078700_pir__A47156 hexamer-binding protein HEXBP - Leishmania major >gi_159342 (M94390) HEXBP DNA binding protein [Leishmania major]

Seq. No.	391179
Contig ID	24315_1.R1084
5'-most EST	LIB3475-009-P1-K1-C6

Seq. No.	391180
Contig ID	24322_1.R1084
5'-most EST	g3768145

Seq. No.	391181
Contig ID	24323_1.R1084
5'-most EST	LIB3434-041-P1-K1-C9

Seq. No.	391182
Contig ID	24324_1.R1084
5'-most EST	LIB3477-005-P1-K1-F7
Method	BLASTX
NCBI GI	g4490292
BLAST score	326
E value	5.0e-30
Match length	89
% identity	67
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	391183
Contig ID	24342_1.R1084
5'-most EST	LIB3475-012-P1-K1-C10
Method	BLASTX
NCBI GI	g4584525
BLAST score	874
E value	3.0e-94
Match length	204
% identity	78

NCBI Description	(AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	391184
Contig ID	24347_1.R1084
5'-most EST	LIB3434-041-P1-K1-F1
Method	BLASTX
NCBI GI	g5732705
BLAST score	424
E value	1.0e-41
Match length	111
% identity	75
NCBI Description	(AF159388) thioredoxin-like protein [Phalaris coerulescens] >gi_5732707_gb_AAD49234.1_AF159389_1 (AF159389) thioredoxin-like protein [Phalaris coerulescens]

Seq. No.	391185
Contig ID	24353_1.R1084
5'-most EST	g568983
Method	BLASTX
NCBI GI	g1196835
BLAST score	614
E value	2.0e-88
Match length	159
% identity	99
NCBI Description	(L76377) osmotin [Oryza sativa]

Seq. No.	391186
Contig ID	24354_1.R1084
5'-most EST	g5771107
Method	BLASTX
NCBI GI	g3882211
BLAST score	161
E value	9.0e-11
Match length	62
% identity	50
NCBI Description	(AB018288) KIAA0745 protein [Homo sapiens]

Seq. No.	391187
Contig ID	24372_1.R1084
5'-most EST	LIB3434-042-P1-K1-A12
Method	BLASTX
NCBI GI	g5031283
BLAST score	371
E value	3.0e-35
Match length	152
% identity	51
NCBI Description	(AF139500) unknown [Prunus armeniaca]

Seq. No.	391188
Contig ID	24374_1.R1084
5'-most EST	g5771089
Method	BLASTX
NCBI GI	g4895185
BLAST score	407
E value	1.0e-39
Match length	127

% identity	57
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No.	391189
Contig ID	24375_1.R1084
5'-most EST	LIB3434-042-P1-K1-A4
Method	BLASTX
NCBI GI	g5668814
BLAST score	457
E value	2.0e-45
Match length	148
% identity	58
NCBI Description	(AC007519) ESTs gb_H36253 and gb_AA04251 come from this gene. [Arabidopsis thaliana]

Seq. No.	391190
Contig ID	24390_1.R1084
5'-most EST	LIB3434-042-P1-K1-B8
Method	BLASTX
NCBI GI	g3452263
BLAST score	731
E value	3.0e-77
Match length	235
% identity	81
NCBI Description	(AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis thaliana]

Seq. No.	391191
Contig ID	24403_1.R1084
5'-most EST	LIB3434-042-P1-K1-D10

Seq. No.	391192
Contig ID	24405_1.R1084
5'-most EST	LIB3434-042-P1-K1-D12
Method	BLASTX
NCBI GI	g5689035
BLAST score	385
E value	9.0e-40
Match length	179
% identity	46
NCBI Description	(AB022053) prolyl oligopeptidase [Mus musculus]

Seq. No.	391193
Contig ID	24423_1.R1084
5'-most EST	LIB3434-042-P1-K1-E9
Method	BLASTX
NCBI GI	g6056194
BLAST score	121
E value	2.0e-14
Match length	102
% identity	43
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	391194
Contig ID	24426_1.R1084
5'-most EST	LIB3434-042-P1-K1-F11
Method	BLASTX

NCBI GI	g1617270
BLAST score	521
E value	7.0e-53
Match length	127
% identity	75
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	391195
Contig ID	24429_1.R1084
5'-most EST	g5004549
Method	BLASTX
NCBI GI	g4586056
BLAST score	224
E value	3.0e-18
Match length	149
% identity	36
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	391196
Contig ID	24434_1.R1084
5'-most EST	LIB3434-042-P1-K1-F9

Seq. No.	391197
Contig ID	24447_1.R1084
5'-most EST	g2863994

Seq. No.	391198
Contig ID	24450_1.R1084
5'-most EST	g3767528
Method	BLASTX
NCBI GI	g3033397
BLAST score	741
E value	2.0e-78
Match length	167
% identity	82
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	391199
Contig ID	24451_1.R1084
5'-most EST	LIB3434-042-P1-K1-H3
Method	BLASTX
NCBI GI	g4586049
BLAST score	534
E value	3.0e-54
Match length	217
% identity	43
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391200
Contig ID	24559_1.R1084
5'-most EST	LIB3474-001-P1-K1-A11
Method	BLASTX
NCBI GI	g2586083
BLAST score	174
E value	2.0e-12
Match length	78
% identity	50

NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	391201
Contig ID	24567_1.R1084
5'-most EST	g4879179
Method	BLASTX
NCBI GI	g2809238
BLAST score	275
E value	4.0e-24
Match length	83
% identity	57
NCBI Description	(AC002560) F21B7.7 [Arabidopsis thaliana]

Seq. No.	391202
Contig ID	24570_1.R1084
5'-most EST	LIB3474-001-P1-K1-B12
Method	BLASTX
NCBI GI	g1346840
BLAST score	689
E value	9.0e-73
Match length	130
% identity	100
NCBI Description	PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN) (PHOTOSYSTEM II PROTEIN D1) >gi_1363615_pir__S58531 photosystem II protein D1 - maize chloroplast >gi_902201_emb_CAA60265_ (X86563) PSII 32 KDa protein [Zea mays]

Seq. No.	391203
Contig ID	24572_1.R1084
5'-most EST	LIB3474-001-P1-K1-B3
Method	BLASTX
NCBI GI	g1169736
BLAST score	741
E value	5.0e-80
Match length	265
% identity	59
NCBI Description	FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN) >gi_1083778_pir__A54837 rapamycin/FKBP12 target 1 - rat >gi_511229 (U11681) rapamycin and FKBP12 target-1 protein [Rattus norvegicus] >gi_561858 (L37085) rapamycin target [Rattus norvegicus]

Seq. No.	391204
Contig ID	24575_1.R1084
5'-most EST	g4715426
Method	BLASTX
NCBI GI	g4678345
BLAST score	154
E value	1.0e-09
Match length	143
% identity	26
NCBI Description	(AL049659) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	391205

Contig ID	24579_1.R1084
5'-most EST	LIB3474-001-P1-K1-C1

Seq. No.	391206
Contig ID	24581_1.R1084
5'-most EST	LIB3474-001-P1-K1-C11

Seq. No.	391207
Contig ID	24591_1.R1084
5'-most EST	LIB3474-001-P1-K1-D1
Method	BLASTX
NCBI GI	g2674203
BLAST score	640
E value	6.0e-67
Match length	149
% identity	88
NCBI Description	(AF036328) CLP protease regulatory subunit CLPX [Arabidopsis thaliana]

Seq. No.	391208
Contig ID	24613_1.R1084
5'-most EST	uC-osf1M202051c05b1

Seq. No.	391209
Contig ID	24618_1.R1084
5'-most EST	LIB3474-001-P1-K1-F5
Method	BLASTX
NCBI GI	g3152559
BLAST score	222
E value	6.0e-18
Match length	52
% identity	77
NCBI Description	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No.	391210
Contig ID	24622_1.R1084
5'-most EST	uC-osf1cyp009d10b1
Method	BLASTX
NCBI GI	g3096910
BLAST score	373
E value	2.0e-35
Match length	119
% identity	61
NCBI Description	(AJ005813) neoxanthin cleavage enzyme [Arabidopsis thaliana]

Seq. No.	391211
Contig ID	24623_1.R1084
5'-most EST	uC-osf1M202095f01b1
Method	BLASTX
NCBI GI	g3202030
BLAST score	295
E value	1.0e-26
Match length	98
% identity	62

NCBI Description	(AF069318) geranylgeranyl hydrogenase [Mesembryanthemum crystallinum]

Seq. No.	391212
Contig ID	24629_1.R1084
5'-most EST	g2309646

Seq. No.	391213
Contig ID	24660_1.R1084
5'-most EST	LIB3475-009-P1-K1-H12
Method	BLASTX
NCBI GI	g4938503
BLAST score	346
E value	2.0e-32
Match length	176
% identity	32
NCBI Description	(AL078465) hnRNP-like protein [Arabidopsis thaliana]

Seq. No.	391214
Contig ID	24666_1.R1084
5'-most EST	uC-osflcyp014a01b1
Method	BLASTX
NCBI GI	g1170029
BLAST score	422
E value	2.0e-41
Match length	88
% identity	91
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_100581_pir__A35789 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - barley >gi_506383 (M31545) glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]

Seq. No.	391215
Contig ID	24679_1.R1084
5'-most EST	LIB3474-002-P1-K1-D10

Seq. No.	391216
Contig ID	24684_1.R1084
5'-most EST	g426510

Seq. No.	391217
Contig ID	24687_1.R1084
5'-most EST	LIB3474-002-P1-K1-D9

Seq. No.	391218
Contig ID	24690_1.R1084
5'-most EST	LIB3474-002-P1-K1-E11
Method	BLASTX
NCBI GI	g81601
BLAST score	513
E value	5.0e-52
Match length	154
% identity	72
NCBI Description	chaperonin 60 beta - Arabidopsis thaliana

Seq. No.	391219

Contig ID	24693_1.R1084
5'-most EST	uC-osroM202018g11b1
Seq. No.	391220
Contig ID	24702_1.R1084
5'-most EST	LIB3474-002-P1-K1-F12
Method	BLASTN
NCBI GI	g5852170
BLAST score	275
E value	1.0e-153
Match length	362
% identity	99
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804
Seq. No.	391221
Contig ID	24705_1.R1084
5'-most EST	LIB3474-002-P1-K1-F4
Method	BLASTX
NCBI GI	g2088648
BLAST score	230
E value	7.0e-19
Match length	65
% identity	60
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana]
Seq. No.	391222
Contig ID	24706_1.R1084
5'-most EST	LIB3474-002-P1-K1-F5
Method	BLASTX
NCBI GI	g285741
BLAST score	233
E value	8.0e-19
Match length	181
% identity	32
NCBI Description	(D14550) EDGP precursor [Daucus carota]
Seq. No.	391223
Contig ID	24711_1.R1084
5'-most EST	uC-osflcyp029e03a1
Method	BLASTN
NCBI GI	g2245377
BLAST score	35
E value	1.0e-09
Match length	83
% identity	86
NCBI Description	Arabidopsis thaliana auxin response factor 1 (ARF1) mRNA, complete cds
Seq. No.	391224
Contig ID	24713_1.R1084
5'-most EST	uC-osflM202043h01b1
Method	BLASTX
NCBI GI	g461532
BLAST score	432
E value	1.0e-42
Match length	112

% identity	67
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1362500_pir__D49993 ADP-ribosylation factor - Ajellomyces capsulata >gi_407693 (L25117) ADP-ribosylation factor [Histoplasma capsulatum]

Seq. No.	391225
Contig ID	24716_1.R1084
5'-most EST	LIB3474-002-P1-K1-G4
Method	BLASTX
NCBI GI	g4938484
BLAST score	322
E value	2.0e-29
Match length	205
% identity	43
NCBI Description	(AL078464) transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	391226
Contig ID	24729_1.R1084
5'-most EST	LIB3474-002-P1-K1-H6
Method	BLASTX
NCBI GI	g2190550
BLAST score	393
E value	5.0e-38
Match length	152
% identity	55
NCBI Description	(AC001229) ESTs gb_T45673,gb_N37512 come from this gene. [Arabidopsis thaliana]

Seq. No.	391227
Contig ID	24743_1.R1084
5'-most EST	LIB3475-008-P1-K1-H3
Method	BLASTN
NCBI GI	g6015437
BLAST score	34
E value	2.0e-09
Match length	38
% identity	97
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	391228
Contig ID	24747_1.R1084
5'-most EST	LIB3474-003-P1-K1-B11
Method	BLASTX
NCBI GI	g4585976
BLAST score	664
E value	2.0e-69
Match length	174
% identity	69
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	391229
Contig ID	24751_1.R1084
5'-most EST	LIB3474-003-P1-K1-B4
Method	BLASTX
NCBI GI	g4508069
BLAST score	639

E value	2.0e-66
Match length	214
% identity	57
NCBI Description	(AC005882) 12246 [Arabidopsis thaliana]

Seq. No.	391230
Contig ID	24752_1.R1084
5'-most EST	uC-osflm202113a11b1
Method	BLASTX
NCBI GI	g4679028
BLAST score	192
E value	7.0e-19
Match length	94
% identity	49
NCBI Description	(AF077207) HSPC021 [Homo sapiens] >gi_5106781_gb_AAD39841.1_ (AF083243) HSPC025 [Homo sapiens]

Seq. No.	391231
Contig ID	24752_2.R1084
5'-most EST	LIB3474-003-P1-K1-B5
Method	BLASTX
NCBI GI	g4679028
BLAST score	280
E value	1.0e-24
Match length	116
% identity	48
NCBI Description	(AF077207) HSPC021 [Homo sapiens] >gi_5106781_gb_AAD39841.1_ (AF083243) HSPC025 [Homo sapiens]

Seq. No.	391232
Contig ID	24752_3.R1084
5'-most EST	uC-osflM202020a05b1
Method	BLASTX
NCBI GI	g4679028
BLAST score	220
E value	9.0e-22
Match length	125
% identity	44
NCBI Description	(AF077207) HSPC021 [Homo sapiens] >gi_5106781_gb_AAD39841.1_ (AF083243) HSPC025 [Homo sapiens]

Seq. No.	391233
Contig ID	24757_1.R1084
5'-most EST	uC-osflcyp078g01b1

Seq. No.	391234
Contig ID	24767_1.R1084
5'-most EST	g572151
Method	BLASTX
NCBI GI	g3914005
BLAST score	511
E value	7.0e-52
Match length	119
% identity	87

NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays]
Seq. No.	391235
Contig ID	24769_1.R1084
5'-most EST	uC-osflcyp155b09b1
Method	BLASTX
NCBI GI	g4960156
BLAST score	283
E value	5.0e-25
Match length	104
% identity	53
NCBI Description	(AF153284) putative progesterone-binding protein homolog [Arabidopsis thaliana]
Seq. No.	391236
Contig ID	24773_1.R1084
5'-most EST	LIB3474-003-P1-K1-D4
Seq. No.	391237
Contig ID	24774_1.R1084
5'-most EST	g4879045
Method	BLASTX
NCBI GI	g4835765
BLAST score	436
E value	5.0e-43
Match length	126
% identity	67
NCBI Description	(AC007202) Is a member of the PF_00171 aldehyde dehydrogenase family. ESTs gb_T21534, gb_N65241 and gb_AA395614 come from this gene. [Arabidopsis thaliana]
Seq. No.	391238
Contig ID	24777_1.R1084
5'-most EST	LIB3474-003-P1-K1-D9
Seq. No.	391239
Contig ID	24786_1.R1084
5'-most EST	LIB3474-003-P1-K1-E7
Seq. No.	391240
Contig ID	24787_1.R1084
5'-most EST	LIB3474-003-P1-K1-E8
Seq. No.	391241
Contig ID	24794_1.R1084
5'-most EST	LIB3474-003-P1-K1-F4
Method	BLASTX
NCBI GI	g2245004
BLAST score	399
E value	1.0e-38
Match length	143
% identity	55
NCBI Description	(Z97341) membrane transporter like protein [Arabidopsis thaliana]
Seq. No.	391242

Contig ID	24806_1.R1084
5'-most EST	LIB3474-003-P1-K1-G4
Method	BLASTX
NCBI GI	g3413717
BLAST score	180
E value	1.0e-12
Match length	49
% identity	73
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi_3643590 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	391243
Contig ID	24807_1.R1084
5'-most EST	uC-osf1M2020114d07a1

Seq. No.	391244
Contig ID	24813_1.R1084
5'-most EST	uC-osf1m202108f10b1
Method	BLASTX
NCBI GI	g1168609
BLAST score	437
E value	4.0e-43
Match length	133
% identity	64
NCBI Description	AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir__S35071 auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana] >gi_448755_prf__1917337A ubiquitin-activating enzyme E1 [Arabidopsis thaliana]

Seq. No.	391245
Contig ID	24824_1.R1084
5'-most EST	LIB3474-004-P1-K1-A2
Method	BLASTX
NCBI GI	g476752
BLAST score	588
E value	5.0e-87
Match length	213
% identity	77
NCBI Description	(L24073) rubisco large subunit [Oryza sativa] >gi_1583954_prf__2121489A RuBisCO:SUBUNIT=large:ISOTYPE=truncated [Oryza sativa]

Seq. No.	391246
Contig ID	24829_1.R1084
5'-most EST	LIB3474-004-P1-K1-A9

Seq. No.	391247
Contig ID	24831_1.R1084
5'-most EST	LIB3474-004-P1-K1-B12
Method	BLASTX
NCBI GI	g2130024
BLAST score	256
E value	5.0e-22

Match length	82
% identity	71
NCBI Description	DNA-binding protein ABF2 - wild oat >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]

Seq. No.	391248
Contig ID	24837_1.R1084
5'-most EST	g4715583

Seq. No.	391249
Contig ID	24846_1.R1084
5'-most EST	LIB3474-004-P1-K1-C9

Seq. No.	391250
Contig ID	24863_1.R1084
5'-most EST	g702358

Seq. No.	391251
Contig ID	24864_1.R1084
5'-most EST	g428427
Method	BLASTX
NCBI GI	g5262202
BLAST score	364
E value	1.0e-34
Match length	116
% identity	60
NCBI Description	(AL080252) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	391252
Contig ID	24866_1.R1084
5'-most EST	uC-osflcyp108f10b1
Method	BLASTX
NCBI GI	g4512667
BLAST score	548
E value	7.0e-56
Match length	139
% identity	75
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	391253
Contig ID	24867_1.R1084
5'-most EST	uC-osrocyp009c12b1

Seq. No.	391254
Contig ID	24868_1.R1084
5'-most EST	LIB3474-004-P1-K1-F10

Seq. No.	391255
Contig ID	24878_1.R1084
5'-most EST	LIB3474-004-P1-K1-G2
Method	BLASTN
NCBI GI	g5822826
BLAST score	86
E value	2.0e-40
Match length	117
% identity	65

NCBI Description	Oryza sativa D1 gene for alpha-subunit of GTP-binding protein, wild type, partial sequence
Seq. No.	391256
Contig ID	24884_1.R1084
5'-most EST	uC-osflm202101e06b1
Method	BLASTX
NCBI GI	g3292814
BLAST score	213
E value	7.0e-17
Match length	45
% identity	89
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	391257
Contig ID	24888_1.R1084
5'-most EST	g569028
Seq. No.	391258
Contig ID	24893_1.R1084
5'-most EST	LIB3479-009-Q6-K1-F10
Method	BLASTX
NCBI GI	g399942
BLAST score	853
E value	1.0e-152
Match length	324
% identity	85
NCBI Description	CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN PRECURSOR >gi_421881_pir__S32818 heat shock protein, 70K, chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi_871515_emb_CAA49147_ (X69213) Psst70 (stress 70 protein) [Pisum sativum]
Seq. No.	391259
Contig ID	24899_1.R1084
5'-most EST	uC-osflcyp055e08b1
Seq. No.	391260
Contig ID	24901_1.R1084
5'-most EST	g4879712
Seq. No.	391261
Contig ID	24903_1.R1084
5'-most EST	g700911
Method	BLASTX
NCBI GI	g4895239
BLAST score	153
E value	5.0e-10
Match length	57
% identity	58
NCBI Description	(AC007659) hypothetical protein [Arabidopsis thaliana]
Seq. No.	391262
Contig ID	24912_1.R1084
5'-most EST	uC-osflM202123f04b1
Method	BLASTX
NCBI GI	g3785989

BLAST score	601
E value	2.0e-62
Match length	131
% identity	87
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	391263
Contig ID	24913_1.R1084
5'-most EST	LIB3479-001-Q6-K2-A8
Method	BLASTX
NCBI GI	g465763
BLAST score	456
E value	4.0e-45
Match length	235
% identity	44
NCBI Description	HYPOTHETICAL 70.9 KD PROTEIN C06G4.2 IN CHROMOSOME III >gi_630525_pir__S44749 C06G4.2 protein - Caenorhabditis elegans >gi_409293 (L25598) homology with calpain; putative [Caenorhabditis elegans]

Seq. No.	391264
Contig ID	24914_1.R1084
5'-most EST	g3761426

Seq. No.	391265
Contig ID	24918_1.R1084
5'-most EST	LIB3474-005-P1-K1-C1
Method	BLASTX
NCBI GI	g3913732
BLAST score	165
E value	3.0e-11
Match length	138
% identity	37
NCBI Description	HYDROXYACYLGLUTATHIONE HYDROLASE MITOCHONDRIAL ISOZYME PRECURSOR (GLYOXALASE II) (GLX II) >gi_2570340 (U90928) glyoxalase II mitochondrial isozyme [Arabidopsis thaliana]

Seq. No.	391266
Contig ID	24953_1.R1084
5'-most EST	g2317552
Method	BLASTX
NCBI GI	g4699942
BLAST score	537
E value	1.0e-97
Match length	297
% identity	62
NCBI Description	(AC007166) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	391267
Contig ID	24955_1.R1084
5'-most EST	LIB3474-005-P1-K1-G1

Seq. No.	391268
Contig ID	24957_1.R1084
5'-most EST	LIB3474-005-P1-K1-G12
Method	BLASTX

NCBI GI	g5689035
BLAST score	559
E value	1.0e-57
Match length	143
% identity	68
NCBI Description	(AB022053) prolyl oligopeptidase [Mus musculus]

Seq. No.	391269
Contig ID	24959_1.R1084
5'-most EST	g2443078
Method	BLASTX
NCBI GI	g3319776
BLAST score	348
E value	4.0e-43
Match length	125
% identity	77
NCBI Description	(AJ007665) seryl-tRNA synthetase [Zea mays]

Seq. No.	391270
Contig ID	24959_2.R1084
5'-most EST	LIB3477-009-P1-K1-B5
Method	BLASTX
NCBI GI	g3319776
BLAST score	183
E value	6.0e-14
Match length	46
% identity	78
NCBI Description	(AJ007665) seryl-tRNA synthetase [Zea mays]

Seq. No.	391271
Contig ID	24962_1.R1084
5'-most EST	LIB3477-002-P1-K1-C3
Method	BLASTX
NCBI GI	g400986
BLAST score	226
E value	2.0e-18
Match length	64
% identity	69
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_81947_pir__S18001 ribosomal protein L15 precursor, chloroplast - garden pea (fragment) >gi_20867_emb_CAA77595_ (Z11510) Plastid ribosomal protein CL15 [Pisum sativum]

Seq. No.	391272
Contig ID	24984_1.R1084
5'-most EST	g2310588
Method	BLASTX
NCBI GI	g5734639
BLAST score	575
E value	4.0e-59
Match length	113
% identity	100
NCBI Description	(AP000391) ESTs AU056036(S20239),C72753(E2173), AU056035(S20239) correspond to a region of the predicted gene.; Similar to putative cytochrome P-450 (AC003680) [Oryza sativa]

Seq. No.	391273
Contig ID	24987_1.R1084
5'-most EST	LIB3474-006-P1-K1-B11
Method	BLASTX
NCBI GI	g3080412
BLAST score	271
E value	1.0e-23
Match length	154
% identity	37
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	391274
Contig ID	24989_1.R1084
5'-most EST	LIB3474-006-P1-K1-B12
Method	BLASTN
NCBI GI	g5042437
BLAST score	41
E value	2.0e-13
Match length	137
% identity	64
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	391275
Contig ID	24990_1.R1084
5'-most EST	LIB3474-006-P1-K1-B2
Method	BLASTX
NCBI GI	g3059061
BLAST score	149
E value	6.0e-09
Match length	198
% identity	24
NCBI Description	(AL022401) dJ93L7.1 (RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein) [Homo sapiens]

Seq. No.	391276
Contig ID	24991_1.R1084
5'-most EST	uC-osf1M202052b07b1
Method	BLASTX
NCBI GI	g1705678
BLAST score	588
E value	7.0e-61
Match length	134
% identity	86
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No.	391277
Contig ID	24992_1.R1084
5'-most EST	g4714144

Seq. No.	391278
Contig ID	24996_1.R1084
5'-most EST	uC-osf1M202064h01a1
Method	BLASTX

NCBI GI	g4972052
BLAST score	230
E value	6.0e-19
Match length	57
% identity	41
NCBI Description	(AL078470) putative protein [Arabidopsis thaliana]

Seq. No.	391279
Contig ID	25003_1.R1084
5'-most EST	uC-osrocyp007h07b1
Method	BLASTX
NCBI GI	g2500036
BLAST score	939
E value	1.0e-102
Match length	219
% identity	80
NCBI Description	DIHYDROOROTASE PRECURSOR (DHOASE) >gi_2121273 (AF000146) dihydroorotase [Arabidopsis thaliana] >gi_3292818_emb_CAA19808.1_ (AL031018) dihydroorotase [Arabidopsis thaliana]

Seq. No.	391280
Contig ID	25008_1.R1084
5'-most EST	LIB3474-006-P1-K1-C9

Seq. No.	391281
Contig ID	25014_1.R1084
5'-most EST	LIB3474-006-P1-K1-D3

Seq. No.	391282
Contig ID	25018_1.R1084
5'-most EST	LIB3474-008-P1-K1-G2
Method	BLASTX
NCBI GI	g4337192
BLAST score	363
E value	4.0e-35
Match length	151
% identity	54
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391283
Contig ID	25020_1.R1084
5'-most EST	g2310148
Method	BLASTX
NCBI GI	g3080433
BLAST score	290
E value	1.0e-46
Match length	151
% identity	63
NCBI Description	(AL022605) putative gamma-glutamyltransferase [Arabidopsis thaliana]

Seq. No.	391284
Contig ID	25033_1.R1084
5'-most EST	g5607610
Method	BLASTX
NCBI GI	g5453379

BLAST score	513
E value	8.0e-52
Match length	179
% identity	54
NCBI Description	(AF155124) bacterial-induced peroxidase precursor [Gossypium hirsutum]

Seq. No.	391285
Contig ID	25052_1.R1084
5'-most EST	uC-osflcyp172e06b1

Seq. No.	391286
Contig ID	25058_1.R1084
5'-most EST	LIB3477-009-P1-K1-E8
Method	BLASTX
NCBI GI	g1743412
BLAST score	307
E value	6.0e-30
Match length	92
% identity	76
NCBI Description	(Y09826) amino acid transporter [Solanum tuberosum]

Seq. No.	391287
Contig ID	25062_1.R1084
5'-most EST	LIB3474-007-P1-K1-A10
Method	BLASTX
NCBI GI	g2289010
BLAST score	220
E value	1.0e-17
Match length	45
% identity	84
NCBI Description	(AC002335) FKBP type peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No.	391288
Contig ID	25065_1.R1084
5'-most EST	LIB3475-004-P1-K2-F2
Method	BLASTX
NCBI GI	g4468798
BLAST score	461
E value	5.0e-46
Match length	145
% identity	63
NCBI Description	(AJ010440) GST7 protein [Zea mays]

Seq. No.	391289
Contig ID	25074_1.R1084
5'-most EST	LIB3474-007-P1-K1-B12
Method	BLASTX
NCBI GI	g4544449
BLAST score	286
E value	2.0e-25
Match length	82
% identity	67
NCBI Description	(AC006592) putative peroxidase [Arabidopsis thaliana]

Seq. No.	391290

Contig ID 25092_1.R1084
5'-most EST LIB3474-007-P1-K1-C7
Method BLASTX
NCBI GI g3386546
BLAST score 391
E value 1.0e-37
Match length 154
% identity 53
NCBI Description (AF079503) H-protein promoter binding factor-2a [Arabidopsis thaliana]

Seq. No. 391291
Contig ID 25105_1.R1084
5'-most EST uC-osflm202110h08b1
Method BLASTX
NCBI GI g3044214
BLAST score 1256
E value 1.0e-150
Match length 330
% identity 78
NCBI Description (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No. 391292
Contig ID 25115_1.R1084
5'-most EST LIB3474-007-P1-K1-F10
Method BLASTX
NCBI GI g6006801
BLAST score 412
E value 5.0e-40
Match length 110
% identity 69
NCBI Description (AF156783) apyrase [Arabidopsis thaliana]

Seq. No. 391293
Contig ID 25120_1.R1084
5'-most EST LIB3474-007-P1-K1-F4
Method BLASTX
NCBI GI g5080800
BLAST score 186
E value 4.0e-20
Match length 136
% identity 38
NCBI Description (AC007576) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 391294
Contig ID 25122_1.R1084
5'-most EST g4878367
Method BLASTX
NCBI GI g6041824
BLAST score 168
E value 2.0e-11
Match length 95
% identity 41
NCBI Description (AC009918) hypothetical protein [Arabidopsis thaliana]

Seq. No. 391295
Contig ID 25125_1.R1084

09660-4609 "09660-4609

5'-most EST	LIB3477-004-P1-K1-B10
Method	BLASTX
NCBI GI	g3169174
BLAST score	326
E value	4.0e-30
Match length	121
% identity	50
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	391296
Contig ID	25130_1.R1084
5'-most EST	g3768305
Method	BLASTX
NCBI GI	g3702323
BLAST score	260
E value	3.0e-22
Match length	102
% identity	45
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	391297
Contig ID	25131_1.R1084
5'-most EST	LIB3474-007-P1-K1-G5

Seq. No.	391298
Contig ID	25132_1.R1084
5'-most EST	g4879977
Method	BLASTX
NCBI GI	g4680491
BLAST score	722
E value	1.0e-102
Match length	198
% identity	92
NCBI Description	(AF119222) hypothetical protein [Oryza sativa]

Seq. No.	391299
Contig ID	25147_1.R1084
5'-most EST	uC-osflcyp155d10b1

Seq. No.	391300
Contig ID	25148_1.R1084
5'-most EST	uC-osroM202030b03b1
Method	BLASTX
NCBI GI	g2244813
BLAST score	425
E value	2.0e-41
Match length	233
% identity	49
NCBI Description	(Z97336) acylaminoacyl-peptidase like protein [Arabidopsis thaliana]

Seq. No.	391301
Contig ID	25154_1.R1084
5'-most EST	uC-osflcyp123e02b1
Method	BLASTX
NCBI GI	g5922612

BLAST score	776
E value	1.0e-118
Match length	450
% identity	51
NCBI Description	(AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa]

Seq. No.	391302
Contig ID	25157_1.R1084
5'-most EST	uC-osroM202018b02b1
Method	BLASTX
NCBI GI	g4206195
BLAST score	184
E value	2.0e-13
Match length	48
% identity	65
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391303
Contig ID	25161_1.R1084
5'-most EST	uC-osflcyp041g11b1

Seq. No.	391304
Contig ID	25162_1.R1084
5'-most EST	LIB3474-008-P1-K1-B7
Method	BLASTX
NCBI GI	g5107831
BLAST score	475
E value	3.0e-47
Match length	302
% identity	11
NCBI Description	(AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]

Seq. No.	391305
Contig ID	25165_1.R1084
5'-most EST	LIB3474-008-P1-K1-C1

Seq. No.	391306
Contig ID	25170_1.R1084
5'-most EST	g572228
Method	BLASTX
NCBI GI	g3885328
BLAST score	276
E value	4.0e-24
Match length	84
% identity	61
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 391307

Contig ID	25175_1.R1084
5'-most EST	LIB3474-008-P1-K1-C8
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	36
% identity	59
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	391308
Contig ID	25178_2.R1084
5'-most EST	g4880033

Seq. No.	391309
Contig ID	25183_1.R1084
5'-most EST	uC-osrocyp015g12a1
Method	BLASTX
NCBI GI	g130718
BLAST score	345
E value	2.0e-32
Match length	119
% identity	58
NCBI Description	ACID PHOSPHATASE PRECURSOR 1 >gi_170370 (M83211) acid phosphatase type 1 [Lycopersicon esculentum] >gi_170372 (M67474) acid phosphatase type 5 [Lycopersicon esculentum] >gi_445121_prf__1908427A acid phosphatase 1 [Lycopersicon esculentum]

Seq. No.	391310
Contig ID	25184_1.R1084
5'-most EST	uC-osflcyp092a10b1
Method	BLASTX
NCBI GI	g5006857
BLAST score	235
E value	1.0e-19
Match length	61
% identity	77
NCBI Description	(AF145730) homeodomain leucine zipper protein [Oryza sativa]

Seq. No.	391311
Contig ID	25193_1.R1084
5'-most EST	LIB3474-008-P1-K1-E9

Seq. No.	391312
Contig ID	25203_1.R1084
5'-most EST	g3548923

Seq. No.	391313
Contig ID	25224_1.R1084
5'-most EST	LIB3474-008-P1-K1-H7
Method	BLASTX
NCBI GI	g4426964
BLAST score	579
E value	1.0e-59
Match length	157

% identity	68
NCBI Description	(AF126255) purple acid phosphatase precursor [Anchusa officinalis]

Seq. No.	391314
Contig ID	25231_1.R1084
5'-most EST	g701194
Method	BLASTX
NCBI GI	g3928088
BLAST score	290
E value	8.0e-26
Match length	107
% identity	53
NCBI Description	(AC005770) putative peroxidase [Arabidopsis thaliana]

Seq. No.	391315
Contig ID	25244_1.R1084
5'-most EST	LIB3474-012-P1-K1-H3

Seq. No.	391316
Contig ID	25251_1.R1084
5'-most EST	uC-osrocyp013e05b1

Seq. No.	391317
Contig ID	25266_1.R1084
5'-most EST	g2800252
Method	BLASTX
NCBI GI	g4468980
BLAST score	418
E value	7.0e-41
Match length	116
% identity	68
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	391318
Contig ID	25271_1.R1084
5'-most EST	LIB3477-004-P1-K1-E8
Method	BLASTX
NCBI GI	g4115377
BLAST score	325
E value	5.0e-30
Match length	88
% identity	75
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	391319
Contig ID	25273_1.R1084
5'-most EST	LIB3474-009-P1-K1-E10

Seq. No.	391320
Contig ID	25275_2.R1084
5'-most EST	g426648

Seq. No.	391321
Contig ID	25279_1.R1084
5'-most EST	LIB3474-009-P1-K1-E5
Method	BLASTN

NCBI GI	g6015437
BLAST score	37
E value	3.0e-11
Match length	39
% identity	61
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	391322
Contig ID	25283_1.R1084
5'-most EST	LIB3474-009-P1-K1-E9
Method	BLASTX
NCBI GI	g2598575
BLAST score	241
E value	1.0e-26
Match length	88
% identity	72
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	391323
Contig ID	25285_1.R1084
5'-most EST	g2311519

Seq. No.	391324
Contig ID	25287_1.R1084
5'-most EST	uC-osflcyp106e02b1
Method	BLASTX
NCBI GI	g4138343
BLAST score	971
E value	1.0e-122
Match length	327
% identity	66
NCBI Description	(AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]

Seq. No.	391325
Contig ID	25290_1.R1084
5'-most EST	uC-osflM202050f11b1

Seq. No.	391326
Contig ID	25297_1.R1084
5'-most EST	LIB3474-009-P1-K1-G11

Seq. No.	391327
Contig ID	25300_1.R1084
5'-most EST	uC-osroM202041c06b1
Method	BLASTX
NCBI GI	g2435519
BLAST score	1047
E value	1.0e-123
Match length	353
% identity	65
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	391328
Contig ID	25310_1.R1084
5'-most EST	uC-osrocyp032h08b1

Method	BLASTN
NCBI GI	g4959460
BLAST score	36
E value	2.0e-10
Match length	36
% identity	38
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	391329
Contig ID	25314_1.R1084
5'-most EST	LIB3474-009-P1-K1-H8

Seq. No.	391330
Contig ID	25322_1.R1084
5'-most EST	g3760914
Method	BLASTX
NCBI GI	g4850384
BLAST score	536
E value	2.0e-54
Match length	129
% identity	71
NCBI Description	(AC007357) F3F19.3 [Arabidopsis thaliana]

Seq. No.	391331
Contig ID	25337_1.R1084
5'-most EST	uC-osflcyp014c01b1
Method	BLASTX
NCBI GI	g531389
BLAST score	229
E value	8.0e-19
Match length	112
% identity	44
NCBI Description	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq. No.	391332
Contig ID	25339_1.R1084
5'-most EST	LIB3474-010-P1-K1-C9
Method	BLASTX
NCBI GI	g4827060
BLAST score	280
E value	9.0e-25
Match length	105
% identity	51
NCBI Description	xylulokinase (H. influenzae) homolog >gi_3298502_dbj_BAA31527_ (AB015046) xylulokinase [Homo sapiens]

Seq. No.	391333
Contig ID	25345_1.R1084
5'-most EST	g287250
Method	BLASTX
NCBI GI	g2632105
BLAST score	1048
E value	1.0e-114
Match length	258
% identity	77

NCBI Description	(Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana] >gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.	391334
Contig ID	25352_1.R1084
5'-most EST	LIB3474-010-P1-K1-E7
Seq. No.	391335
Contig ID	25359_1.R1084
5'-most EST	LIB3474-010-P1-K1-F7
Seq. No.	391336
Contig ID	25363_1.R1084
5'-most EST	LIB3474-010-P1-K1-G11
Seq. No.	391337
Contig ID	25369_1.R1084
5'-most EST	LIB3474-010-P1-K1-G8
Method	BLASTN
NCBI GI	g6015437
BLAST score	34
E value	4.0e-09
Match length	40
% identity	60
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	391338
Contig ID	25375_1.R1084
5'-most EST	g1631822
Method	BLASTX
NCBI GI	g3928150
BLAST score	442
E value	4.0e-50
Match length	129
% identity	82
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]
Seq. No.	391339
Contig ID	25381_1.R1084
5'-most EST	LIB3474-011-P1-K1-A4
Seq. No.	391340
Contig ID	25387_1.R1084
5'-most EST	LIB3474-011-P1-K1-B10
Method	BLASTX
NCBI GI	g3522929
BLAST score	776
E value	6.0e-83
Match length	153
% identity	95
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.	391341
Contig ID	25393_1.R1084

Docket No. 9660.4000-00

5'-most EST	LIB3474-011-P1-K1-B6
Seq. No.	391342
Contig ID	25396_1.R1084
5'-most EST	g428267
Seq. No.	391343
Contig ID	25409_1.R1084
5'-most EST	LIB3474-011-P1-K1-D10
Method	BLASTX
NCBI GI	g1174470
BLAST score	534
E value	2.0e-54
Match length	187
% identity	56
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]
Seq. No.	391344
Contig ID	25412_1.R1084
5'-most EST	LIB3474-011-P1-K1-D2
Method	BLASTN
NCBI GI	g175854
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	O.sativa 28S large subunit rRNA, 5' end
Seq. No.	391345
Contig ID	25414_1.R1084
5'-most EST	g4968864
Seq. No.	391346
Contig ID	25415_1.R1084
5'-most EST	LIB3474-011-P1-K1-D6
Seq. No.	391347
Contig ID	25419_1.R1084
5'-most EST	g286930
Seq. No.	391348
Contig ID	25422_1.R1084
5'-most EST	uC-osf1cyp034b10b1
Method	BLASTX
NCBI GI	g3980378
BLAST score	870
E value	1.0e-125
Match length	249
% identity	84
NCBI Description	(AC004561) putative RNA binding protein [Arabidopsis thaliana]
Seq. No.	391349
Contig ID	25425_1.R1084

5'-most EST	g2428001
Seq. No.	391350
Contig ID	25426_1.R1084
5'-most EST	LIB3474-011-P1-K1-E7
Method	BLASTX
NCBI GI	g2244771
BLAST score	340
E value	2.0e-36
Match length	124
% identity	58
NCBI Description	(Z97335) kinesin like protein [Arabidopsis thaliana]
Seq. No.	391351
Contig ID	25429_1.R1084
5'-most EST	g3090523
Method	BLASTX
NCBI GI	g1418990
BLAST score	150
E value	3.0e-09
Match length	63
% identity	51
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]
Seq. No.	391352
Contig ID	25447_1.R1084
5'-most EST	g2310233
Method	BLASTX
NCBI GI	g2058456
BLAST score	660
E value	1.0e-130
Match length	289
% identity	81
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]
Seq. No.	391353
Contig ID	25449_1.R1084
5'-most EST	g5005494
Method	BLASTX
NCBI GI	g3063444
BLAST score	196
E value	6.0e-15
Match length	73
% identity	52
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana] >gi_4973256_gb_AAD35005.1_AF144387_1 (AF144387) thioredoxin-like 1 [Arabidopsis thaliana]
Seq. No.	391354
Contig ID	25465_1.R1084
5'-most EST	LIB3474-012-P1-K1-A5
Seq. No.	391355
Contig ID	25476_1.R1084
5'-most EST	g2310198

Method	BLASTX
NCBI GI	g3150415
BLAST score	305
E value	1.0e-27
Match length	108
% identity	36
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	391356
Contig ID	25490_1.R1084
5'-most EST	LIB3474-012-P1-K1-C8
Method	BLASTX
NCBI GI	g3327957
BLAST score	152
E value	8.0e-10
Match length	48
% identity	58
NCBI Description	(AF060490) TLS-associated protein TASR-2 [Mus musculus] >gi_3327976 (AF067730) TLS-associated protein TASR-2 [Homo sapiens]

Seq. No.	391357
Contig ID	25493_1.R1084
5'-most EST	g5003707
Method	BLASTN
NCBI GI	g5803242
BLAST score	79
E value	5.0e-36
Match length	359
% identity	87
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	391358
Contig ID	25505_1.R1084
5'-most EST	g4880939
Method	BLASTX
NCBI GI	g4519671
BLAST score	334
E value	7.0e-31
Match length	163
% identity	42
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No.	391359
Contig ID	25518_1.R1084
5'-most EST	g5701335

Seq. No.	391360
Contig ID	25519_1.R1084
5'-most EST	LIB3474-012-P1-K1-F5
Method	BLASTX
NCBI GI	g3080442
BLAST score	209
E value	1.0e-16
Match length	66

% identity	56
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]
Seq. No.	391361
Contig ID	25520_1.R1084
5'-most EST	LIB3474-012-P1-K1-F6
Seq. No.	391362
Contig ID	25528_1.R1084
5'-most EST	LIB3474-012-P1-K1-G2
Seq. No.	391363
Contig ID	25529_1.R1084
5'-most EST	LIB3474-012-P1-K1-G3
Method	BLASTX
NCBI GI	g2735764
BLAST score	146
E value	4.0e-09
Match length	37
% identity	76
NCBI Description	(AF008651) MADS transcriptional factor; STMADS16 [Solanum tuberosum]
Seq. No.	391364
Contig ID	25531_1.R1084
5'-most EST	g2799775
Method	BLASTX
NCBI GI	g4105798
BLAST score	844
E value	3.0e-99
Match length	239
% identity	60
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.	391365
Contig ID	25531_2.R1084
5'-most EST	LIB3599-001-P1-K6-F3
Method	BLASTX
NCBI GI	g4105798
BLAST score	840
E value	3.0e-90
Match length	200
% identity	63
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.	391366
Contig ID	25534_1.R1084
5'-most EST	LIB3474-012-P1-K1-H1
Method	BLASTX
NCBI GI	g3047124
BLAST score	279
E value	6.0e-26
Match length	120
% identity	53
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	391367

Contig ID 25541_1.R1084
5'-most EST g5002884

Seq. No. 391368
Contig ID 25545_1.R1084
5'-most EST jC-osleLIB3474037a02a1
Method BLASTX
NCBI GI g1170619
BLAST score 471
E value 5.0e-47
Match length 108
% identity 83
NCBI Description KINESIN-LIKE PROTEIN A >gi_479594_pir__S34830 kinesin-related protein katA - Arabidopsis thaliana >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor protein heavy chain [Arabidopsis thaliana] >gi_2911084_emb_CAA17546.1_ (AL021960) kinesin-related protein katA [Arabidopsis thaliana]

Seq. No. 391369
Contig ID 25547_1.R1084
5'-most EST jC-osleLIB3474037a04a1

Seq. No. 391370
Contig ID 25552_1.R1084
5'-most EST jC-osleLIB3474037a09a1
Method BLASTX
NCBI GI g2104691
BLAST score 235
E value 4.0e-19
Match length 147
% identity 37
NCBI Description (U92794) alpha glucosidase II, beta subunit [Mus musculus]

Seq. No. 391371
Contig ID 25554_1.R1084
5'-most EST uC-osroM202020e03a1
Method BLASTX
NCBI GI g2062169
BLAST score 335
E value 4.0e-31
Match length 106
% identity 42
NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No. 391372
Contig ID 25556_1.R1084
5'-most EST g2317583
Method BLASTX
NCBI GI g2252830
BLAST score 218
E value 3.0e-17
Match length 113
% identity 43
NCBI Description (AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana] >gi_6049872_gb_AAF02787.1_AF195115_7

09854605.3.0.0

(AF195115) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	391373
Contig ID	25559_1.R1084
5'-most EST	g4714132
Method	BLASTX
NCBI GI	g1345946
BLAST score	427
E value	1.0e-41
Match length	101
% identity	78
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III PRECURSOR (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) >gi_541820_pir__JQ2386 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) III precursor, chloroplast - spinach >gi_311686_emb_CAA80452_ (Z22771) 3-ketoacyl-acyl carrier protein synthase III (KAS III) [Spinacia oleracea]

Seq. No.	391374
Contig ID	25574_1.R1084
5'-most EST	jC-osleLIB3474037c11a1
Method	BLASTX
NCBI GI	g4185139
BLAST score	420
E value	5.0e-41
Match length	112
% identity	66
NCBI Description	(AC005724) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	391375
Contig ID	25578_1.R1084
5'-most EST	jC-osleLIB3474037d03a1

Seq. No.	391376
Contig ID	25586_1.R1084
5'-most EST	jC-osleLIB3474037f09a1
Method	BLASTX
NCBI GI	g4325342
BLAST score	170
E value	1.0e-11
Match length	38
% identity	79
NCBI Description	(AF128393) No definition line found [Arabidopsis thaliana]

Seq. No.	391377
Contig ID	25592_1.R1084
5'-most EST	jC-osleLIB3474037e08a1
Method	BLASTX
NCBI GI	g5081555
BLAST score	248
E value	4.0e-27
Match length	189
% identity	31
NCBI Description	(AF132001) PHAP2A protein [Petunia x hybrida]

Seq. No.	391378
Contig ID	25594_1.R1084
5'-most EST	uC-osflcyp096g11a1
Method	BLASTX
NCBI GI	g2454182
BLAST score	765
E value	6.0e-81
Match length	348
% identity	63
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	391379
Contig ID	25600_1.R1084
5'-most EST	g5900758
Method	BLASTX
NCBI GI	g3402282
BLAST score	172
E value	1.0e-11
Match length	104
% identity	41
NCBI Description	(AJ000997) proline-rich protein [Solanum tuberosum]

Seq. No.	391380
Contig ID	25600_2.R1084
5'-most EST	g3762219
Method	BLASTX
NCBI GI	g3402282
BLAST score	173
E value	8.0e-12
Match length	113
% identity	39
NCBI Description	(AJ000997) proline-rich protein [Solanum tuberosum]

Seq. No.	391381
Contig ID	25600_3.R1084
5'-most EST	g3762406

Seq. No.	391382
Contig ID	25600_4.R1084
5'-most EST	g5056143
Method	BLASTX
NCBI GI	g3402282
BLAST score	187
E value	2.0e-13
Match length	147
% identity	37
NCBI Description	(AJ000997) proline-rich protein [Solanum tuberosum]

Seq. No.	391383
Contig ID	25600_5.R1084
5'-most EST	uC-osflcyp153h09b1

Seq. No.	391384
Contig ID	25626_1.R1084
5'-most EST	uC-osflcyp156b05a1

Seq. No.	391385
Contig ID	25636_1.R1084
5'-most EST	uC-osflm202110g10b1
Method	BLASTX
NCBI GI	g4522009
BLAST score	370
E value	6.0e-35
Match length	131
% identity	58
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	391386
Contig ID	25639_1.R1084
5'-most EST	LIB3475-001-P1-K2-B6
Method	BLASTX
NCBI GI	g4469023
BLAST score	670
E value	3.0e-70
Match length	223
% identity	64
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	391387
Contig ID	25640_1.R1084
5'-most EST	uC-osrocyp028b05a1

Seq. No.	391388
Contig ID	25647_1.R1084
5'-most EST	LIB3475-001-P1-K2-C4

Seq. No.	391389
Contig ID	25650_1.R1084
5'-most EST	LIB3475-001-P1-K2-C7
Method	BLASTX
NCBI GI	g2827631
BLAST score	443
E value	2.0e-67
Match length	231
% identity	58
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	391390
Contig ID	25677_1.R1084
5'-most EST	LIB3475-001-P1-K2-F5
Method	BLASTN
NCBI GI	g20177
BLAST score	34
E value	2.0e-09
Match length	54
% identity	91
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	391391
Contig ID	25681_1.R1084
5'-most EST	uC-osrocyp016h08b1
Method	BLASTX

NCBI GI	g2708624
BLAST score	467
E value	1.0e-46
Match length	128
% identity	67
NCBI Description	(AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	391392
Contig ID	25685_1.R1084
5'-most EST	LIB3475-001-P1-K2-G4
Method	BLASTX
NCBI GI	g2661412
BLAST score	684
E value	6.0e-72
Match length	192
% identity	70
NCBI Description	(AJ000728) MAP kinase kinase [Lycopersicon esculentum]

Seq. No.	391393
Contig ID	25687_1.R1084
5'-most EST	uC-osflcyp157h12b1

Seq. No.	391394
Contig ID	25688_1.R1084
5'-most EST	LIB3475-001-P1-K2-G7
Method	BLASTX
NCBI GI	g2244749
BLAST score	603
E value	1.0e-62
Match length	155
% identity	74
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	391395
Contig ID	25691_1.R1084
5'-most EST	LIB3475-001-P1-K2-H2

Seq. No.	391396
Contig ID	25698_1.R1084
5'-most EST	g3761395
Method	BLASTX
NCBI GI	g1055161
BLAST score	140
E value	2.0e-17
Match length	150
% identity	25
NCBI Description	(U40029) Contains similarity to Pfam domain: PF00567 (TUDOR), Score=62.7, E-value=2.5e-15, N=1 [Caenorhabditis elegans]

Seq. No.	391397
Contig ID	25702_1.R1084
5'-most EST	g5039087

Seq. No.	391398
Contig ID	25707_1.R1084
5'-most EST	g699879

Seq. No.	391399
Contig ID	25708_1.R1084
5'-most EST	uC-osroM202036h04b1

Seq. No.	391400
Contig ID	25714_1.R1084
5'-most EST	uC-osflm202101c12b1

Seq. No.	391401
Contig ID	25719_1.R1084
5'-most EST	LIB3475-002-P1-K2-C11
Method	BLASTX
NCBI GI	g4544443
BLAST score	170
E value	6.0e-12
Match length	35
% identity	94
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	391402
Contig ID	25730_1.R1084
5'-most EST	g572243
Method	BLASTX
NCBI GI	g4678332
BLAST score	250
E value	3.0e-21
Match length	117
% identity	43
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	391403
Contig ID	25735_1.R1084
5'-most EST	LIB3475-002-P1-K2-D9

Seq. No.	391404
Contig ID	25736_1.R1084
5'-most EST	uC-osrocyp031d02b1
Method	BLASTX
NCBI GI	g4587525
BLAST score	276
E value	4.0e-24
Match length	105
% identity	53
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	391405
Contig ID	25742_1.R1084
5'-most EST	g426569

Seq. No.	391406
Contig ID	25744_1.R1084

5'-most EST	LIB3475-002-P1-K2-E6
Method	BLASTX
NCBI GI	g4512702
BLAST score	596
E value	9.0e-62
Match length	178
% identity	65
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391407
Contig ID	25747_1.R1084
5'-most EST	LIB3475-002-P1-K2-F1

Seq. No.	391408
Contig ID	25753_1.R1084
5'-most EST	LIB3475-002-P1-K2-F4
Method	BLASTX
NCBI GI	g4835242
BLAST score	302
E value	5.0e-27
Match length	264
% identity	34
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	391409
Contig ID	25755_2.R1084
5'-most EST	LIB3475-002-P1-K2-F6

Seq. No.	391410
Contig ID	25780_1.R1084
5'-most EST	LIB3475-002-P1-K2-H9
Method	BLASTX
NCBI GI	g4325372
BLAST score	218
E value	2.0e-17
Match length	103
% identity	46
NCBI Description	(AF128396) contains similarity to protein disulfide isomerases [Arabidopsis thaliana]

Seq. No.	391411
Contig ID	25787_1.R1084
5'-most EST	LIB3475-003-P1-K2-A6
Method	BLASTX
NCBI GI	g4704613
BLAST score	534
E value	2.0e-54
Match length	126
% identity	77
NCBI Description	(AF109695) monodehydroascorbate reductase [Brassica juncea]

Seq. No.	391412
Contig ID	25788_1.R1084
5'-most EST	LIB3475-003-P1-K2-A8

Seq. No.	391413
Contig ID	25792_1.R1084

5'-most EST	g568984
Method	BLASTN
NCBI GI	g4512233
BLAST score	415
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Oryza sativa copia-type retrotransposon RIRE7 DNA, partial sequence

Seq. No.	391414
Contig ID	25796_1.R1084
5'-most EST	LIB3475-003-P1-K2-B4

Seq. No.	391415
Contig ID	25797_1.R1084
5'-most EST	LIB3477-007-P1-K1-B1
Method	BLASTX
NCBI GI	g1350625
BLAST score	165
E value	3.0e-11
Match length	56
% identity	64
NCBI Description	50S RIBOSOMAL PROTEIN L1, CHLOROPLAST PRECURSOR >gi_577089_emb_CAA58020_ (X82776) chloroplast ribosomal protein L1 [Pisum sativum]

Seq. No.	391416
Contig ID	25807_1.R1084
5'-most EST	LIB3475-003-P1-K2-C4
Method	BLASTX
NCBI GI	g3941480
BLAST score	155
E value	4.0e-10
Match length	46
% identity	63
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	391417
Contig ID	25807_2.R1084
5'-most EST	g5055999
Method	BLASTX
NCBI GI	g1488647
BLAST score	171
E value	9.0e-12
Match length	68
% identity	47
NCBI Description	(X99937) RNA helicase [Spinacia oleracea]

Seq. No.	391418
Contig ID	25826_1.R1084
5'-most EST	LIB3475-003-P1-K2-E11
Method	BLASTX
NCBI GI	g3885968
BLAST score	573
E value	7.0e-59

Match length	146
% identity	76
NCBI Description	(AF100985) phosphopyruvate hydratase [Penaeus monodon]

Seq. No.	391419
Contig ID	25829_1.R1084
5'-most EST	g2443070
Method	BLASTX
NCBI GI	g1888357
BLAST score	266
E value	3.0e-38
Match length	305
% identity	32
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	391420
Contig ID	25833_1.R1084
5'-most EST	LIB3475-003-P1-K2-F1

Seq. No.	391421
Contig ID	25835_1.R1084
5'-most EST	LIB3475-003-P1-K2-F11

Seq. No.	391422
Contig ID	25838_1.R1084
5'-most EST	uC-osf1M202094h05b1

Seq. No.	391423
Contig ID	25846_2.R1084
5'-most EST	uC-osf1cyp075g03b1
Method	BLASTX
NCBI GI	g5231113
BLAST score	365
E value	1.0e-34
Match length	201
% identity	38
NCBI Description	(AF141202) EIN2 [Arabidopsis thaliana] >gi_5231115_gb_AAD41077.1_AF141203_1 (AF141203) EIN2 [Arabidopsis thaliana]

Seq. No.	391424
Contig ID	25851_1.R1084
5'-most EST	g4969212
Method	BLASTX
NCBI GI	g3184082
BLAST score	418
E value	2.0e-58
Match length	351
% identity	38
NCBI Description	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]

Seq. No.	391425
Contig ID	25857_1.R1084
5'-most EST	LIB3479-001-Q6-K1-G11

Seq. No.	391426
Contig ID	25857_2.R1084
5'-most EST	LIB3475-003-P1-K2-H3

Seq. No.	391427
Contig ID	25860_1.R1084
5'-most EST	LIB3475-003-P1-K2-H7
Method	BLASTX
NCBI GI	g4538911
BLAST score	143
E value	1.0e-08
Match length	76
% identity	46
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391428
Contig ID	25862_1.R1084
5'-most EST	uC-osroM202025c05b1
Method	BLASTX
NCBI GI	g1353516
BLAST score	439
E value	3.0e-43
Match length	174
% identity	49
NCBI Description	(U38651) sugar transporter [Medicago truncatula]

Seq. No.	391429
Contig ID	25866_1.R1084
5'-most EST	g6025170
Method	BLASTX
NCBI GI	g3021508
BLAST score	607
E value	8.0e-63
Match length	177
% identity	69
NCBI Description	(AJ001769) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	391430
Contig ID	25874_1.R1084
5'-most EST	LIB3475-004-P1-K2-B10
Method	BLASTX
NCBI GI	g3258569
BLAST score	129
E value	5.0e-14
Match length	98
% identity	49
NCBI Description	(U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]

Seq. No.	391431
Contig ID	25884_1.R1084
5'-most EST	g5055964
Method	BLASTX
NCBI GI	g4545130
BLAST score	150

E value	2.0e-09
Match length	54
% identity	50
NCBI Description	(AF091326) histone deacetylase [Plasmodium falciparum]

Seq. No.	391432
Contig ID	25890_1.R1084
5'-most EST	g3762740

Seq. No.	391433
Contig ID	25901_1.R1084
5'-most EST	LIB3475-004-P1-K2-D5

Seq. No.	391434
Contig ID	25912_1.R1084
5'-most EST	LIB3475-004-P1-K2-E9
Method	BLASTX
NCBI GI	g2129825
BLAST score	347
E value	2.0e-32
Match length	120
% identity	59
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No.	391435
Contig ID	25914_1.R1084
5'-most EST	uC-osflcyp172h06b1
Method	BLASTX
NCBI GI	g2827551
BLAST score	193
E value	3.0e-14
Match length	144
% identity	44
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	391436
Contig ID	25918_1.R1084
5'-most EST	g4880206

Seq. No.	391437
Contig ID	25929_1.R1084
5'-most EST	g3760073
Method	BLASTX
NCBI GI	g2829911
BLAST score	1001
E value	1.0e-108
Match length	334
% identity	59
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	391438
Contig ID	25932_1.R1084
5'-most EST	uC-osflm202099a07b1
Method	BLASTX
NCBI GI	g6041792
BLAST score	885

E value	2.0e-95
Match length	218
% identity	79
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]

Seq. No.	391439
Contig ID	25934_1.R1084
5'-most EST	LIB3475-004-P1-K2-H10
Method	BLASTN
NCBI GI	g5730046
BLAST score	33
E value	1.0e-08
Match length	40
% identity	67
NCBI Description	Homo sapiens solute carrier family 17 (sodium phosphate), member 3 (SLC17A3) mRNA >gi_2062691_gb_U90545_HSU90545 Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No.	391440
Contig ID	25935_1.R1084
5'-most EST	LIB3475-004-P1-K2-H11

Seq. No.	391441
Contig ID	25942_1.R1084
5'-most EST	LIB3475-004-P1-K2-H9
Method	BLASTX
NCBI GI	g2398679
BLAST score	274
E value	5.0e-24
Match length	53
% identity	96
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	391442
Contig ID	25959_1.R1084
5'-most EST	LIB3475-005-P1-K1-B2
Method	BLASTX
NCBI GI	g3550661
BLAST score	216
E value	4.0e-17
Match length	91
% identity	29
NCBI Description	(AJ001310) 39 kDa EF-Hand containing protein [Solanum tuberosum]

Seq. No.	391443
Contig ID	25967_1.R1084
5'-most EST	uC-osroM202005g10b1

Seq. No.	391444
Contig ID	25977_1.R1084
5'-most EST	g3761298

Seq. No.	391445
Contig ID	25981_1.R1084

5'-most EST	g5455318
Method	BLASTX
NCBI GI	g2979552
BLAST score	285
E value	4.0e-25
Match length	67
% identity	76
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	391446
Contig ID	25985_1.R1084
5'-most EST	uC-osroM202031e12b1

Seq. No.	391447
Contig ID	25992_1.R1084
5'-most EST	g4879110
Method	BLASTX
NCBI GI	g3426064
BLAST score	188
E value	6.0e-14
Match length	138
% identity	35
NCBI Description	(AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]

Seq. No.	391448
Contig ID	26003_1.R1084
5'-most EST	LIB3475-005-P1-K1-F3
Method	BLASTX
NCBI GI	g4914419
BLAST score	160
E value	1.0e-10
Match length	52
% identity	73
NCBI Description	(AL050352) putative protein [Arabidopsis thaliana]

Seq. No.	391449
Contig ID	26004_1.R1084
5'-most EST	uC-osroM202034g07b1
Method	BLASTX
NCBI GI	g4895219
BLAST score	224
E value	5.0e-18
Match length	106
% identity	47
NCBI Description	(AC007660) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391450
Contig ID	26006_1.R1084
5'-most EST	g3462541
Method	BLASTX
NCBI GI	g3334276
BLAST score	1188
E value	1.0e-131
Match length	424
% identity	57

NCBI Description	AUTOANTIGEN NGP-1 >gi_179285_gb_AAC37588.1_ (L05425) nucleolar GTPase [Homo sapiens]

Seq. No.	391451
Contig ID	26006_2.R1084
5'-most EST	uC-osflcyp110b05a1

Seq. No.	391452
Contig ID	26017_1.R1084
5'-most EST	LIB3475-005-P1-K1-H1
Method	BLASTX
NCBI GI	g3402684
BLAST score	318
E value	5.0e-33
Match length	113
% identity	63
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391453
Contig ID	26021_1.R1084
5'-most EST	LIB3477-010-P1-K1-A5
Method	BLASTX
NCBI GI	g4587562
BLAST score	582
E value	4.0e-60
Match length	124
% identity	86
NCBI Description	(AC006550) Belongs to PF_00583 Acetyltransfersase (GNAT) family. [Arabidopsis thaliana]

Seq. No.	391454
Contig ID	26023_1.R1084
5'-most EST	LIB3475-005-P1-K1-H4
Method	BLASTX
NCBI GI	g5816992
BLAST score	224
E value	4.0e-18
Match length	63
% identity	67
NCBI Description	(AL110123) putative protein [Arabidopsis thaliana]

Seq. No.	391455
Contig ID	26024_1.R1084
5'-most EST	g3061108
Method	BLASTX
NCBI GI	g3927831
BLAST score	799
E value	2.0e-98
Match length	264
% identity	68
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	391456
Contig ID	26025_1.R1084
5'-most EST	LIB3475-005-P1-K1-H6
Method	BLASTX

NCBI GI	g3860333
BLAST score	382
E value	1.0e-36
Match length	100
% identity	66
NCBI Description	(AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No.	391457
Contig ID	26033_1.R1084
5'-most EST	LIB3475-006-P1-K1-A3

Seq. No.	391458
Contig ID	26037_1.R1084
5'-most EST	uC-osrocyp015b04b1
Method	BLASTX
NCBI GI	g3264767
BLAST score	194
E value	1.0e-14
Match length	52
% identity	69
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	391459
Contig ID	26038_1.R1084
5'-most EST	g5667342

Seq. No.	391460
Contig ID	26039_1.R1084
5'-most EST	LIB3475-006-P1-K1-B10
Method	BLASTN
NCBI GI	g1245938
BLAST score	33
E value	6.0e-09
Match length	33
% identity	62
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	391461
Contig ID	26047_1.R1084
5'-most EST	g2443059
Method	BLASTX
NCBI GI	g1711508
BLAST score	427
E value	6.0e-42
Match length	119
% identity	76
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 1 (SRP54) >gi_1020000 (L48284) signal recognition particle 54 kDa subunit [Hordeum vulgare]

Seq. No.	391462
Contig ID	26057_1.R1084
5'-most EST	g2311109

Seq. No.	391463
Contig ID	26059_1.R1084

5'-most EST	LIB3475-006-P1-K1-C9
Method	BLASTX
NCBI GI	g5281034
BLAST score	620
E value	1.0e-82
Match length	177
% identity	81
NCBI Description	(AL080318) putative protein [Arabidopsis thaliana]

Seq. No.	391464
Contig ID	26060_1.R1084
5'-most EST	LIB3475-006-P1-K1-D10
Method	BLASTX
NCBI GI	g2062164
BLAST score	379
E value	2.0e-36
Match length	140
% identity	32
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	391465
Contig ID	26061_1.R1084
5'-most EST	g2312644
Method	BLASTX
NCBI GI	g5453129
BLAST score	190
E value	3.0e-14
Match length	92
% identity	42
NCBI Description	(AF107838) 26S proteasome subunit p40.5 [Mus musculus]

Seq. No.	391466
Contig ID	26063_1.R1084
5'-most EST	LIB3475-006-P1-K1-D2
Method	BLASTX
NCBI GI	g3860688
BLAST score	156
E value	6.0e-10
Match length	167
% identity	34
NCBI Description	(AJ235270) unknown [Rickettsia prowazekii]

Seq. No.	391467
Contig ID	26064_1.R1084
5'-most EST	LIB3475-006-P1-K1-D3

Seq. No.	391468
Contig ID	26066_1.R1084
5'-most EST	g2310671
Method	BLASTX
NCBI GI	g4580575
BLAST score	350
E value	3.0e-57
Match length	211
% identity	60
NCBI Description	(AF082176) auxin response factor 9 [Arabidopsis thaliana]

>gi_4972102_emb_CAB43898.1_ (AL078468) auxin response factor 9 (ARF9) [Arabidopsis thaliana]

Seq. No.	391469
Contig ID	26070_1.R1084
5'-most EST	LIB3479-007-Q6-K1-D11
Method	BLASTX
NCBI GI	g893294
BLAST score	291
E value	5.0e-26
Match length	159
% identity	40
NCBI Description	(L43362) 4-coumarate:CoA ligase isoform 2 [Oryza sativa]

Seq. No.	391470
Contig ID	26074_1.R1084
5'-most EST	LIB3475-006-P1-K1-E4
Method	BLASTX
NCBI GI	g119784
BLAST score	838
E value	4.0e-90
Match length	179
% identity	88
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_100555_pir__A39356 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) I beta chain precursor, chloroplast - barley >gi_167065 (M60410) beta-ketoacyl-ACP synthase I [Hordeum vulgare]

Seq. No.	391471
Contig ID	26086_1.R1084
5'-most EST	g2428640
Method	BLASTX
NCBI GI	g4678264
BLAST score	452
E value	1.0e-44
Match length	183
% identity	54
NCBI Description	(AL049657) putative protein [Arabidopsis thaliana]

Seq. No.	391472
Contig ID	26087_1.R1084
5'-most EST	LIB3475-009-P1-K1-D7
Method	BLASTX
NCBI GI	g3169065
BLAST score	200
E value	3.0e-15
Match length	185
% identity	32
NCBI Description	(AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe]

Seq. No.	391473
Contig ID	26088_1.R1084
5'-most EST	uC-osf1M202016b01b1
Method	BLASTX

NCBI GI	g5817110
BLAST score	189
E value	5.0e-14
Match length	80
% identity	57
NCBI Description	(AL110193) hypothetical protein [Homo sapiens]

Seq. No.	391474
Contig ID	26090_1.R1084
5'-most EST	g6025168
Method	BLASTX
NCBI GI	g3142300
BLAST score	908
E value	4.0e-98
Match length	275
% identity	63
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	391475
Contig ID	26098_1.R1084
5'-most EST	LIB3475-006-P1-K1-H1

Seq. No.	391476
Contig ID	26110_1.R1084
5'-most EST	g5456490
Method	BLASTX
NCBI GI	g4206122
BLAST score	170
E value	2.0e-13
Match length	71
% identity	65
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	391477
Contig ID	26143_1.R1084
5'-most EST	uC-osflcyp108d12b1
Method	BLASTX
NCBI GI	g4580389
BLAST score	695
E value	4.0e-73
Match length	204
% identity	66
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	391478
Contig ID	26155_1.R1084
5'-most EST	LIB3475-007-P1-K1-E1
Method	BLASTX
NCBI GI	g4160579
BLAST score	200
E value	5.0e-15
Match length	113
% identity	36

NCBI Description	(AL035218) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	391479
Contig ID	26157_1.R1084
5'-most EST	uC-osrocyp015h05b1
Method	BLASTX
NCBI GI	g4538911
BLAST score	334
E value	7.0e-44
Match length	118
% identity	72
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391480
Contig ID	26170_1.R1084
5'-most EST	uC-osflm202106a08b1
Method	BLASTX
NCBI GI	g5441874
BLAST score	209
E value	4.0e-16
Match length	101
% identity	41
NCBI Description	(AP000366) Similar to maize transposon MuDR mudrA-like protein. (AC002340) [Oryza sativa]

Seq. No.	391481
Contig ID	26173_1.R1084
5'-most EST	g2309693
Method	BLASTX
NCBI GI	g4836904
BLAST score	141
E value	3.0e-26
Match length	121
% identity	60
NCBI Description	(AC007369) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	391482
Contig ID	26176_1.R1084
5'-most EST	uC-osflcyp023f11b1
Method	BLASTX
NCBI GI	g1323748
BLAST score	382
E value	2.0e-36
Match length	187
% identity	47
NCBI Description	(U32430) thiol protease [Triticum aestivum]

Seq. No.	391483
Contig ID	26180_1.R1084
5'-most EST	g3107678
Method	BLASTX
NCBI GI	g4938487
BLAST score	428
E value	8.0e-47
Match length	172
% identity	63

NCBI Description	(AL078464) cadmium-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No.	391484
Contig ID	26181_1.R1084
5'-most EST	g2311227
Method	BLASTX
NCBI GI	g4006854
BLAST score	389
E value	2.0e-37
Match length	148
% identity	57
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	391485
Contig ID	26184_1.R1084
5'-most EST	uC-osflcyp082g12b1
Method	BLASTX
NCBI GI	g5668645
BLAST score	506
E value	5.0e-51
Match length	247
% identity	49
NCBI Description	(AL109619) putative protein [Arabidopsis thaliana]

Seq. No.	391486
Contig ID	26193_1.R1084
5'-most EST	LIB3475-007-P1-K1-H4
Method	BLASTX
NCBI GI	g2529663
BLAST score	472
E value	4.0e-47
Match length	209
% identity	45
NCBI Description	(AC002535) putative lysophospholipase [Arabidopsis thaliana] >gi_3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	391487
Contig ID	26196_1.R1084
5'-most EST	g2428059
Method	BLASTX
NCBI GI	g4678349
BLAST score	1192
E value	1.0e-131
Match length	375
% identity	19
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	391488
Contig ID	26199_1.R1084
5'-most EST	LIB3475-008-P1-K1-A1

Seq. No.	391489
Contig ID	26204_1.R1084
5'-most EST	g2428228
Method	BLASTX

NCBI GI	g3219969
BLAST score	157
E value	3.0e-10
Match length	56
% identity	48
NCBI Description	HYPOTHETICAL 22.4 KD PROTEIN C6G10.10C IN CHROMOSOME I >gi_2330874_emb_CAB11296.1_ (Z98603) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	391490
Contig ID	26220_1.R1084
5'-most EST	LIB3475-008-P1-K1-C2

Seq. No.	391491
Contig ID	26222_1.R1084
5'-most EST	uC-osflM202115g02b1
Method	BLASTX
NCBI GI	g2104679
BLAST score	318
E value	4.0e-29
Match length	200
% identity	35
NCBI Description	(X97906) transcription factor [Vicia faba]

Seq. No.	391492
Contig ID	26225_1.R1084
5'-most EST	g3768483
Method	BLASTX
NCBI GI	g2708750
BLAST score	149
E value	3.0e-09
Match length	110
% identity	35
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	391493
Contig ID	26236_1.R1084
5'-most EST	g2427944
Method	BLASTX
NCBI GI	g4680340
BLAST score	264
E value	9.0e-23
Match length	66
% identity	77
NCBI Description	(AF128457) putative nucleolysin [Oryza sativa subsp. indica]

Seq. No.	391494
Contig ID	26237_1.R1084
5'-most EST	uC-osroM202023f05b1
Method	BLASTX
NCBI GI	g3182981
BLAST score	441
E value	2.0e-88
Match length	218
% identity	76

NCBI Description	CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_ (D86494) diminuto [Pisum sativum]

Seq. No.	391495
Contig ID	26244_1.R1084
5'-most EST	g2427838

Seq. No.	391496
Contig ID	26247_1.R1084
5'-most EST	LIB3477-004-P1-K1-A8
Method	BLASTX
NCBI GI	g4580461
BLAST score	306
E value	3.0e-27
Match length	210
% identity	28
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	391497
Contig ID	26255_1.R1084
5'-most EST	LIB3475-008-P1-K1-F7
Method	BLASTX
NCBI GI	g4056490
BLAST score	364
E value	5.0e-44
Match length	188
% identity	51
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391498
Contig ID	26261_1.R1084
5'-most EST	uC-osroM202040f06b1
Method	BLASTX
NCBI GI	g4929621
BLAST score	486
E value	1.0e-48
Match length	156
% identity	58
NCBI Description	(AF151834) CGI-76 protein [Homo sapiens]

Seq. No.	391499
Contig ID	26266_1.R1084
5'-most EST	LIB3475-008-P1-K1-G7
Method	BLASTN
NCBI GI	g2895865
BLAST score	270
E value	1.0e-150
Match length	282
% identity	99
NCBI Description	Oryza sativa methylmalonate semi-aldehyde dehydrogenase (MMSDH1) mRNA, complete cds

Seq. No.	391500
Contig ID	26267_1.R1084
5'-most EST	g286634
Method	BLASTX
NCBI GI	g4049341

BLAST score	155
E value	4.0e-10
Match length	45
% identity	58
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	391501
Contig ID	26282_1.R1084
5'-most EST	uC-osrocyp006g02b1

Seq. No.	391502
Contig ID	26292_1.R1084
5'-most EST	uC-osroM202012g07b1
Method	BLASTX
NCBI GI	g2541876
BLAST score	287
E value	2.0e-25
Match length	165
% identity	41
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	391503
Contig ID	26314_1.R1084
5'-most EST	LIB3475-009-P1-K1-E5

Seq. No.	391504
Contig ID	26315_1.R1084
5'-most EST	LIB3479-004-Q6-K1-F4
Method	BLASTX
NCBI GI	g4539335
BLAST score	332
E value	1.0e-34
Match length	151
% identity	45
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	391505
Contig ID	26322_1.R1084
5'-most EST	LIB3475-009-P1-K1-F4

Seq. No.	391506
Contig ID	26327_1.R1084
5'-most EST	g4715287
Method	BLASTX
NCBI GI	g6017114
BLAST score	438
E value	4.0e-43
Match length	170
% identity	57
NCBI Description	(AC009895) unknown protein [Arabidopsis thaliana]

Seq. No.	391507
Contig ID	26330_1.R1084
5'-most EST	LIB3475-009-P1-K1-G12
Method	BLASTX
NCBI GI	g4415933

BLAST score	355
E value	3.0e-33
Match length	145
% identity	52
NCBI Description	(AC006418) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana] >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana]

Seq. No.	391508
Contig ID	26347_1.R1084
5'-most EST	uC-osroM202008c02a1
Method	BLASTX
NCBI GI	g3786005
BLAST score	608
E value	7.0e-63
Match length	180
% identity	35
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	391509
Contig ID	26352_1.R1084
5'-most EST	LIB3475-010-P1-K1-A8

Seq. No.	391510
Contig ID	26353_1.R1084
5'-most EST	g701411
Method	BLASTX
NCBI GI	g1279654
BLAST score	277
E value	5.0e-25
Match length	103
% identity	57
NCBI Description	(X97351) peroxidase [Populus balsamifera subsp. trichocarpa]

Seq. No.	391511
Contig ID	26361_1.R1084
5'-most EST	uC-osf1M202039g03b1
Method	BLASTX
NCBI GI	g2633727
BLAST score	179
E value	7.0e-13
Match length	109
% identity	40
NCBI Description	(Z99111) ykrT [Bacillus subtilis]

Seq. No.	391512
Contig ID	26362_1.R1084
5'-most EST	LIB3475-010-P1-K1-B7
Method	BLASTX
NCBI GI	g3355480
BLAST score	312
E value	2.0e-28
Match length	156

% identity	35
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	391513
Contig ID	26364_1.R1084
5'-most EST	LIB3475-010-P1-K1-B9

Seq. No.	391514
Contig ID	26373_1.R1084
5'-most EST	uC-osroM202004a01b1
Method	BLASTX
NCBI GI	g4760700
BLAST score	245
E value	1.0e-20
Match length	78
% identity	60
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]

Seq. No.	391515
Contig ID	26377_1.R1084
5'-most EST	LIB3475-010-P1-K1-D1

Seq. No.	391516
Contig ID	26378_1.R1084
5'-most EST	LIB3475-010-P1-K1-D10
Method	BLASTX
NCBI GI	g4455227
BLAST score	320
E value	2.0e-42
Match length	123
% identity	73
NCBI Description	(AL035440) SNF8 like protein [Arabidopsis thaliana]

Seq. No.	391517
Contig ID	26379_1.R1084
5'-most EST	uC-osrocyp005c12b1
Method	BLASTX
NCBI GI	g5262154
BLAST score	217
E value	2.0e-17
Match length	135
% identity	39
NCBI Description	(AL080237) putative protein [Arabidopsis thaliana]

Seq. No.	391518
Contig ID	26397_1.R1084
5'-most EST	LIB3475-010-P1-K1-F11
Method	BLASTX
NCBI GI	g4235430
BLAST score	216
E value	5.0e-32
Match length	107
% identity	68
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	391519

Contig ID	26400_1.R1084
5'-most EST	uC-osflM202066d04b1
Method	BLASTX
NCBI GI	g4115377
BLAST score	793
E value	1.0e-84
Match length	251
% identity	63
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	391520
Contig ID	26408_1.R1084
5'-most EST	LIB3475-010-P1-K1-G2
Method	BLASTX
NCBI GI	g4033469
BLAST score	162
E value	5.0e-11
Match length	37
% identity	73
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	391521
Contig ID	26414_1.R1084
5'-most EST	uC-osflcyp033b01a1

Seq. No.	391522
Contig ID	26420_1.R1084
5'-most EST	LIB3475-010-P1-K1-H4

Seq. No.	391523
Contig ID	26427_1.R1084
5'-most EST	LIB3475-011-P1-K1-A10

Seq. No.	391524
Contig ID	26429_1.R1084
5'-most EST	uC-osroM202004d12b1
Method	BLASTX
NCBI GI	g2213629
BLAST score	519
E value	9.0e-53
Match length	123
% identity	75
NCBI Description	(AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No.	391525
Contig ID	26430_1.R1084
5'-most EST	LIB3475-011-P1-K1-A4
Method	BLASTX
NCBI GI	g2253411
BLAST score	309
E value	6.0e-28
Match length	139
% identity	41
NCBI Description	(AF007219) PP2A inhibitor [Tetraodon fluviatilis]

Seq. No.	391526
Contig ID	26436_1.R1084
5'-most EST	LIB3475-011-P1-K1-B11
Method	BLASTX
NCBI GI	g3913525
BLAST score	484
E value	9.0e-49
Match length	135
% identity	75
NCBI Description	DNA POLYMERASE DELTA CATALYTIC CHAIN >gi_2895198 (AF020193) DNA polymerase delta [Glycine max]

Seq. No.	391527
Contig ID	26438_1.R1084
5'-most EST	g5039072
Method	BLASTN
NCBI GI	g5777612
BLAST score	56
E value	3.0e-22
Match length	187
% identity	59
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	391528
Contig ID	26444_1.R1084
5'-most EST	g4714766
Method	BLASTX
NCBI GI	g6006869
BLAST score	389
E value	2.0e-37
Match length	101
% identity	77
NCBI Description	(AC009540) putative cationic amino acid transporter [Arabidopsis thaliana]

Seq. No.	391529
Contig ID	26449_1.R1084
5'-most EST	uC-osroM202037f01b1

Seq. No.	391530
Contig ID	26461_1.R1084
5'-most EST	LIB3475-011-P1-K1-D6
Method	BLASTX
NCBI GI	g6056374
BLAST score	554
E value	7.0e-57
Match length	154
% identity	64
NCBI Description	(AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	391531
Contig ID	26461_2.R1084
5'-most EST	g2317644
Method	BLASTX
NCBI GI	g6056372
BLAST score	285

E value	2.0e-25
Match length	90
% identity	59
NCBI Description	(AC009894) Very similar to receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	391532
Contig ID	26468_1.R1084
5'-most EST	uC-osrocyp031d04a1

Seq. No.	391533
Contig ID	26479_1.R1084
5'-most EST	LIB3475-011-P1-K1-G1
Method	BLASTX
NCBI GI	g4512659
BLAST score	874
E value	2.0e-94
Match length	223
% identity	77
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	391534
Contig ID	26483_1.R1084
5'-most EST	LIB3475-011-P1-K1-G8
Method	BLASTX
NCBI GI	g2129550
BLAST score	683
E value	1.0e-71
Match length	178
% identity	72
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	391535
Contig ID	26491_1.R1084
5'-most EST	uC-osroM202016b12b1
Method	BLASTX
NCBI GI	g82410
BLAST score	349
E value	8.0e-33
Match length	98
% identity	67
NCBI Description	peroxidase (EC 1.11.1.7) BP1 precursor - barley >gi_167081 (M73234) peroxidase BP 1 [Hordeum vulgare]

Seq. No.	391536
Contig ID	26501_1.R1084
5'-most EST	g3768668
Method	BLASTX

NCBI GI	g3024764
BLAST score	137
E value	8.0e-16
Match length	104
% identity	50
NCBI Description	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (UBIQUITIN THIOLESTERASE T) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T) (DEUBIQUITINATING ENZYME T) (ISOPEPTIDASE T) >gi_3287373 (AC002397) ISOT [Mus musculus]

Seq. No.	391537
Contig ID	26504_1.R1084
5'-most EST	g3061208

Seq. No.	391538
Contig ID	26513_1.R1084
5'-most EST	g426645
Method	BLASTX
NCBI GI	g1085002
BLAST score	234
E value	2.0e-19
Match length	88
% identity	27
NCBI Description	mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans >gi_472902_emb_CAA53721_ (X76115) carrier protein (c1) [Caenorhabditis elegans] >gi_829102_emb_CAA88283_ (Z48240) DIF-1 [Caenorhabditis elegans]

Seq. No.	391539
Contig ID	26516_1.R1084
5'-most EST	uC-osroM202041c08b1

Seq. No.	391540
Contig ID	26538_1.R1084
5'-most EST	uC-osflcyp081g09b1

Seq. No.	391541
Contig ID	26540_1.R1084
5'-most EST	uC-osflcyp154g04b1
Method	BLASTX
NCBI GI	g3327204
BLAST score	510
E value	4.0e-58
Match length	186
% identity	62
NCBI Description	(AB014595) KIAA0695 protein [Homo sapiens]

Seq. No.	391542
Contig ID	26545_1.R1084
5'-most EST	uC-osrocyp008e07b1
Method	BLASTX
NCBI GI	g4567232
BLAST score	298
E value	9.0e-27
Match length	72
% identity	81

NCBI Description	(AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana]

Seq. No.	391543
Contig ID	26545_2.R1084
5'-most EST	g427541
Method	BLASTX
NCBI GI	g1173234
BLAST score	276
E value	4.0e-24
Match length	71
% identity	77
NCBI Description	40S RIBOSOMAL PROTEIN S25 >gi_481909_pir__S40089 ribosomal protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi_1584836_prf__2123431A ribosomal protein S25 [Lycopersicon esculentum]

Seq. No.	391544
Contig ID	26545_3.R1084
5'-most EST	LIB3475-012-P1-K1-F8
Method	BLASTX
NCBI GI	g1173234
BLAST score	283
E value	3.0e-25
Match length	72
% identity	79
NCBI Description	40S RIBOSOMAL PROTEIN S25 >gi_481909_pir__S40089 ribosomal protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi_1584836_prf__2123431A ribosomal protein S25 [Lycopersicon esculentum]

Seq. No.	391545
Contig ID	26546_1.R1084
5'-most EST	uC-osroM202036b11b1

Seq. No.	391546
Contig ID	26548_1.R1084
5'-most EST	LIB3475-012-P1-K1-G10

Seq. No.	391547
Contig ID	26554_1.R1084
5'-most EST	LIB3475-012-P1-K1-G6
Method	BLASTX
NCBI GI	g4512699
BLAST score	944
E value	1.0e-102
Match length	365
% identity	54
NCBI Description	(AC006569) putative NADH-ubiquinone oxireductase [Arabidopsis thaliana]

Seq. No.	391548
Contig ID	26565_1.R1084
5'-most EST	g2799530

Seq. No.	391549
Contig ID	26573_1.R1084
5'-most EST	g2800204

Seq. No.	391550
Contig ID	26575_1.R1084
5'-most EST	LIB3477-001-P1-K1-A5

Seq. No.	391551
Contig ID	26579_1.R1084
5'-most EST	g2312772
Method	BLASTX
NCBI GI	g4519507
BLAST score	1190
E value	1.0e-131
Match length	322
% identity	71
NCBI Description	(D88434) protein abundantly expressed during apple fruit development [Malus domestica]

Seq. No.	391552
Contig ID	26593_1.R1084
5'-most EST	LIB3477-001-P1-K1-C10
Method	BLASTX
NCBI GI	g5733873
BLAST score	309
E value	3.0e-28
Match length	143
% identity	45
NCBI Description	(AC007932) Contains similarity to gb_AB023235 KIAA1018 protein from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	391553
Contig ID	26600_1.R1084
5'-most EST	uC-osflcyp120c11b1

Seq. No.	391554
Contig ID	26604_1.R1084
5'-most EST	LIB3477-001-P1-K1-D1
Method	BLASTX
NCBI GI	g4185140
BLAST score	418
E value	9.0e-41
Match length	88
% identity	94
NCBI Description	(AC005724) putative small nuclear ribonucleoprotein E (snRNP-E) [Arabidopsis thaliana]

Seq. No.	391555
Contig ID	26604_2.R1084
5'-most EST	LIB3477-003-P1-K1-D8
Method	BLASTX
NCBI GI	g4185140
BLAST score	401
E value	6.0e-39
Match length	85
% identity	92

NCBI Description	(AC005724) putative small nuclear ribonucleoprotein E (snRNP-E) [Arabidopsis thaliana]

Seq. No.	391556
Contig ID	26606_1.R1084
5'-most EST	g1632692
Method	BLASTX
NCBI GI	g225102
BLAST score	287
E value	3.0e-25
Match length	130
% identity	48
NCBI Description	trypsin/amylase inhibitor pUP13 [Hordeum vulgare var. distichum]

Seq. No.	391557
Contig ID	26606_2.R1084
5'-most EST	g1632642
Method	BLASTX
NCBI GI	g225102
BLAST score	176
E value	3.0e-21
Match length	126
% identity	49
NCBI Description	trypsin/amylase inhibitor pUP13 [Hordeum vulgare var. distichum]

Seq. No.	391558
Contig ID	26611_1.R1084
5'-most EST	LIB3477-002-P1-K1-H1
Method	BLASTX
NCBI GI	g5921934
BLAST score	366
E value	7.0e-35
Match length	108
% identity	64
NCBI Description	CYTOCHROME P450 CYP99A1 >gi_2766450 (AF029857) cytochrome P450 CYP99A1 [Sorghum bicolor]

Seq. No.	391559
Contig ID	26615_1.R1084
5'-most EST	g2276038
Method	BLASTX
NCBI GI	g4097573
BLAST score	160
E value	2.0e-10
Match length	72
% identity	40
NCBI Description	(U64917) GMFP7 [Glycine max]

Seq. No.	391560
Contig ID	26617_1.R1084
5'-most EST	LIB3477-001-P1-K1-E10
Method	BLASTX
NCBI GI	g3122858
BLAST score	1798
E value	0.0e+00

Match length	496
% identity	72
NCBI Description	D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (PGDH) >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate dehydrogenase [Arabidopsis thaliana] >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]

Seq. No.	391561
Contig ID	26618_1.R1084
5'-most EST	g426178

Seq. No.	391562
Contig ID	26619_1.R1084
5'-most EST	g4969295

Seq. No.	391563
Contig ID	26625_1.R1084
5'-most EST	LIB3477-001-P1-K1-E7
Method	BLASTX
NCBI GI	g5257272
BLAST score	293
E value	1.0e-30
Match length	70
% identity	99
NCBI Description	(AP000364) ESTs C96816(C11212),AU063547(C62696), AU075331(C11212) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	391564
Contig ID	26626_1.R1084
5'-most EST	LIB3477-001-P1-K1-E8

Seq. No.	391565
Contig ID	26627_1.R1084
5'-most EST	LIB3477-001-P1-K1-E9

Seq. No.	391566
Contig ID	26637_1.R1084
5'-most EST	g4969143
Method	BLASTX
NCBI GI	g4678263
BLAST score	525
E value	3.0e-53
Match length	189
% identity	55
NCBI Description	(AL049657) brefeldin A-sensitive Golgi protein-like [Arabidopsis thaliana]

Seq. No.	391567
Contig ID	26639_1.R1084
5'-most EST	LIB3477-001-P1-K1-F9
Method	BLASTX
NCBI GI	g5262775
BLAST score	414
E value	2.0e-40
Match length	119

% identity	67
NCBI Description	(AL080282) putative protein [Arabidopsis thaliana]

Seq. No.	391568
Contig ID	26640_1.R1084
5'-most EST	uC-osrocyp030e09b1
Method	BLASTX
NCBI GI	g3885334
BLAST score	599
E value	8.0e-62
Match length	227
% identity	56
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	391569
Contig ID	26653_1.R1084
5'-most EST	g4878220
Method	BLASTX
NCBI GI	g1421730
BLAST score	224
E value	5.0e-18
Match length	95
% identity	56
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	391570
Contig ID	26661_1.R1084
5'-most EST	g3761883

Seq. No.	391571
Contig ID	26667_1.R1084
5'-most EST	uC-osroM202022f12b1

Seq. No.	391572
Contig ID	26676_1.R1084
5'-most EST	LIB3477-002-P1-K1-B12

Seq. No.	391573
Contig ID	26677_1.R1084
5'-most EST	LIB3477-002-P1-K1-B3
Method	BLASTX
NCBI GI	g4584541
BLAST score	319
E value	2.0e-29
Match length	80
% identity	75
NCBI Description	(AL049608) 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein [Arabidopsis thaliana]

Seq. No.	391574
Contig ID	26680_1.R1084
5'-most EST	LIB3477-002-P1-K1-B6

Seq. No.	391575
Contig ID	26686_1.R1084
5'-most EST	g4878549

Method	BLASTX
NCBI GI	g4263710
BLAST score	369
E value	4.0e-35
Match length	91
% identity	53
NCBI Description	(AC006223) putative pur-alpha transcriptional activator protein [Arabidopsis thaliana]

Seq. No.	391576
Contig ID	26691_1.R1084
5'-most EST	LIB3477-002-P1-K1-C5
Method	BLASTX
NCBI GI	g4926827
BLAST score	585
E value	3.0e-94
Match length	278
% identity	68
NCBI Description	(AC004135) T17H7.12 [Arabidopsis thaliana]

Seq. No.	391577
Contig ID	26693_1.R1084
5'-most EST	g5004357
Method	BLASTX
NCBI GI	g4886522
BLAST score	290
E value	8.0e-26
Match length	129
% identity	50
NCBI Description	(AL050291) hypothetical protein [Homo sapiens]

Seq. No.	391578
Contig ID	26694_1.R1084
5'-most EST	LIB3477-002-P1-K1-C8

Seq. No.	391579
Contig ID	26701_1.R1084
5'-most EST	g3768133

Seq. No.	391580
Contig ID	26703_2.R1084
5'-most EST	g428274

Seq. No.	391581
Contig ID	26704_1.R1084
5'-most EST	g2800479
Method	BLASTX
NCBI GI	g2266672
BLAST score	686
E value	4.0e-72
Match length	175
% identity	73
NCBI Description	(Y14214) phosphate transporter [Lycopersicon esculentum]

Seq. No.	391582
Contig ID	26716_1.R1084
5'-most EST	LIB3477-002-P1-K1-E6

Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	6.0e-10
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	391583
Contig ID	26719_1.R1084
5'-most EST	LIB3477-002-P1-K1-E9

Seq. No.	391584
Contig ID	26725_1.R1084
5'-most EST	LIB3477-002-P1-K1-F3

Seq. No.	391585
Contig ID	26731_1.R1084
5'-most EST	uC-osflcyp106b05b1
Method	BLASTX
NCBI GI	g2493131
BLAST score	1050
E value	1.0e-115
Match length	228
% identity	93
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No.	391586
Contig ID	26735_1.R1084
5'-most EST	g5667362

Seq. No.	391587
Contig ID	26736_1.R1084
5'-most EST	uC-osroM202028e01b1

Seq. No.	391588
Contig ID	26740_1.R1084
5'-most EST	g2427510
Method	BLASTX
NCBI GI	g2739279
BLAST score	272
E value	6.0e-24
Match length	102
% identity	54
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	391589
Contig ID	26746_1.R1084
5'-most EST	g3762159

Seq. No.	391590
Contig ID	26749_1.R1084
5'-most EST	g427741

Method	BLASTX
NCBI GI	g2832681
BLAST score	145
E value	5.0e-09
Match length	62
% identity	44
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	391591
Contig ID	26752_1.R1084
5'-most EST	LIB3477-010-P1-K1-H2
Method	BLASTX
NCBI GI	g544018
BLAST score	449
E value	2.0e-44
Match length	122
% identity	72
NCBI Description	NITRATE/CHLORATE TRANSPORTER >gi_1076359_pir__A45772 nitrate-inducible nitrate transporter - Arabidopsis thaliana >gi_166668 (L10357) CHL1 [Arabidopsis thaliana] >gi_3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb_L10357 from A. thaliana. ESTs gb_H37533 and gb_R29790, gb_T46117, gb_T46068, gb_T75688, gb_R29817, gb_R29862, gb_Z34634 and gb_Z34258 come from this gene. [Arabidopsis thaliana]

Seq. No.	391592
Contig ID	26754_1.R1084
5'-most EST	LIB3477-002-P1-K1-H9
Method	BLASTX
NCBI GI	g2801536
BLAST score	842
E value	3.0e-90
Match length	256
% identity	61
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	391593
Contig ID	26755_1.R1084
5'-most EST	uC-osflcyp143g10b1
Method	BLASTX
NCBI GI	g5733874
BLAST score	325
E value	6.0e-47
Match length	210
% identity	50
NCBI Description	(AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No.	391594
Contig ID	26768_1.R1084
5'-most EST	uC-osflcyp088g09b1
Method	BLASTX
NCBI GI	g3874563
BLAST score	484
E value	2.0e-48
Match length	230
% identity	41

NCBI Description	(Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDN... >gi_3924825_emb_CAB05549.1_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDN

Seq. No.	391595
Contig ID	26770_1.R1084
5'-most EST	LIB3479-002-Q6-K2-C11
Method	BLASTX
NCBI GI	g5257292
BLAST score	638
E value	2.0e-66
Match length	174
% identity	74
NCBI Description	(AF124740) unknown [Zea mays]

Seq. No.	391596
Contig ID	26773_1.R1084
5'-most EST	LIB3477-008-P1-K1-E8

Seq. No.	391597
Contig ID	26783_1.R1084
5'-most EST	LIB3477-003-P1-K1-C6
Method	BLASTX
NCBI GI	g1173137
BLAST score	845
E value	1.0e-90
Match length	173
% identity	92
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5) >gi_322700_pir__B44457 RNA polymerase II fifth largest subunit - Glycine max=soybeans >gi_170052 (M90504) RNA polymerase II [Glycine max]

Seq. No.	391598
Contig ID	26789_1.R1084
5'-most EST	g2312560
Method	BLASTX
NCBI GI	g1170242
BLAST score	204
E value	6.0e-21
Match length	107
% identity	67
NCBI Description	FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) >gi_474966_dbj_BAA05101_ (D26105) ferrochelatase [Hordeum vulgare]

Seq. No.	391599
Contig ID	26795_1.R1084
5'-most EST	LIB3477-003-P1-K1-D7
Method	BLASTX
NCBI GI	g5733886

BLAST score	345
E value	3.0e-32
Match length	79
% identity	85
NCBI Description	(AC007932) F11A17.20 [Arabidopsis thaliana]

Seq. No.	391600
Contig ID	26797_1.R1084
5'-most EST	LIB3477-003-P1-K1-D9

Seq. No.	391601
Contig ID	26810_1.R1084
5'-most EST	g4716668

Seq. No.	391602
Contig ID	26826_1.R1084
5'-most EST	LIB3477-003-P1-K1-G7

Seq. No.	391603
Contig ID	26830_1.R1084
5'-most EST	LIB3477-003-P1-K1-H12
Method	BLASTX
NCBI GI	g3093294
BLAST score	681
E value	1.0e-71
Match length	180
% identity	45
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana] >gi_5730126_emb_CAB52460.1_ (AL109796) putative villin [Arabidopsis thaliana]

Seq. No.	391604
Contig ID	26835_1.R1084
5'-most EST	g4879726
Method	BLASTX
NCBI GI	g464470
BLAST score	650
E value	8.0e-68
Match length	125
% identity	95
NCBI Description	PROFILIN 3 >gi_422033_pir__S35798 profilin 3 - maize >gi_313142_emb_CAA51720_ (X73281) profilin 3 [Zea mays]

Seq. No.	391605
Contig ID	26835_2.R1084
5'-most EST	uC-osflcyp074f09b1
Method	BLASTX
NCBI GI	g3914422
BLAST score	616
E value	3.0e-64
Match length	120
% identity	93
NCBI Description	PROFILIN >gi_2154728_emb_CAA69669_ (Y08389) profilin 2 [Cynodon dactylon] >gi_2154730_emb_CAA69670_ (Y08390) profilin 1 [Cynodon dactylon]

Seq. No.	391606

Contig ID	26837_1.R1084
5'-most EST	LIB3477-003-P1-K1-H8

Seq. No.	391607
Contig ID	26838_1.R1084
5'-most EST	uC-osroM202019d06b1
Method	BLASTX
NCBI GI	g4760700
BLAST score	299
E value	6.0e-27
Match length	89
% identity	70
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]

Seq. No.	391608
Contig ID	26844_1.R1084
5'-most EST	LIB3477-004-P1-K1-A3
Method	BLASTN
NCBI GI	g6015437
BLAST score	38
E value	1.0e-11
Match length	38
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	391609
Contig ID	26848_1.R1084
5'-most EST	g2310674

Seq. No.	391610
Contig ID	26850_1.R1084
5'-most EST	LIB3477-004-P1-K1-A9
Method	BLASTX
NCBI GI	g4567312
BLAST score	510
E value	2.0e-51
Match length	143
% identity	64
NCBI Description	(AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391611
Contig ID	26851_1.R1084
5'-most EST	uC-osroM202008g03b1
Method	BLASTX
NCBI GI	g1657621
BLAST score	590
E value	5.0e-94
Match length	405
% identity	68
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]

Seq. No.	391612
Contig ID	26857_1.R1084
5'-most EST	g2280924

Method	BLASTX
NCBI GI	g6093512
BLAST score	172
E value	1.0e-16
Match length	81
% identity	53
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (NSLTP) (SDI-9) >gi_1050918_emb_CAA63340_ (X92648) lipid transfer protein [Helianthus annuus]

Seq. No.	391613
Contig ID	26857_2.R1084
5'-most EST	g3763369
Method	BLASTN
NCBI GI	g416316
BLAST score	36
E value	2.0e-10
Match length	64
% identity	88
NCBI Description	Yeast integrative vector pRS405 with LEU2 marker, complete sequence

Seq. No.	391614
Contig ID	26866_1.R1084
5'-most EST	g2310924
Method	BLASTX
NCBI GI	g4585980
BLAST score	479
E value	6.0e-48
Match length	188
% identity	52
NCBI Description	(AC005287) Very similar to TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	391615
Contig ID	26876_1.R1084
5'-most EST	LIB3477-004-P1-K1-D2

Seq. No.	391616
Contig ID	26880_1.R1084
5'-most EST	LIB3477-004-P1-K1-D6

Seq. No.	391617
Contig ID	26883_1.R1084
5'-most EST	LIB3477-004-P1-K1-D9
Method	BLASTX
NCBI GI	g4191785
BLAST score	364
E value	1.0e-34
Match length	165
% identity	49
NCBI Description	(AC005917) putative hydrolase [Arabidopsis thaliana]

Seq. No.	391618
Contig ID	26885_1.R1084
5'-most EST	LIB3477-005-P1-K1-D3
Method	BLASTX

NCBI GI	g3075391
BLAST score	156
E value	6.0e-10
Match length	149
% identity	34
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	391619
Contig ID	26897_1.R1084
5'-most EST	uC-osroM202038e01b1
Method	BLASTX
NCBI GI	g4538968
BLAST score	373
E value	1.0e-35
Match length	156
% identity	48
NCBI Description	(AL049488) putative protein kinase [Arabidopsis thaliana]

Seq. No.	391620
Contig ID	26906_1.R1084
5'-most EST	LIB3477-004-P1-K1-G11

Seq. No.	391621
Contig ID	26906_2.R1084
5'-most EST	g3761822
Method	BLASTN
NCBI GI	g4680488
BLAST score	74
E value	4.0e-33
Match length	94
% identity	95
NCBI Description	Oryza sativa BAC clone 1.H19, complete sequence

Seq. No.	391622
Contig ID	26906_4.R1084
5'-most EST	uC-osf1M202037e06b1
Method	BLASTN
NCBI GI	g5091496
BLAST score	43
E value	1.0e-14
Match length	99
% identity	62
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	391623
Contig ID	26910_1.R1084
5'-most EST	uC-osflcyp032e08b1

Seq. No.	391624
Contig ID	26916_1.R1084
5'-most EST	uC-osflcyp005a11b1
Method	BLASTX
NCBI GI	g4826572
BLAST score	518
E value	5.0e-96
Match length	248

% identity	69
NCBI Description	(AJ238848) polygalacturonase [Phleum pratense]

Seq. No.	391625
Contig ID	26916_2.R1084
5'-most EST	uC-osflcyp029g10b1
Method	BLASTX
NCBI GI	g129940
BLAST score	404
E value	1.0e-75
Match length	222
% identity	64
NCBI Description	EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi_100911_pir__S18570 polygalacturonase (EC 3.2.1.15) precursor - maize >gi_22417_emb_CAA40850_ (X57627) polygalacturonase [Zea mays] >gi_22419_emb_CAA44249_ (X62385) polygalacturonase [Zea mays] >gi_288374_emb_CAA46679_ (X65844) polygalacturonase [Zea mays]

Seq. No.	391626
Contig ID	26930_1.R1084
5'-most EST	LIB3477-005-P1-K1-A4
Method	BLASTX
NCBI GI	g1403522
BLAST score	623
E value	7.0e-82
Match length	239
% identity	62
NCBI Description	(X57187) chitinase [Phaseolus vulgaris]

Seq. No.	391627
Contig ID	26933_1.R1084
5'-most EST	LIB3477-005-P1-K1-A7
Method	BLASTX
NCBI GI	g4218535
BLAST score	430
E value	2.0e-42
Match length	123
% identity	68
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	391628
Contig ID	26937_1.R1084
5'-most EST	uC-osflM202092d08b1

Seq. No.	391629
Contig ID	26941_1.R1084
5'-most EST	LIB3477-005-P1-K1-B3

Seq. No.	391630
Contig ID	26971_1.R1084
5'-most EST	LIB3477-005-P1-K1-E11

Seq. No.	391631
Contig ID	26974_1.R1084

5'-most EST	uC-osflcyp125f07b1
Method	BLASTX
NCBI GI	g3337361
BLAST score	1079
E value	1.0e-118
Match length	270
% identity	71
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	391632
Contig ID	26985_1.R1084
5'-most EST	LIB3477-005-P1-K1-F4
Method	BLASTX
NCBI GI	g5919219
BLAST score	256
E value	1.0e-21
Match length	234
% identity	10
NCBI Description	(AF186273) leucine-rich repeats containing F-box protein FBL3 [Homo sapiens]

Seq. No.	391633
Contig ID	26986_1.R1084
5'-most EST	LIB3477-005-P1-K1-F6
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	4.0e-11
Match length	37
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	391634
Contig ID	26990_1.R1084
5'-most EST	g700922
Method	BLASTX
NCBI GI	g2191150
BLAST score	731
E value	5.0e-77
Match length	196
% identity	39
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No.	391635
Contig ID	26995_1.R1084
5'-most EST	uC-osrocyp033a01a1
Method	BLASTX
NCBI GI	g4008006
BLAST score	139
E value	6.0e-09
Match length	45
% identity	60
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	391636

Contig ID	27004_1.R1084
5'-most EST	uC-osrocyp010h08a1

Seq. No.	391637
Contig ID	27018_1.R1084
5'-most EST	LIB3477-006-P1-K1-C10
Method	BLASTX
NCBI GI	g2459435
BLAST score	429
E value	2.0e-42
Match length	134
% identity	60
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	391638
Contig ID	27035_1.R1084
5'-most EST	LIB3477-006-P1-K1-E11
Method	BLASTX
NCBI GI	g4895190
BLAST score	622
E value	2.0e-64
Match length	213
% identity	61
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No.	391639
Contig ID	27038_1.R1084
5'-most EST	LIB3477-006-P1-K1-E6

Seq. No.	391640
Contig ID	27043_1.R1084
5'-most EST	g3767352
Method	BLASTX
NCBI GI	g2407800
BLAST score	312
E value	2.0e-29
Match length	86
% identity	87
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	391641
Contig ID	27046_1.R1084
5'-most EST	uC-osflM202068g03b1
Method	BLASTX
NCBI GI	g6056373
BLAST score	677
E value	6.0e-73
Match length	168
% identity	89
NCBI Description	(AC009894) elongation factor EF-2 [Arabidopsis thaliana]

Seq. No.	391642
Contig ID	27048_1.R1084
5'-most EST	LIB3477-010-P1-K1-F5
Method	BLASTX
NCBI GI	g4490316

BLAST score	191
E value	4.0e-16
Match length	88
% identity	50
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	391643
Contig ID	27050_1.R1084
5'-most EST	LIB3477-006-P1-K1-G2
Method	BLASTN
NCBI GI	g20283
BLAST score	78
E value	1.0e-35
Match length	106
% identity	95
NCBI Description	Rice (O. sativa) gene for proliferating cell nuclear antigen (PCNA)

Seq. No.	391644
Contig ID	27055_1.R1084
5'-most EST	LIB3477-006-P1-K1-G8
Method	BLASTX
NCBI GI	g4204294
BLAST score	192
E value	6.0e-16
Match length	95
% identity	60
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	391645
Contig ID	27063_1.R1084
5'-most EST	g3767671

Seq. No.	391646
Contig ID	27069_1.R1084
5'-most EST	uC-osrocyp005e10b1
Method	BLASTX
NCBI GI	g3184100
BLAST score	129
E value	4.0e-16
Match length	162
% identity	34
NCBI Description	(AL023777) rna binding protein [Schizosaccharomyces pombe]

Seq. No.	391647
Contig ID	27073_1.R1084
5'-most EST	g3761707
Method	BLASTX
NCBI GI	g4105794
BLAST score	256
E value	6.0e-29
Match length	104
% identity	63
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	391648

Contig ID	27073_2.R1084
5'-most EST	LIB3477-007-P1-K1-A9
Method	BLASTX
NCBI GI	g4105794
BLAST score	390
E value	2.0e-37
Match length	124
% identity	59
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	391649
Contig ID	27075_1.R1084
5'-most EST	g2800005
Method	BLASTX
NCBI GI	g4512673
BLAST score	1185
E value	1.0e-130
Match length	268
% identity	80
NCBI Description	(AC006931) putative phosphoprotein phosphatase [Arabidopsis thaliana]

Seq. No.	391650
Contig ID	27077_1.R1084
5'-most EST	LIB3477-007-P1-K1-B12

Seq. No.	391651
Contig ID	27080_1.R1084
5'-most EST	uC-osroM202005b12b1
Method	BLASTX
NCBI GI	g2760844
BLAST score	382
E value	2.0e-36
Match length	132
% identity	55
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391652
Contig ID	27087_1.R1084
5'-most EST	LIB3477-007-P1-K1-C11
Method	BLASTX
NCBI GI	g4587549
BLAST score	581
E value	5.0e-72
Match length	216
% identity	42
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t

Seq. No.	391653
Contig ID	27089_1.R1084
5'-most EST	g4715158

Seq. No.	391654
Contig ID	27090_1.R1084

5'-most EST	uC-osroM202020e12b1
Method	BLASTX
NCBI GI	g2618686
BLAST score	291
E value	5.0e-26
Match length	177
% identity	36
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391655
Contig ID	27093_1.R1084
5'-most EST	g2427398
Method	BLASTX
NCBI GI	g2342494
BLAST score	295
E value	4.0e-32
Match length	153
% identity	52
NCBI Description	(D14058) bromelain [Ananas comosus] >gi_2463582_dbj_BAA22543_ (D38531) FB31 precursor (FB13 precursor) [Ananas comosus]

Seq. No.	391656
Contig ID	27097_1.R1084
5'-most EST	g2428154

Seq. No.	391657
Contig ID	27110_1.R1084
5'-most EST	g2427847
Method	BLASTX
NCBI GI	g1171577
BLAST score	365
E value	9.0e-35
Match length	119
% identity	58
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.	391658
Contig ID	27111_1.R1084
5'-most EST	LIB3477-007-P1-K1-E12

Seq. No.	391659
Contig ID	27115_1.R1084
5'-most EST	LIB3477-007-P1-K1-E5
Method	BLASTX
NCBI GI	g4678321
BLAST score	382
E value	2.0e-36
Match length	178
% identity	48
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	391660
Contig ID	27118_1.R1084
5'-most EST	g2317603
Method	BLASTX
NCBI GI	g5734642

BLAST score	662
E value	5.0e-69
Match length	250
% identity	82
NCBI Description	(AP000391) ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484) [Oryza sativa] >gi_6006357_dbj_BAA84787.1_ (AP000559) ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484) [Oryza sativa]

Seq. No.	391661
Contig ID	27124_1.R1084
5'-most EST	LIB3477-007-P1-K1-F2

Seq. No.	391662
Contig ID	27126_1.R1084
5'-most EST	LIB3477-007-P1-K1-F4
Method	BLASTX
NCBI GI	g4753658
BLAST score	203
E value	9.0e-16
Match length	54
% identity	74
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	391663
Contig ID	27127_1.R1084
5'-most EST	LIB3477-007-P1-K1-F5
Method	BLASTX
NCBI GI	g2580499
BLAST score	836
E value	8.0e-90
Match length	206
% identity	73
NCBI Description	(U67186) NADPH:ferrihemoprotein oxidoreductase [Eschscholzia californica]

Seq. No.	391664
Contig ID	27129_1.R1084
5'-most EST	g5005504
Method	BLASTX
NCBI GI	g2109293
BLAST score	216
E value	3.0e-17
Match length	120
% identity	44
NCBI Description	(U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	391665
Contig ID	27130_1.R1084
5'-most EST	LIB3477-007-P1-K1-F9
Method	BLASTX
NCBI GI	g602292
BLAST score	543

E value	3.0e-55
Match length	214
% identity	50
NCBI Description	(U17987) RCH2 protein [Brassica napus]

Seq. No.	391666
Contig ID	27132_1.R1084
5'-most EST	LIB3477-009-P1-K1-E2
Method	BLASTX
NCBI GI	g5478530
BLAST score	815
E value	5.0e-87
Match length	288
% identity	16
NCBI Description	(AF130441) UVB-resistance protein UVR8 [Arabidopsis thaliana]

Seq. No.	391667
Contig ID	27136_1.R1084
5'-most EST	uC-osflcyp009h03b1
Method	BLASTX
NCBI GI	g1076809
BLAST score	384
E value	6.0e-37
Match length	104
% identity	70
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - maize >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase [Zea mays]

Seq. No.	391668
Contig ID	27137_1.R1084
5'-most EST	LIB3477-007-P1-K1-G4
Method	BLASTX
NCBI GI	g629561
BLAST score	150
E value	2.0e-13
Match length	84
% identity	50
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana] >gi_5734767_gb_AAD50032.1_AC007651_27 (AC007651) SRG1 Protein [Arabidopsis thaliana]

Seq. No.	391669
Contig ID	27142_1.R1084
5'-most EST	LIB3477-007-P1-K1-G9
Method	BLASTX
NCBI GI	g1076748
BLAST score	221
E value	9.0e-18
Match length	91
% identity	28
NCBI Description	major intrinsic protein - rice >gi_440869_dbj_BAA04257_ (D17443) major intrinsic protein [Oryza sativa]

Seq. No.	391670

Contig ID	27145_1.R1084
5'-most EST	g440865
Method	BLASTX
NCBI GI	g2497752
BLAST score	148
E value	1.0e-09
Match length	53
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1321911_emb_CAA65475_ (X96714) lipid transfer protein [Prunus dulcis]

Seq. No.	391671
Contig ID	27147_1.R1084
5'-most EST	g568613
Method	BLASTX
NCBI GI	g6013206
BLAST score	475
E value	1.0e-47
Match length	128
% identity	71
NCBI Description	(AF177990) gamma-soluble NSF attachment protein; gamma-SNAP [Arabidopsis thaliana]

Seq. No.	391672
Contig ID	27155_1.R1084
5'-most EST	LIB3477-008-P1-K1-A11
Method	BLASTX
NCBI GI	g6065749
BLAST score	662
E value	3.0e-87
Match length	256
% identity	63
NCBI Description	(AJ250341) beta-amylase enzyme [Arabidopsis thaliana]

Seq. No.	391673
Contig ID	27158_1.R1084
5'-most EST	uC-osflcyp140d10b1

Seq. No.	391674
Contig ID	27160_1.R1084
5'-most EST	LIB3477-008-P1-K1-B2
Method	BLASTX
NCBI GI	g3281853
BLAST score	236
E value	1.0e-29
Match length	110
% identity	60
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	391675
Contig ID	27178_1.R1084
5'-most EST	g2442474
Method	BLASTX
NCBI GI	g4038471
BLAST score	390
E value	1.0e-37

Match length	86
% identity	86
NCBI Description	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No.	391676
Contig ID	27194_1.R1084
5'-most EST	LIB3477-011-P1-K1-E2
Method	BLASTX
NCBI GI	g1708421
BLAST score	386
E value	1.0e-42
Match length	125
% identity	75
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG IRL >gi_1205986 (U33318) sulfur starvation induced isoflavone reductase-like IRL [Zea mays]

Seq. No.	391677
Contig ID	27195_1.R1084
5'-most EST	g570196
Method	BLASTX
NCBI GI	g3738326
BLAST score	145
E value	4.0e-09
Match length	48
% identity	50
NCBI Description	(AC005170) putative nodulin [Arabidopsis thaliana]

Seq. No.	391678
Contig ID	27200_1.R1084
5'-most EST	g5004922

Seq. No.	391679
Contig ID	27210_1.R1084
5'-most EST	uC-osflcyp169d07b1
Method	BLASTX
NCBI GI	g2494041
BLAST score	363
E value	2.0e-34
Match length	106
% identity	64
NCBI Description	DIAMINOPIMELATE EPIMERASE (DAP EPIMERASE) >gi_1653875_dbj_BAA18785_ (D90917) diaminopimelate epimerase [Synechocystis sp.]

Seq. No.	391680
Contig ID	27212_1.R1084
5'-most EST	uC-osrocyp017f08b1
Method	BLASTX
NCBI GI	g2688824
BLAST score	163
E value	4.0e-11
Match length	102
% identity	42
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	391681
Contig ID	27218_1.R1084
5'-most EST	uC-osf1cyp002d03b1
Method	BLASTX
NCBI GI	g4522012
BLAST score	435
E value	6.0e-43
Match length	117
% identity	68
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391682
Contig ID	27225_1.R1084
5'-most EST	LIB3477-009-P1-K1-C4
Method	BLASTX
NCBI GI	g2289001
BLAST score	223
E value	4.0e-18
Match length	142
% identity	44
NCBI Description	(AC002335) small nuclear ribonucleoprotein isolog [Arabidopsis thaliana]

Seq. No.	391683
Contig ID	27227_1.R1084
5'-most EST	g572293
Method	BLASTX
NCBI GI	g4210449
BLAST score	524
E value	3.0e-53
Match length	193
% identity	56
NCBI Description	(AB016471) ARR1 protein [Arabidopsis thaliana]

Seq. No.	391684
Contig ID	27234_1.R1084
5'-most EST	LIB3477-009-P1-K1-D2
Method	BLASTX
NCBI GI	g5917664
BLAST score	192
E value	2.0e-27
Match length	151
% identity	29
NCBI Description	(AF159296) extensin-like protein [Lycopersicon esculentum]

Seq. No.	391685
Contig ID	27241_1.R1084
5'-most EST	LIB3477-009-P1-K1-E1
Method	BLASTX
NCBI GI	g3482979
BLAST score	179
E value	6.0e-13
Match length	49
% identity	63
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana] >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391686
Contig ID	27249_1.R1084
5'-most EST	uC-osroM202030a02b1
Method	BLASTX
NCBI GI	g2440029
BLAST score	228
E value	8.0e-19
Match length	59
% identity	71
NCBI Description	(Y14851) DAL1 protein [Arabidopsis thaliana] >gi_2440031_emb_CAA75115_ (Y14850) DAL1 protein [Arabidopsis thaliana]

Seq. No.	391687
Contig ID	27250_1.R1084
5'-most EST	uC-osflM202074g10a1

Seq. No.	391688
Contig ID	27256_1.R1084
5'-most EST	g568800
Method	BLASTX
NCBI GI	g2058456
BLAST score	225
E value	2.0e-18
Match length	46
% identity	98
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No.	391689
Contig ID	27257_1.R1084
5'-most EST	LIB3477-009-P1-K1-F3
Method	BLASTX
NCBI GI	g4097948
BLAST score	320
E value	2.0e-29
Match length	90
% identity	77
NCBI Description	(U72255) beta-1,3-glucanase precursor [Oryza sativa]

Seq. No.	391690
Contig ID	27261_1.R1084
5'-most EST	LIB3477-009-P1-K1-F7

Seq. No.	391691
Contig ID	27263_1.R1084
5'-most EST	g3762154
Method	BLASTN
NCBI GI	g3127105
BLAST score	54
E value	3.0e-21
Match length	65
% identity	97
NCBI Description	Helicella itala clone B2 microsatellite

Seq. No.	391692
Contig ID	27265_1.R1084
5'-most EST	LIB3477-009-P1-K1-G11

Seq. No.	391693
Contig ID	27266_1.R1084
5'-most EST	LIB3477-009-P1-K1-H4

Seq. No.	391694
Contig ID	27277_1.R1084
5'-most EST	uC-osflcyp125c01b1

Seq. No.	391695
Contig ID	27284_1.R1084
5'-most EST	uC-osroM202035g09b1

Seq. No.	391696
Contig ID	27285_1.R1084
5'-most EST	g4879394

Seq. No.	391697
Contig ID	27288_1.R1084
5'-most EST	LIB3477-010-P1-K1-A4

Seq. No.	391698
Contig ID	27295_1.R1084
5'-most EST	LIB3477-010-P1-K1-B10

Seq. No.	391699
Contig ID	27296_1.R1084
5'-most EST	g3090671
Method	BLASTX
NCBI GI	g1171008
BLAST score	490
E value	3.0e-49
Match length	134
% identity	63
NCBI Description	POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I) >gi_629812_pir__S44182 allergen Phl p I - common timothy >gi_473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum pratense]

Seq. No.	391700
Contig ID	27298_1.R1084
5'-most EST	LIB3477-010-P1-K1-B2
Method	BLASTX
NCBI GI	g1931647
BLAST score	527
E value	3.0e-62
Match length	275
% identity	39
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	391701
Contig ID	27301_1.R1084
5'-most EST	LIB3477-010-P1-K1-B5

Method	BLASTX
NCBI GI	g3522937
BLAST score	174
E value	4.0e-12
Match length	141
% identity	33
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	391702
Contig ID	27303_1.R1084
5'-most EST	LIB3477-010-P1-K1-B7
Method	BLASTX
NCBI GI	g4582436
BLAST score	486
E value	5.0e-49
Match length	135
% identity	67
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	391703
Contig ID	27309_1.R1084
5'-most EST	g5443721
Method	BLASTX
NCBI GI	g3914210
BLAST score	439
E value	5.0e-81
Match length	235
% identity	69
NCBI Description	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR (E2) (E2K) >gi_1117958 (U40758) dihydrolipoamide succinyltransferase [Fugu rubripes]

Seq. No.	391704
Contig ID	27310_1.R1084
5'-most EST	LIB3477-010-P1-K1-C3

Seq. No.	391705
Contig ID	27311_1.R1084
5'-most EST	g2280794

Seq. No.	391706
Contig ID	27312_1.R1084
5'-most EST	LIB3477-010-P1-K1-C5
Method	BLASTX
NCBI GI	g3935148
BLAST score	227
E value	2.0e-18
Match length	70
% identity	63
NCBI Description	(AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No.	391707
Contig ID	27316_1.R1084
5'-most EST	g2428122

Seq. No. 391708

Contig ID	27316_2.R1084
5'-most EST	g4879255
Seq. No.	391709
Contig ID	27317_1.R1084
5'-most EST	g2309940
Seq. No.	391710
Contig ID	27320_1.R1084
5'-most EST	LIB3477-010-P1-K1-D2
Method	BLASTX
NCBI GI	g5815233
BLAST score	217
E value	2.0e-17
Match length	93
% identity	49
NCBI Description	(AF173378) 60S acidic ribosomal protein PO [Homo sapiens]
Seq. No.	391711
Contig ID	27338_1.R1084
5'-most EST	LIB3477-010-P1-K1-E9
Seq. No.	391712
Contig ID	27344_1.R1084
5'-most EST	g2309894
Seq. No.	391713
Contig ID	27351_1.R1084
5'-most EST	g5455589
Method	BLASTX
NCBI GI	g2827709
BLAST score	331
E value	1.0e-30
Match length	94
% identity	66
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.	391714
Contig ID	27351_2.R1084
5'-most EST	LIB3477-010-P1-K1-G10
Seq. No.	391715
Contig ID	27353_1.R1084
5'-most EST	g4968882
Method	BLASTX
NCBI GI	g4680190
BLAST score	507
E value	2.0e-51
Match length	142
% identity	77
NCBI Description	(AF111710) putative dnaJ-like protein [Oryza sativa subsp. indica]
Seq. No.	391716
Contig ID	27356_1.R1084
5'-most EST	LIB3477-010-P1-K1-G4

Seq. No.	391717
Contig ID	27359_1.R1084
5'-most EST	g569159
Method	BLASTX
NCBI GI	g4539452
BLAST score	1344
E value	1.0e-149
Match length	377
% identity	64
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	391718
Contig ID	27360_1.R1084
5'-most EST	uC-osflcyp009g06b1
Method	BLASTX
NCBI GI	g4929725
BLAST score	344
E value	4.0e-32
Match length	124
% identity	55
NCBI Description	(AF151886) CGI-128 protein [Homo sapiens]

Seq. No.	391719
Contig ID	27370_1.R1084
5'-most EST	LIB3477-011-P1-K1-A10

Seq. No.	391720
Contig ID	27371_1.R1084
5'-most EST	g427064
Method	BLASTX
NCBI GI	g1842111
BLAST score	393
E value	5.0e-38
Match length	110
% identity	68
NCBI Description	(U87586) decoy [Arabidopsis thaliana] >gi_1931612_gb_AAB51588.1_ (U93308) decoy [Arabidopsis thaliana]

Seq. No.	391721
Contig ID	27373_1.R1084
5'-most EST	LIB3477-011-P1-K1-A2

Seq. No.	391722
Contig ID	27374_1.R1084
5'-most EST	LIB3477-011-P1-K1-A3

Seq. No.	391723
Contig ID	27376_1.R1084
5'-most EST	uC-osflcyp012g08b1
Method	BLASTX
NCBI GI	g5453603
BLAST score	603
E value	4.0e-70
Match length	169
% identity	78

NCBI Description	chaperonin containing TCP1, subunit 2 (beta) >gi_6094436_sp_P78371_TCPB_HUMAN T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_2559012 (AF026293) chaperonin containing t-complex polypeptide 1, beta subunit; CCT-beta [Homo sapiens] >gi_4090929 (AF026166) chaperonin-containing TCP-1 beta subunit homolog [Homo sapiens]

Seq. No.	391724
Contig ID	27379_1.R1084
5'-most EST	g1632332
Method	BLASTX
NCBI GI	g133867
BLAST score	573
E value	4.0e-59
Match length	126
% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	391725
Contig ID	27404_1.R1084
5'-most EST	LIB3477-011-P1-K1-D11
Method	BLASTX
NCBI GI	g4507857
BLAST score	157
E value	3.0e-10
Match length	184
% identity	27
NCBI Description	Herpes virus-associated ubiquitin-specific protease >gi_2501460_sp_Q93009_UBPH_HUMAN PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >gi_1545952_emb_CAA96580_ (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]

Seq. No.	391726
Contig ID	27408_1.R1084
5'-most EST	g702293
Method	BLASTX
NCBI GI	g3395431
BLAST score	193
E value	2.0e-14
Match length	215
% identity	31
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	391727
Contig ID	27411_1.R1084
5'-most EST	LIB3477-011-P1-K1-E1

Seq. No.	391728
Contig ID	27413_1.R1084
5'-most EST	g2312069

Seq. No.	391729
Contig ID	27416_1.R1084
5'-most EST	LIB3477-011-P1-K1-E4

Seq. No.	391730
Contig ID	27420_1.R1084
5'-most EST	LIB3477-011-P1-K1-E8

Seq. No.	391731
Contig ID	27421_1.R1084
5'-most EST	LIB3477-011-P1-K1-E9
Method	BLASTX
NCBI GI	g118306
BLAST score	149
E value	2.0e-20
Match length	132
% identity	42
NCBI Description	AROMATIC-L-AMINO-ACID DECARBOXYLASE (DOPA DECARBOXYLASE) (TRYPTOPHAN DECARBOXYLASE) >gi_68027_pir__DCJAAP aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) - Madagascar periwinkle >gi_18226_emb_CAA47898_ (X67662) tryptophan decarboxylase [Catharanthus roseus] >gi_167490 (M25151) tryptophan decarboxylase (EC 4.1.1.28) [Catharanthus roseus]

Seq. No.	391732
Contig ID	27422_1.R1084
5'-most EST	uC-osflm202112e06b1
Method	BLASTX
NCBI GI	g3660471
BLAST score	504
E value	6.0e-51
Match length	122
% identity	79
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No.	391733
Contig ID	27428_1.R1084
5'-most EST	g3760448
Method	BLASTX
NCBI GI	g4585907
BLAST score	585
E value	2.0e-60
Match length	151
% identity	72
NCBI Description	(AC006298) unknown protein [Arabidopsis thaliana]

Seq. No.	391734
Contig ID	27436_1.R1084
5'-most EST	uC-osroM202036h06b1
Method	BLASTX
NCBI GI	g5732040
BLAST score	350
E value	6.0e-33
Match length	93

% identity	70
NCBI Description	(AF147262) contains similarity to mouse and human SL15 proteins (GB:AF038961 and U41996) [Arabidopsis thaliana]

Seq. No.	391735
Contig ID	27451_1.R1084
5'-most EST	g428081
Method	BLASTX
NCBI GI	g4098521
BLAST score	987
E value	1.0e-107
Match length	212
% identity	86
NCBI Description	(U79160) HMG-CoA synthase [Arabidopsis thaliana] >gi_4098523 (U79161) HMG-CoA synthase [Arabidopsis thaliana] >gi_5002517_emb_CAB44320.1_ (AL078606) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]

Seq. No.	391736
Contig ID	27454_1.R1084
5'-most EST	LIB3479-001-Q6-K1-A1
Method	BLASTX
NCBI GI	g4455302
BLAST score	355
E value	1.0e-46
Match length	167
% identity	60
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	391737
Contig ID	27461_1.R1084
5'-most EST	LIB3479-001-Q6-K1-A7

Seq. No.	391738
Contig ID	27465_1.R1084
5'-most EST	LIB3479-001-Q6-K1-B12
Method	BLASTX
NCBI GI	g1381154
BLAST score	306
E value	8.0e-28
Match length	106
% identity	59
NCBI Description	(U58278) WCOR719 [Triticum aestivum]

Seq. No.	391739
Contig ID	27470_1.R1084
5'-most EST	uC-osf1cyp021d10b1

Seq. No.	391740
Contig ID	27471_1.R1084
5'-most EST	LIB3479-001-Q6-K2-B8
Method	BLASTX
NCBI GI	g3482974
BLAST score	528
E value	6.0e-54
Match length	164
% identity	65

NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]
Seq. No.	391741
Contig ID	27472_1.R1084
5'-most EST	LIB3479-001-Q6-K1-C11
Method	BLASTX
NCBI GI	g4903006
BLAST score	394
E value	3.0e-38
Match length	134
% identity	59
NCBI Description	(AB027458) ACE [Arabidopsis thaliana] >gi_5903086_gb_AAD55644.1_AC008017_17 (AC008017) ACE [Arabidopsis thaliana]
Seq. No.	391742
Contig ID	27473_1.R1084
5'-most EST	g5771040
Seq. No.	391743
Contig ID	27475_1.R1084
5'-most EST	g3061074
Method	BLASTX
NCBI GI	g3643085
BLAST score	499
E value	4.0e-50
Match length	292
% identity	55
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]
Seq. No.	391744
Contig ID	27477_1.R1084
5'-most EST	LIB3479-001-Q6-K1-C5
Seq. No.	391745
Contig ID	27478_1.R1084
5'-most EST	LIB3479-012-Q6-K1-C12
Seq. No.	391746
Contig ID	27484_1.R1084
5'-most EST	LIB3479-001-Q6-K2-D4
Method	BLASTX
NCBI GI	g2245136
BLAST score	397
E value	1.0e-38
Match length	121
% identity	64
NCBI Description	(Z97344) trehalose-6-phosphate synthase like protein [Arabidopsis thaliana]
Seq. No.	391747
Contig ID	27489_1.R1084
5'-most EST	LIB3479-001-Q6-K1-E10
Method	BLASTX
NCBI GI	g3023275

BLAST score	525
E value	3.0e-59
Match length	148
% identity	79
NCBI Description	ALPHA-GLUCOSIDASE PRECURSOR (MALTASE) >gi_2130027_pir__S65057 alpha-glucosidase (EC 3.2.1.20) - barley >gi_944901 (U22450) alpha-glucosidase [Hordeum vulgare]

Seq. No.	391748
Contig ID	27491_1.R1084
5'-most EST	uC-osrocyp013b10b1

Seq. No.	391749
Contig ID	27493_1.R1084
5'-most EST	LIB3479-001-Q6-K2-E5

Seq. No.	391750
Contig ID	27497_1.R1084
5'-most EST	LIB3479-001-Q6-K1-F1

Seq. No.	391751
Contig ID	27498_1.R1084
5'-most EST	LIB3479-001-Q6-K1-F10
Method	BLASTN
NCBI GI	g5091496
BLAST score	122
E value	8.0e-62
Match length	174
% identity	28
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	391752
Contig ID	27500_1.R1084
5'-most EST	LIB3479-001-Q6-K1-F12

Seq. No.	391753
Contig ID	27500_2.R1084
5'-most EST	g3762358
Method	BLASTN
NCBI GI	g1184321
BLAST score	66
E value	2.0e-28
Match length	117
% identity	91
NCBI Description	Cloning vector pCRSCRIPT SK[+], complete sequence

Seq. No.	391754
Contig ID	27506_1.R1084
5'-most EST	g3107319

Seq. No.	391755
Contig ID	27510_1.R1084
5'-most EST	LIB3479-001-Q6-K2-G12
Method	BLASTN
NCBI GI	g5257255

BLAST score	347
E value	0.0e+00
Match length	396
% identity	97
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	391756
Contig ID	27513_1.R1084
5'-most EST	LIB3479-001-Q6-K2-G4
Method	BLASTX
NCBI GI	g4982499
BLAST score	775
E value	9.0e-83
Match length	171
% identity	75
NCBI Description	(AC000107) F17F8.5 [Arabidopsis thaliana]

Seq. No.	391757
Contig ID	27518_1.R1084
5'-most EST	uC-osflM202071f06b1
Method	BLASTX
NCBI GI	g5669871
BLAST score	446
E value	7.0e-44
Match length	289
% identity	41
NCBI Description	(AF135014) dihydrolipoamide S-acetyltransferase [Zea mays]

Seq. No.	391758
Contig ID	27519_1.R1084
5'-most EST	LIB3479-001-Q6-K2-H1

Seq. No.	391759
Contig ID	27523_1.R1084
5'-most EST	g2798879
Method	BLASTN
NCBI GI	g3402815
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	Cloning Vector pGreen

Seq. No.	391760
Contig ID	27526_1.R1084
5'-most EST	g1632195
Method	BLASTX
NCBI GI	g4126695
BLAST score	127
E value	4.0e-13
Match length	142
% identity	35
NCBI Description	(AB016505) prolamin [Oryza sativa]

Seq. No.	391761
Contig ID	27531_1.R1084
5'-most EST	LIB3479-001-Q6-K2-A3

Method	BLASTN
NCBI GI	g5921664
BLAST score	40
E value	6.0e-13
Match length	99
% identity	91
NCBI Description	Pseudomonas putida FliK (fliK), FliL, FliM (fliM), FliN (fliN), FliO (fliO), FliP (fliP), FliQ (fliQ), FliR (fliR), and FlhB (flhB) genes, complete cds; and unknown gene

Seq. No.	391762
Contig ID	27605_1.R1084
5'-most EST	g2312192
Method	BLASTX
NCBI GI	g2351374
BLAST score	213
E value	6.0e-17
Match length	47
% identity	89
NCBI Description	(U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No.	391763
Contig ID	27607_1.R1084
5'-most EST	LIB3479-003-Q6-K2-C5
Method	BLASTX
NCBI GI	g5531484
BLAST score	553
E value	6.0e-57
Match length	122
% identity	93
NCBI Description	(Y17898) OCL1 homeobox protein [Zea mays]

Seq. No.	391764
Contig ID	27609_1.R1084
5'-most EST	uC-osflcyp031e08b1

Seq. No.	391765
Contig ID	27611_1.R1084
5'-most EST	LIB3479-002-Q6-K2-B12

Seq. No.	391766
Contig ID	27612_1.R1084
5'-most EST	LIB3479-002-Q6-K2-B2

Seq. No.	391767
Contig ID	27613_1.R1084
5'-most EST	LIB3479-002-Q6-K2-B3

Seq. No.	391768
Contig ID	27616_1.R1084
5'-most EST	LIB3479-002-Q6-K1-C1
Method	BLASTX
NCBI GI	g4455276
BLAST score	182
E value	7.0e-22
Match length	92

% identity	68
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	391769
Contig ID	27623_1.R1084
5'-most EST	LIB3479-002-Q6-K1-D10

Seq. No.	391770
Contig ID	27627_1.R1084
5'-most EST	LIB3479-002-Q6-K2-D7

Seq. No.	391771
Contig ID	27631_1.R1084
5'-most EST	LIB3479-002-Q6-K1-E12

Seq. No.	391772
Contig ID	27635_1.R1084
5'-most EST	LIB3479-002-Q6-K2-E5
Method	BLASTX
NCBI GI	g1737492
BLAST score	468
E value	1.0e-46
Match length	107
% identity	49
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	391773
Contig ID	27636_1.R1084
5'-most EST	g2310044
Method	BLASTX
NCBI GI	g4263827
BLAST score	119
E value	9.0e-13
Match length	137
% identity	42
NCBI Description	(AC006067) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	391774
Contig ID	27640_1.R1084
5'-most EST	LIB3479-002-Q6-K2-F1

Seq. No.	391775
Contig ID	27642_1.R1084
5'-most EST	LIB3479-002-Q6-K1-F3

Seq. No.	391776
Contig ID	27644_1.R1084
5'-most EST	LIB3479-002-Q6-K2-G1
Method	BLASTX
NCBI GI	g1345132
BLAST score	312
E value	2.0e-28
Match length	110
% identity	11
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana]

>gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	391777
Contig ID	27645_1.R1084
5'-most EST	LIB3479-002-Q6-K2-G10
Method	BLASTX
NCBI GI	g4006893
BLAST score	380
E value	1.0e-36
Match length	94
% identity	79
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	391778
Contig ID	27646_1.R1084
5'-most EST	uC-osroM202005a02b1

Seq. No.	391779
Contig ID	27647_1.R1084
5'-most EST	LIB3479-002-Q6-K2-G2
Method	BLASTN
NCBI GI	g5852077
BLAST score	236
E value	1.0e-130
Match length	273
% identity	96
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone: b6015

Seq. No.	391780
Contig ID	27656_1.R1084
5'-most EST	LIB3479-002-Q6-K2-H12

Seq. No.	391781
Contig ID	27684_1.R1084
5'-most EST	g3106575

Seq. No.	391782
Contig ID	27688_1.R1084
5'-most EST	LIB3479-003-Q6-K2-E1
Method	BLASTX
NCBI GI	g4586244
BLAST score	175
E value	1.0e-12
Match length	114
% identity	35
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	391783
Contig ID	27724_1.R1084
5'-most EST	uC-osflcyp030d11b1
Method	BLASTX
NCBI GI	g5668813
BLAST score	299
E value	5.0e-27

Match length	115
% identity	47
NCBI Description	(AC007519) Similar to gb_X77136 HSR203J protein from Nicotiana tabacum and is a member of the PF_00135 Carboxylesterase family. ESTs gb_Z25688 and gb_F14025 come from this gene. [Arabidopsis thaliana]

Seq. No.	391784
Contig ID	27725_1.R1084
5'-most EST	LIB3479-003-Q6-K1-A11

Seq. No.	391785
Contig ID	27731_1.R1084
5'-most EST	LIB3479-003-Q6-K2-A6

Seq. No.	391786
Contig ID	27741_1.R1084
5'-most EST	LIB3479-003-Q6-K1-C12
Method	BLASTX
NCBI GI	g4680207
BLAST score	435
E value	7.0e-43
Match length	163
% identity	53
NCBI Description	(AF114171) disease resistance protein RPM1 homolog [Sorghum bicolor]

Seq. No.	391787
Contig ID	27747_1.R1084
5'-most EST	LIB3479-003-Q6-K2-C7
Method	BLASTX
NCBI GI	g3461850
BLAST score	379
E value	2.0e-36
Match length	147
% identity	48
NCBI Description	(AC005315) putative ligand-gated ionic channel [Arabidopsis thaliana]

Seq. No.	391788
Contig ID	27750_1.R1084
5'-most EST	LIB3479-003-Q6-K2-D12
Method	BLASTX
NCBI GI	g4467148
BLAST score	138
E value	1.0e-15
Match length	143
% identity	40
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	391789
Contig ID	27765_1.R1084
5'-most EST	LIB3479-003-Q6-K2-F10
Method	BLASTX
NCBI GI	g731871
BLAST score	201
E value	2.0e-15

Match length	143
% identity	29
NCBI Description	HYPOTHETICAL 269.9 KD PROTEIN IN FKH1-MET18 INTERGENIC REGION >gi_626325_pir__S48405 probable membrane protein YIL129c - yeast (Saccharomyces cerevisiae) >gi_557794_emb_CAA86149_ (Z38059) orf, len: 2376, CAI: 0.14 [Saccharomyces cerevisiae]

Seq. No.	391790
Contig ID	27770_1.R1084
5'-most EST	g4715808

Seq. No.	391791
Contig ID	27772_1.R1084
5'-most EST	uC-osflcyp030e09b1
Method	BLASTX
NCBI GI	g5921647
BLAST score	734
E value	1.0e-77
Match length	214
% identity	64
NCBI Description	(AF155332) flavonoid 3'-hydroxylase [Petunia x hybrida]

Seq. No.	391792
Contig ID	27772_2.R1084
5'-most EST	g3768215
Method	BLASTX
NCBI GI	g5921647
BLAST score	422
E value	2.0e-52
Match length	180
% identity	61
NCBI Description	(AF155332) flavonoid 3'-hydroxylase [Petunia x hybrida]

Seq. No.	391793
Contig ID	27776_1.R1084
5'-most EST	LIB3479-003-Q6-K1-G8
Method	BLASTX
NCBI GI	g6063541
BLAST score	893
E value	1.0e-96
Match length	178
% identity	98
NCBI Description	(AP000615) EST AU068209(C12438) corresponds to a region of the predicted gene.; similar to Dis3p protein - human. (JE0110) [Oryza sativa]

Seq. No.	391794
Contig ID	27779_1.R1084
5'-most EST	LIB3479-003-Q6-K1-H10
Method	BLASTX
NCBI GI	g4768968
BLAST score	279
E value	2.0e-24
Match length	101
% identity	64
NCBI Description	(AF140219) nuclear cap-binding protein; CBP20 [Arabidopsis

thaliana]

Seq. No.	391795
Contig ID	27781_1.R1084
5'-most EST	LIB3479-003-Q6-K2-H3

Seq. No.	391796
Contig ID	27783_1.R1084
5'-most EST	LIB3479-003-Q6-K2-H8
Method	BLASTX
NCBI GI	g2982293
BLAST score	361
E value	3.0e-34
Match length	83
% identity	81
NCBI Description	(AF051231) ISP42-like protein [Picea mariana]

Seq. No.	391797
Contig ID	27824_1.R1084
5'-most EST	uC-osflcyp169g10b1
Method	BLASTX
NCBI GI	g4309732
BLAST score	155
E value	7.0e-10
Match length	53
% identity	53
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391798
Contig ID	27848_1.R1084
5'-most EST	LIB3479-004-Q6-K2-A1
Method	BLASTN
NCBI GI	g5777612
BLAST score	431
E value	0.0e+00
Match length	559
% identity	99
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	391799
Contig ID	27853_1.R1084
5'-most EST	LIB3479-004-Q6-K1-A4
Method	BLASTX
NCBI GI	g1076758
BLAST score	833
E value	2.0e-89
Match length	201
% identity	80
NCBI Description	heat-shock protein precursor - rye >gi_2130093_pir__S65776 heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]

Seq. No.	391800
Contig ID	27855_1.R1084
5'-most EST	LIB3479-004-Q6-K1-A6

Seq. No.	391801
Contig ID	27856_1.R1084
5'-most EST	LIB3479-004-Q6-K2-A7
Method	BLASTX
NCBI GI	g401237
BLAST score	238
E value	8.0e-43
Match length	94
% identity	90
NCBI Description	UBIQUITIN-ACTIVATING ENZYME E1 2 >gi_170684 (M90663) ubiquitin activating enyme [Triticum aestivum]

Seq. No.	391802
Contig ID	27860_1.R1084
5'-most EST	LIB3479-004-Q6-K2-B10
Method	BLASTX
NCBI GI	g3169171
BLAST score	175
E value	2.0e-12
Match length	74
% identity	45
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445213_gb_AAC32443.1_ (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	391803
Contig ID	27862_1.R1084
5'-most EST	LIB3479-004-Q6-K2-B2
Method	BLASTX
NCBI GI	g3925363
BLAST score	240
E value	3.0e-20
Match length	111
% identity	48
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	391804
Contig ID	27864_1.R1084
5'-most EST	LIB3479-004-Q6-K2-B6
Method	BLASTX
NCBI GI	g121477
BLAST score	562
E value	7.0e-58
Match length	140
% identity	77
NCBI Description	GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa] >gi_226767_prf__1604474A glutelin [Oryza sativa]

Seq. No.	391805
Contig ID	27865_1.R1084
5'-most EST	LIB3479-004-Q6-K2-B7

Seq. No.	391806
Contig ID	27875_1.R1084
5'-most EST	LIB3479-004-Q6-K2-C9

Method	BLASTX
NCBI GI	g3128213
BLAST score	243
E value	2.0e-20
Match length	85
% identity	54
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391807
Contig ID	27878_1.R1084
5'-most EST	LIB3479-004-Q6-K1-D2

Seq. No.	391808
Contig ID	27880_1.R1084
5'-most EST	LIB3479-004-Q6-K2-D6
Method	BLASTX
NCBI GI	g5881778
BLAST score	178
E value	9.0e-13
Match length	79
% identity	51
NCBI Description	(AL117386) putative protein [Arabidopsis thaliana]

Seq. No.	391809
Contig ID	27884_1.R1084
5'-most EST	LIB3479-004-Q6-K2-E1

Seq. No.	391810
Contig ID	27885_1.R1084
5'-most EST	LIB3479-004-Q6-K2-E10
Method	BLASTN
NCBI GI	g4159706
BLAST score	36
E value	1.0e-10
Match length	80
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	391811
Contig ID	27886_1.R1084
5'-most EST	LIB3479-004-Q6-K1-E11
Method	BLASTX
NCBI GI	g2739044
BLAST score	383
E value	8.0e-37
Match length	105
% identity	70
NCBI Description	(AF024651) polyphosphoinositide binding protein Sshlp [Glycine max]

Seq. No.	391812
Contig ID	27893_1.R1084
5'-most EST	LIB3479-004-Q6-K2-E7
Method	BLASTX
NCBI GI	g3924604
BLAST score	195

E value	2.0e-15
Match length	65
% identity	58
NCBI Description	(AF069442) putative leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No.	391813
Contig ID	27894_1.R1084
5'-most EST	LIB3479-004-Q6-K2-E8
Method	BLASTX
NCBI GI	g3738315
BLAST score	385
E value	4.0e-37
Match length	95
% identity	75
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	391814
Contig ID	27898_1.R1084
5'-most EST	LIB3479-004-Q6-K2-F11
Method	BLASTX
NCBI GI	g5263321
BLAST score	285
E value	2.0e-25
Match length	136
% identity	45
NCBI Description	(AC007727) Contains similarity to gb_AF033823 moira protein from Drosophila melanogaster and contains a PF_00249 Myb-like DNA-binding domain. EST gb_Z25609 comes from this gene. [Arabidopsis thaliana]

Seq. No.	391815
Contig ID	27902_1.R1084
5'-most EST	LIB3479-004-Q6-K1-F6
Method	BLASTX
NCBI GI	g2244981
BLAST score	153
E value	9.0e-10
Match length	107
% identity	39
NCBI Description	(Z97340) proline-rich, APG like protein [Arabidopsis thaliana]

Seq. No.	391816
Contig ID	27903_1.R1084
5'-most EST	uC-osflcyp022g05b1

Seq. No.	391817
Contig ID	27903_3.R1084
5'-most EST	LIB3479-004-Q6-K1-F7

Seq. No.	391818
Contig ID	27906_1.R1084
5'-most EST	LIB3479-004-Q6-K2-G10
Method	BLASTX
NCBI GI	g927428
BLAST score	156

E value	4.0e-10
Match length	55
% identity	56
NCBI Description	(X86733) fis1 [Linum usitatissimum]

Seq. No.	391819
Contig ID	27908_1.R1084
5'-most EST	LIB3479-004-Q6-K2-G2

Seq. No.	391820
Contig ID	27911_1.R1084
5'-most EST	g3462531

Seq. No.	391821
Contig ID	27913_1.R1084
5'-most EST	LIB3479-004-Q6-K1-G8

Seq. No.	391822
Contig ID	27914_1.R1084
5'-most EST	LIB3479-004-Q6-K1-G9

Seq. No.	391823
Contig ID	27916_1.R1084
5'-most EST	LIB3479-004-Q6-K2-H10
Method	BLASTX
NCBI GI	g3183310
BLAST score	173
E value	4.0e-12
Match length	112
% identity	39
NCBI Description	HYPOTHETICAL 23.2 KD PROTEIN C5D6.06C IN CHROMOSOME I >gi_2281976_emb_CAB10854.1_ (Z98056) putative glycosyl transferase [Schizosaccharomyces pombe]

Seq. No.	391824
Contig ID	27919_2.R1084
5'-most EST	LIB3479-004-Q6-K1-H2

Seq. No.	391825
Contig ID	27920_1.R1084
5'-most EST	LIB3479-004-Q6-K1-H3

Seq. No.	391826
Contig ID	27921_1.R1084
5'-most EST	LIB3479-004-Q6-K2-H4
Method	BLASTX
NCBI GI	g4337040
BLAST score	292
E value	3.0e-26
Match length	143
% identity	42
NCBI Description	(AF124159) molybdopterin synthase sulphurylase [Arabidopsis thaliana] >gi_4337042_gb_AAD18051_ (AF124160) molybdopterin synthase sulphurylase [Arabidopsis thaliana]

Seq. No.	391827
Contig ID	27924_1.R1084

5'-most EST	LIB3479-004-Q6-K2-H7
Method	BLASTX
NCBI GI	g2827715
BLAST score	438
E value	2.0e-43
Match length	122
% identity	12
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	391828
Contig ID	27944_1.R1084
5'-most EST	LIB3479-004-Q6-K2-B5
Method	BLASTX
NCBI GI	g2443880
BLAST score	225
E value	4.0e-18
Match length	104
% identity	46
NCBI Description	(AC002294) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	391829
Contig ID	27991_1.R1084
5'-most EST	g2800805
Method	BLASTN
NCBI GI	g4760544
BLAST score	59
E value	3.0e-24
Match length	67
% identity	97
NCBI Description	Homo sapiens IDN4-GGTR14 mRNA, partial cds

Seq. No.	391830
Contig ID	27991_2.R1084
5'-most EST	g2427988
Method	BLASTX
NCBI GI	g2055230
BLAST score	226
E value	2.0e-18
Match length	119
% identity	50
NCBI Description	(AB000130) SRC2 [Glycine max]

Seq. No.	391831
Contig ID	28014_1.R1084
5'-most EST	LIB3479-005-Q6-K1-A10

Seq. No.	391832
Contig ID	28016_1.R1084
5'-most EST	LIB3479-005-Q6-K1-A2
Method	BLASTX
NCBI GI	g3426037
BLAST score	463
E value	2.0e-46
Match length	110
% identity	41
NCBI Description	(AC005168) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No.	391833
Contig ID	28017_1.R1084
5'-most EST	g2800799
Method	BLASTX
NCBI GI	g5123547
BLAST score	482
E value	6.0e-48
Match length	208
% identity	48
NCBI Description	(AL079344) putative protein [Arabidopsis thaliana]

Seq. No.	391834
Contig ID	28031_1.R1084
5'-most EST	LIB3479-005-Q6-K1-B8

Seq. No.	391835
Contig ID	28039_1.R1084
5'-most EST	g2428470
Method	BLASTX
NCBI GI	g4584548
BLAST score	377
E value	2.0e-37
Match length	98
% identity	78
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	391836
Contig ID	28040_1.R1084
5'-most EST	uC-osrocyp011g02b1
Method	BLASTX
NCBI GI	g4567204
BLAST score	155
E value	1.0e-09
Match length	82
% identity	44
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	391837
Contig ID	28050_1.R1084
5'-most EST	uC-osflcyp137e10a1

Seq. No.	391838
Contig ID	28059_1.R1084
5'-most EST	uC-osflcyp159f04b1
Method	BLASTX
NCBI GI	g2632252
BLAST score	328
E value	2.0e-30
Match length	66
% identity	97
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	391839
Contig ID	28064_1.R1084
5'-most EST	LIB3479-005-Q6-K1-F4

Seq. No.	391840
Contig ID	28066_1.R1084
5'-most EST	LIB3479-005-Q6-K1-F6
Method	BLASTX
NCBI GI	g3080420
BLAST score	899
E value	6.0e-97
Match length	336
% identity	58
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	391841
Contig ID	28067_1.R1084
5'-most EST	g2312464
Method	BLASTX
NCBI GI	g629881
BLAST score	136
E value	5.0e-10
Match length	125
% identity	34
NCBI Description	myosin-related protein - slime mold (Physarum polycephalum) >gi_511053_emb_CAA79924_ (Z21878) myosin-related protein [Physarum polycephalum]

Seq. No.	391842
Contig ID	28075_1.R1084
5'-most EST	LIB3479-005-Q6-K1-G4

Seq. No.	391843
Contig ID	28079_1.R1084
5'-most EST	uC-osroM202004f07b1
Method	BLASTX
NCBI GI	g2264382
BLAST score	209
E value	9.0e-21
Match length	133
% identity	44
NCBI Description	(AC002354) putative tetracycline transporter-like protein [Arabidopsis thaliana]

Seq. No.	391844
Contig ID	28089_1.R1084
5'-most EST	LIB3479-006-Q6-K1-A10

Seq. No.	391845
Contig ID	28094_1.R1084
5'-most EST	g569998
Method	BLASTX
NCBI GI	g3075394
BLAST score	1592
E value	0.0e+00
Match length	490
% identity	70
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead

protein [Arabidopsis thaliana]

Seq. No.	391846
Contig ID	28094_2.R1084
5'-most EST	g3061093
Method	BLASTX
NCBI GI	g3075394
BLAST score	370
E value	5.0e-35
Match length	119
% identity	60
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	391847
Contig ID	28112_1.R1084
5'-most EST	LIB3479-006-Q6-K1-C7
Method	BLASTX
NCBI GI	g4220474
BLAST score	402
E value	7.0e-39
Match length	193
% identity	49
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	391848
Contig ID	28113_1.R1084
5'-most EST	g4969141
Method	BLASTX
NCBI GI	g2827141
BLAST score	1602
E value	1.0e-179
Match length	356
% identity	81
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4914447_emb_CAB43650.1_ (AL050351) cellulose synthase catalytic subunit (Ath-A) [Arabidopsis thaliana]

Seq. No.	391849
Contig ID	28121_1.R1084
5'-most EST	LIB3479-006-Q6-K1-D5

Seq. No.	391850
Contig ID	28126_1.R1084
5'-most EST	uC-osrocyp036h05a1
Method	BLASTN
NCBI GI	g1805615
BLAST score	44
E value	2.0e-15
Match length	100
% identity	47
NCBI Description	Rice OSH45 gene for OSH42, OSH44 and OSH45 transcripts, exon 2, 3, 4, 5, 6 and 7, complete cds

Seq. No.	391851
Contig ID	28152_1.R1084
5'-most EST	uC-osflcyp011g01b2

Seq. No.	391852
Contig ID	28160_1.R1084
5'-most EST	g1632044
Method	BLASTX
NCBI GI	g3122234
BLAST score	330
E value	2.0e-30
Match length	135
% identity	52
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) (P38) >gi_2306768 (U87163) eIF-2 beta subunit [Triticum aestivum]

Seq. No.	391853
Contig ID	28163_1.R1084
5'-most EST	g4879050

Seq. No.	391854
Contig ID	28168_1.R1084
5'-most EST	g702413
Method	BLASTX
NCBI GI	g2398679
BLAST score	476
E value	9.0e-48
Match length	148
% identity	73
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	391855
Contig ID	28172_1.R1084
5'-most EST	uC-osflM202052h12b1
Method	BLASTX
NCBI GI	g2275202
BLAST score	814
E value	1.0e-122
Match length	403
% identity	56
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	391856
Contig ID	28172_2.R1084
5'-most EST	uC-osflM202073a11a1

Seq. No.	391857
Contig ID	28179_1.R1084
5'-most EST	LIB3479-007-Q6-K1-D10

Seq. No.	391858
Contig ID	28183_1.R1084
5'-most EST	LIB3479-007-Q6-K1-D3
Method	BLASTX

NCBI GI	g3297816
BLAST score	283
E value	6.0e-25
Match length	150
% identity	35
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	391859
Contig ID	28186_1.R1084
5'-most EST	g1631673
Method	BLASTX
NCBI GI	g3063444
BLAST score	207
E value	2.0e-30
Match length	139
% identity	55
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana] >gi_4973256_gb_AAD35005.1_AF144387_1 (AF144387) thioredoxin-like 1 [Arabidopsis thaliana]

Seq. No.	391860
Contig ID	28188_1.R1084
5'-most EST	uC-osflcyp126h10b1
Method	BLASTX
NCBI GI	g4895198
BLAST score	1036
E value	1.0e-113
Match length	289
% identity	69
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No.	391861
Contig ID	28202_1.R1084
5'-most EST	LIB3479-007-Q6-K1-G12
Method	BLASTX
NCBI GI	g3924612
BLAST score	458
E value	2.0e-45
Match length	100
% identity	90
NCBI Description	(AF069442) mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	391862
Contig ID	28205_1.R1084
5'-most EST	LIB3479-007-Q6-K1-H1
Method	BLASTX
NCBI GI	g4850405
BLAST score	566
E value	1.0e-57
Match length	512
% identity	15
NCBI Description	(AC007357) Similar to gb_D64087 nuclear matrix constituent protein 1 (NMCP1) from Daucus carota. [Arabidopsis thaliana]

Seq. No.	391863
Contig ID	28207_1.R1084
5'-most EST	uC-osroM202038a01b1
Method	BLASTX
NCBI GI	g1502430
BLAST score	507
E value	2.0e-51
Match length	125
% identity	77
NCBI Description	(U62331) phosphate transporter [Arabidopsis thaliana] >gi_2564661 (AF022872) phosphate transporter [Arabidopsis thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770) phosphate transporter, AtPT2 [Arabidopsis thaliana]

Seq. No.	391864
Contig ID	28213_1.R1084
5'-most EST	uC-osroM202030e01b1

Seq. No.	391865
Contig ID	28216_1.R1084
5'-most EST	g1101887

Seq. No.	391866
Contig ID	28229_1.R1084
5'-most EST	g427874

Seq. No.	391867
Contig ID	28233_1.R1084
5'-most EST	LIB3479-008-Q6-K1-C6
Method	BLASTX
NCBI GI	g5915838
BLAST score	184
E value	2.0e-13
Match length	112
% identity	30
NCBI Description	CYTOCHROME P450 71D9 (P450 CP3) >gi_3334661_emb_CAA71514_ (Y10490) putative cytochrome P450 [Glycine max]

Seq. No.	391868
Contig ID	28239_1.R1084
5'-most EST	LIB3479-008-Q6-K1-D4

Seq. No.	391869
Contig ID	28254_1.R1084
5'-most EST	uC-osflm202101f02b1
Method	BLASTX
NCBI GI	g3874228
BLAST score	242
E value	4.0e-20
Match length	183
% identity	21
NCBI Description	(Z49909) cDNA EST CEMSF21F comes from this gene; cDNA EST EMBL:D73546 comes from this gene; cDNA EST EMBL:D73669 comes from this gene; cDNA EST EMBL:D70979 comes from this gene; cDNA EST EMBL:D71075 comes from this gene; cDNA

Seq. No.	391870
Contig ID	28260_1.R1084
5'-most EST	g4715819
Method	BLASTX
NCBI GI	g4417267
BLAST score	231
E value	8.0e-19
Match length	187
% identity	32
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391871
Contig ID	28269_1.R1084
5'-most EST	LIB3479-008-Q6-K1-H11
Method	BLASTX
NCBI GI	g585147
BLAST score	215
E value	7.0e-17
Match length	229
% identity	32
NCBI Description	FLUG PROTEIN >gi_1078630_pir__A53186 fluG protein - Emericella nidulans >gi_450258 (L27817) FluG [Emericella nidulans]

Seq. No.	391872
Contig ID	28286_1.R1084
5'-most EST	LIB3479-009-Q6-K1-B12

Seq. No.	391873
Contig ID	28289_1.R1084
5'-most EST	uC-osroM202019c11a1
Method	BLASTX
NCBI GI	g2129578
BLAST score	166
E value	2.0e-11
Match length	43
% identity	72
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	391874
Contig ID	28289_2.R1084
5'-most EST	LIB3479-009-Q6-K1-B4
Method	BLASTN
NCBI GI	g4959460
BLAST score	37
E value	2.0e-11
Match length	42
% identity	36
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	391875
Contig ID	28294_1.R1084
5'-most EST	g6012859

Method	BLASTX
NCBI GI	g3135265
BLAST score	227
E value	2.0e-18
Match length	48
% identity	83
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	391876
Contig ID	28295_1.R1084
5'-most EST	LIB3479-009-Q6-K1-C12

Seq. No.	391877
Contig ID	28296_1.R1084
5'-most EST	g3767505
Method	BLASTX
NCBI GI	g266944
BLAST score	685
E value	5.0e-72
Match length	130
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2) >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic - tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein L2 [Lycopersicon esculentum]

Seq. No.	391878
Contig ID	28299_1.R1084
5'-most EST	LIB3479-012-Q6-K1-D1

Seq. No.	391879
Contig ID	28300_1.R1084
5'-most EST	uC-osroM202023c01b1
Method	BLASTX
NCBI GI	g3169719
BLAST score	545
E value	1.0e-55
Match length	175
% identity	70
NCBI Description	(AF007109) similar to yeast dcp1 [Arabidopsis thaliana]

Seq. No.	391880
Contig ID	28313_1.R1084
5'-most EST	uC-osf1cyp079b02a1
Method	BLASTX
NCBI GI	g442693
BLAST score	569
E value	1.0e-58
Match length	120
% identity	83
NCBI Description	Barwin, Basic Barley Seed Protein (Nmr, 20 Structures) >gi_442694_pdb_1BW4_ Barwin, Basic Barley Seed Protein (Nmr, 20 Structures)

Seq. No.	391881
Contig ID	28317_1.R1084
5'-most EST	uC-osflm202101a05b1

Seq. No.	391882
Contig ID	28325_1.R1084
5'-most EST	uC-osflcyp049d01b1
Seq. No.	391883
Contig ID	28329_1.R1084
5'-most EST	LIB3479-009-Q6-K1-G5
Seq. No.	391884
Contig ID	28330_1.R1084
5'-most EST	uC-osflcyp013b01b1
Seq. No.	391885
Contig ID	28331_1.R1084
5'-most EST	LIB3479-009-Q6-K1-G7
Method	BLASTX
NCBI GI	g544400
BLAST score	513
E value	4.0e-52
Match length	126
% identity	76
NCBI Description	GLUTELIN TYPE-B 2 PRECURSOR >gi_100676_pir__S17763 glutelin gluB-2 precursor - rice >gi_20212_emb_CAA38110_ (X54192) glutelin [Oryza sativa]
Seq. No.	391886
Contig ID	28337_1.R1084
5'-most EST	g5455632
Method	BLASTX
NCBI GI	g5734636
BLAST score	313
E value	2.0e-28
Match length	121
% identity	52
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]
Seq. No.	391887
Contig ID	28340_1.R1084
5'-most EST	g2431506
Method	BLASTX
NCBI GI	g4836883
BLAST score	358
E value	9.0e-34
Match length	173
% identity	38
NCBI Description	(AC007260) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	391888
Contig ID	28347_1.R1084
5'-most EST	g3762172
Seq. No.	391889
Contig ID	28349_1.R1084
5'-most EST	LIB3479-011-Q6-K1-A8

Method	BLASTX
NCBI GI	g5579408
BLAST score	480
E value	3.0e-48
Match length	156
% identity	60
NCBI Description	(AF164434) putative diacylglycerol acyltransferase [Brassica napus]

Seq. No.	391890
Contig ID	28355_1.R1084
5'-most EST	LIB3479-010-Q6-K1-B3

Seq. No.	391891
Contig ID	28361_1.R1084
5'-most EST	uC-osroM202035c11b1

Seq. No.	391892
Contig ID	28364_1.R1084
5'-most EST	g2309976

Seq. No.	391893
Contig ID	28379_1.R1084
5'-most EST	uC-osrocyp003f02a1

Seq. No.	391894
Contig ID	28381_1.R1084
5'-most EST	uC-osflcyp064h10b1
Method	BLASTX
NCBI GI	g4138581
BLAST score	187
E value	8.0e-14
Match length	94
% identity	46
NCBI Description	(X98474) mitochondrial energy transfer protein [Solanum tuberosum]

Seq. No.	391895
Contig ID	28382_1.R1084
5'-most EST	g2312318
Method	BLASTX
NCBI GI	g4512703
BLAST score	205
E value	5.0e-22
Match length	138
% identity	44
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	391896
Contig ID	28387_1.R1084
5'-most EST	uC-osroM202037f08a1
Method	BLASTX
NCBI GI	g5123545
BLAST score	356
E value	2.0e-33
Match length	101
% identity	70

NCBI Description	(AL079344) arginine methyltransferase (pam1) [Arabidopsis thaliana]

Seq. No.	391897
Contig ID	28396_1.R1084
5'-most EST	g1632326
Method	BLASTX
NCBI GI	g1109614
BLAST score	164
E value	3.0e-11
Match length	48
% identity	58
NCBI Description	(D45078) MP28 [Cucurbita sp.]

Seq. No.	391898
Contig ID	28398_1.R1084
5'-most EST	uC-osflcyp023b12b1

Seq. No.	391899
Contig ID	28408_1.R1084
5'-most EST	LIB3479-011-Q6-K1-A9
Method	BLASTX
NCBI GI	g4689034
BLAST score	167
E value	2.0e-11
Match length	69
% identity	49
NCBI Description	(AJ133751) chloroplast ribosome recycling factor protein [Spinacia oleracea]

Seq. No.	391900
Contig ID	28418_1.R1084
5'-most EST	LIB3479-011-Q6-K1-C3
Method	BLASTX
NCBI GI	g5731763
BLAST score	217
E value	2.0e-17
Match length	56
% identity	77
NCBI Description	(X92419) SNAP25A protein [Arabidopsis thaliana] >gi_5731764_emb_CAB52583.1_ (X92420) SNAP25AB protein [Arabidopsis thaliana]

Seq. No.	391901
Contig ID	28422_1.R1084
5'-most EST	g4880540

Seq. No.	391902
Contig ID	28424_2.R1084
5'-most EST	LIB3479-011-Q6-K1-C9
Method	BLASTX
NCBI GI	g1173218
BLAST score	499
E value	4.0e-50
Match length	102
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal

protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	391903
Contig ID	28429_1.R1084
5'-most EST	LIB3479-011-Q6-K1-D4

Seq. No.	391904
Contig ID	28435_1.R1084
5'-most EST	uC-osflcyp112b04b1
Method	BLASTX
NCBI GI	g5911782
BLAST score	357
E value	1.0e-40
Match length	167
% identity	56
NCBI Description	(AJ133786) gigantea protein [Arabidopsis thaliana] >gi_6002680_gb_AAF00092.1_AF105064_1 (AF105064) GIGANTEA [Arabidopsis thaliana]

Seq. No.	391905
Contig ID	28437_1.R1084
5'-most EST	LIB3479-011-Q6-K1-E12
Method	BLASTX
NCBI GI	g267152
BLAST score	204
E value	2.0e-15
Match length	116
% identity	50
NCBI Description	PROBABLE ATP-DEPENDENT TRANSPORTER YCF16 >gi_11938_emb_CAA43151_ (X60752) ORF 756 [Odontella sinensis] >gi_11945_emb_CAA43158_ (X60752) ORF 252 [Odontella sinensis] >gi_1185205_emb_CAA91688_ (Z67753) ORF251 [Odontella sinensis]

Seq. No.	391906
Contig ID	28447_1.R1084
5'-most EST	g3759804

Seq. No.	391907
Contig ID	28456_1.R1084
5'-most EST	uC-osflcyp086d11b1
Method	BLASTX
NCBI GI	g4926867
BLAST score	684
E value	9.0e-72
Match length	210
% identity	63
NCBI Description	(AC007509) serine acetyltransferase (GB:AF112303) [Arabidopsis thaliana]

Seq. No.	391908
Contig ID	28467_1.R1084
5'-most EST	uC-osflcyp043d01b1

Seq. No.	391909
Contig ID	28468_1.R1084

5'-most EST	g2798420
Method	BLASTX
NCBI GI	g121477
BLAST score	265
E value	6.0e-28
Match length	106
% identity	60
NCBI Description	GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa] >gi_226767_prf__1604474A glutelin [Oryza sativa]

Seq. No.	391910
Contig ID	28471_1.R1084
5'-most EST	g568916

Seq. No.	391911
Contig ID	28480_1.R1084
5'-most EST	uC-osflcyp158f09a1
Method	BLASTX
NCBI GI	g3915037
BLAST score	894
E value	2.0e-96
Match length	190
% identity	85
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose synthase [Pisum sativum]

Seq. No.	391912
Contig ID	28482_1.R1084
5'-most EST	g2431132
Method	BLASTX
NCBI GI	g4725941
BLAST score	463
E value	4.0e-46
Match length	115
% identity	70
NCBI Description	(AL049730) putative pollen-specific protein [Arabidopsis thaliana]

Seq. No.	391913
Contig ID	28485_1.R1084
5'-most EST	uC-osflM2020117g11a1
Method	BLASTX
NCBI GI	g6041837
BLAST score	259
E value	4.0e-22
Match length	125
% identity	42
NCBI Description	(AC009853) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391914
Contig ID	28495_1.R1084
5'-most EST	uC-osrocyp007f09a1

Seq. No.	391915

Contig ID	28508_1.R1084
5'-most EST	g3759858
Seq. No.	391916
Contig ID	28521_1.R1084
5'-most EST	uC-osf1M202043g09b1
Method	BLASTX
NCBI GI	g5123943
BLAST score	283
E value	2.0e-37
Match length	116
% identity	67
NCBI Description	(AL079349) serine/threonine-specific protein kinase MHK [Arabidopsis thaliana]
Seq. No.	391917
Contig ID	28528_1.R1084
5'-most EST	g2427962
Method	BLASTX
NCBI GI	g4417286
BLAST score	192
E value	2.0e-14
Match length	104
% identity	47
NCBI Description	(AC007019) putative shikimate kinase [Arabidopsis thaliana]
Seq. No.	391918
Contig ID	28529_1.R1084
5'-most EST	LIB3479-012-Q6-K1-G2
Seq. No.	391919
Contig ID	28540_2.R1084
5'-most EST	uC-osf1cyp028f02b1
Method	BLASTX
NCBI GI	g2462762
BLAST score	260
E value	2.0e-22
Match length	84
% identity	62
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.	391920
Contig ID	28542_1.R1084
5'-most EST	g4715424
Method	BLASTX
NCBI GI	g422391
BLAST score	397
E value	4.0e-78
Match length	338
% identity	47
NCBI Description	glycine--tRNA ligase (EC 6.1.1.14) - silkworm
Seq. No.	391921
Contig ID	28545_1.R1084
5'-most EST	LIB3479-012-Q6-K1-H8
Method	BLASTX

NCBI GI	g2160694
BLAST score	649
E value	6.0e-68
Match length	182
% identity	70
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	391922
Contig ID	28553_1.R1084
5'-most EST	LIB3599-001-P1-N6-B2

Seq. No.	391923
Contig ID	28557_1.R1084
5'-most EST	uC-osf1cyp012g02b1
Method	BLASTX
NCBI GI	g126896
BLAST score	654
E value	6.0e-95
Match length	231
% identity	79
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37) precursor, mitochondrial - watermelon >gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27 to 320) [Citrullus lanatus]

Seq. No.	391924
Contig ID	28564_1.R1084
5'-most EST	uC-osroM202012d10a1

Seq. No.	391925
Contig ID	28565_1.R1084
5'-most EST	LIB3599-001-P1-K6-C6
Method	BLASTX
NCBI GI	g3426043
BLAST score	473
E value	4.0e-47
Match length	113
% identity	68
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	391926
Contig ID	28567_1.R1084
5'-most EST	LIB3599-001-P1-N6-C9

Seq. No.	391927
Contig ID	28571_1.R1084
5'-most EST	uC-osf1cyp151h04b1
Method	BLASTN
NCBI GI	g6016845
BLAST score	329
E value	0.0e+00
Match length	649
% identity	97
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	391928
Contig ID	28571_2.R1084
5'-most EST	LIB3599-001-P1-N6-D3
Method	BLASTN
NCBI GI	g6016845
BLAST score	333
E value	0.0e+00
Match length	474
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	391929
Contig ID	28579_1.R1084
5'-most EST	LIB3599-001-P1-N6-E11

Seq. No.	391930
Contig ID	28580_1.R1084
5'-most EST	g3762420

Seq. No.	391931
Contig ID	28614_1.R1084
5'-most EST	LIB3599-001-P1-K6-A2
Method	BLASTX
NCBI GI	g4263781
BLAST score	260
E value	3.0e-22
Match length	84
% identity	56
NCBI Description	(AC006068) putative membrane transport protein [Arabidopsis thaliana]

Seq. No.	391932
Contig ID	28617_1.R1084
5'-most EST	LIB3599-001-P1-K6-A6
Method	BLASTX
NCBI GI	g5733660
BLAST score	287
E value	2.0e-25
Match length	162
% identity	49
NCBI Description	(AF165939) vacuolar V-H+ATPase subunit E [Citrus limon]

Seq. No.	391933
Contig ID	28627_1.R1084
5'-most EST	LIB3599-001-P1-K6-B5
Method	BLASTX
NCBI GI	g5777592
BLAST score	300
E value	6.0e-27
Match length	137
% identity	36
NCBI Description	(X62091) low molecular weight globulin [Oryza sativa]

Seq. No.	391934
Contig ID	28680_1.R1084
5'-most EST	g2799163
Method	BLASTN

NCBI GI	g413823
BLAST score	42
E value	5.0e-14
Match length	42
% identity	100
NCBI Description	Cloning vector pYEUra3, complete sequence

Seq. No.	391935
Contig ID	28694_1.R1084
5'-most EST	g1037051

Seq. No.	391936
Contig ID	28702_1.R1084
5'-most EST	LIB3599-002-P1-N6-C7

Seq. No.	391937
Contig ID	28729_1.R1084
5'-most EST	LIB3599-002-P1-N6-G5
Method	BLASTX
NCBI GI	g2388580
BLAST score	184
E value	2.0e-13
Match length	60
% identity	50
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	391938
Contig ID	28743_1.R1084
5'-most EST	uC-osflcyp002b02b1
Method	BLASTX
NCBI GI	g732080
BLAST score	166
E value	4.0e-11
Match length	187
% identity	27
NCBI Description	HYPOTHETICAL 32.0 KD PROTEIN IN MRR-TSR INTERGENIC REGION (F284) >gi_1361266_pir__S56578 yjiA protein - Escherichia coli >gi_537194 (U14003) yjiA gene product [Escherichia coli] >gi_1790812 (AE000506) orf, hypothetical protein [Escherichia coli]

Seq. No.	391939
Contig ID	28754_1.R1084
5'-most EST	uC-osflcyp002c08b1
Method	BLASTX
NCBI GI	g3935169
BLAST score	172
E value	5.0e-12
Match length	65
% identity	55
NCBI Description	(AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No.	391940
Contig ID	28763_1.R1084
5'-most EST	g5667546

Seq. No.	391941
Contig ID	28769_1.R1084
5'-most EST	uC-osflcyp002e08b1

Seq. No.	391942
Contig ID	28773_1.R1084
5'-most EST	uC-osflcyp158f02b1
Method	BLASTX
NCBI GI	g4006978
BLAST score	201
E value	3.0e-15
Match length	87
% identity	44
NCBI Description	(AJ131335) pollen allergen (group II) [Cynodon dactylon]

Seq. No.	391943
Contig ID	28773_2.R1084
5'-most EST	uC-osflcyp174b01a1

Seq. No.	391944
Contig ID	28773_4.R1084
5'-most EST	uC-osflcyp011a04b1

Seq. No.	391945
Contig ID	28773_5.R1084
5'-most EST	uC-osflcyp002f04b1
Method	BLASTX
NCBI GI	g4006978
BLAST score	174
E value	4.0e-12
Match length	90
% identity	38
NCBI Description	(AJ131335) pollen allergen (group II) [Cynodon dactylon]

Seq. No.	391946
Contig ID	28774_1.R1084
5'-most EST	uC-osroM202037d02b1
Method	BLASTX
NCBI GI	g5020215
BLAST score	409
E value	1.0e-39
Match length	194
% identity	47
NCBI Description	(AF149917) acyl CoA reductase [Simmondsia chinensis] >gi_5020217_gb_AAD38040.1_AF149918_1 (AF149918) acyl CoA reductase [synthetic construct]

Seq. No.	391947
Contig ID	28774_2.R1084
5'-most EST	uC-osrocyp033f02b1
Method	BLASTX
NCBI GI	g5020215
BLAST score	169
E value	1.0e-23
Match length	124
% identity	53
NCBI Description	(AF149917) acyl CoA reductase [Simmondsia chinensis]

>gi_5020217_gb_AAD38040.1_AF149918_1 (AF149918) acyl CoA reductase [synthetic construct]

Seq. No.	391948
Contig ID	28779_1.R1084
5'-most EST	uC-osflcyp002g07b1

Seq. No.	391949
Contig ID	28788_1.R1084
5'-most EST	uC-osflm202106b08b1
Method	BLASTX
NCBI GI	g4836875
BLAST score	545
E value	1.0e-115
Match length	327
% identity	78
NCBI Description	(AC007260) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	391950
Contig ID	28801_1.R1084
5'-most EST	uC-osflcyp031e11b1

Seq. No.	391951
Contig ID	28804_1.R1084
5'-most EST	uC-osflcyp005b12b1
Method	BLASTX
NCBI GI	g3212865
BLAST score	849
E value	3.0e-91
Match length	257
% identity	66
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	391952
Contig ID	28813_1.R1084
5'-most EST	uC-osflcyp005d05b1
Method	BLASTX
NCBI GI	g1419368
BLAST score	443
E value	6.0e-44
Match length	107
% identity	78
NCBI Description	(X97725) actin depolymerizing factor [Zea mays]

Seq. No.	391953
Contig ID	28819_1.R1084
5'-most EST	uC-osflcyp005e01b1
Method	BLASTX
NCBI GI	g4314388
BLAST score	354
E value	3.0e-33
Match length	115
% identity	61
NCBI Description	(AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	391954

Contig ID	28820_1.R1084
5'-most EST	uC-osflcyp005e03b1
Method	BLASTX
NCBI GI	g3033386
BLAST score	536
E value	2.0e-54
Match length	204
% identity	56
NCBI Description	(AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No.	391955
Contig ID	28821_1.R1084
5'-most EST	uC-osflcyp128g08a1

Seq. No.	391956
Contig ID	28822_1.R1084
5'-most EST	uC-osflcyp005e07b1
Method	BLASTX
NCBI GI	g3695392
BLAST score	293
E value	5.0e-26
Match length	147
% identity	45
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	391957
Contig ID	28825_1.R1084
5'-most EST	uC-osflcyp088a08b1
Method	BLASTX
NCBI GI	g2864624
BLAST score	278
E value	2.0e-24
Match length	185
% identity	17
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	391958
Contig ID	28837_1.R1084
5'-most EST	g2311074

Seq. No.	391959
Contig ID	28839_1.R1084
5'-most EST	uC-osflcyp005h07b1
Method	BLASTX
NCBI GI	g6056372
BLAST score	416
E value	8.0e-41
Match length	128
% identity	65
NCBI Description	(AC009894) Very similar to receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	391960
Contig ID	28846_1.R1084
5'-most EST	uC-osflcyp169g03b1

Seq. No.	391961

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Contig ID	28847_1.R1084
5'-most EST	g5003813
Method	BLASTX
NCBI GI	g1717957
BLAST score	1070
E value	1.0e-117
Match length	272
% identity	75
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_100923_pir__A41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - maize >gi_168607 (M77224) Rieske Fe-S protein [Zea mays]

Seq. No.	391962
Contig ID	28854_1.R1084
5'-most EST	uC-osflcyp006g08b1
Method	BLASTX
NCBI GI	g1871186
BLAST score	947
E value	1.0e-102
Match length	287
% identity	64
NCBI Description	(U90439) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	391963
Contig ID	28858_1.R1084
5'-most EST	uC-osflcyp006c10b1

Seq. No.	391964
Contig ID	28859_1.R1084
5'-most EST	uC-osflM202062f12b1

Seq. No.	391965
Contig ID	28866_1.R1084
5'-most EST	uC-osflcyp011g05b1
Method	BLASTX
NCBI GI	g4886280
BLAST score	296
E value	1.0e-26
Match length	145
% identity	39
NCBI Description	(AL050300) putative protein [Arabidopsis thaliana]

Seq. No.	391966
Contig ID	28872_1.R1084
5'-most EST	uC-osflcyp006e09b1
Method	BLASTX
NCBI GI	g2894598
BLAST score	487
E value	4.0e-49
Match length	110
% identity	76
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	391967
Contig ID	28898_1.R1084

5'-most EST	uC-osflcyp026f04b1
Seq. No.	391968
Contig ID	28898_2.R1084
5'-most EST	uC-osflM202014g08b1
Method	BLASTN
NCBI GI	g5042437
BLAST score	135
E value	1.0e-69
Match length	195
% identity	78
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.	391969
Contig ID	28901_1.R1084
5'-most EST	uC-osroM202031f03b1
Method	BLASTX
NCBI GI	g2832633
BLAST score	752
E value	6.0e-80
Match length	161
% identity	84
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]
Seq. No.	391970
Contig ID	28902_1.R1084
5'-most EST	uC-osflM202066a08b1
Method	BLASTX
NCBI GI	g2739374
BLAST score	279
E value	2.0e-27
Match length	157
% identity	51
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.	391971
Contig ID	28905_1.R1084
5'-most EST	uC-osflcyp007d06b1
Seq. No.	391972
Contig ID	28911_1.R1084
5'-most EST	uC-osflcyp007f06b1
Method	BLASTX
NCBI GI	g1519253
BLAST score	151
E value	7.0e-18
Match length	75
% identity	60
NCBI Description	(U65958) GF14-d protein [Oryza sativa]
Seq. No.	391973
Contig ID	28919_1.R1084
5'-most EST	uC-osflcyp013f10b1
Seq. No.	391974
Contig ID	28922_1.R1084
5'-most EST	uC-osflcyp007h05b1

Method	BLASTX
NCBI GI	g629849
BLAST score	624
E value	7.0e-78
Match length	168
% identity	86
NCBI Description	pectate lyase (EC 4.2.2.2) - maize >gi_405535 (L20140) homology with pectate lyase [Zea mays]

Seq. No.	391975
Contig ID	28926_1.R1084
5'-most EST	uC-osflcyp008b04b1
Method	BLASTX
NCBI GI	g2570160
BLAST score	172
E value	3.0e-20
Match length	69
% identity	70
NCBI Description	(D45181) chitinase [Chenopodium amaranticolor]

Seq. No.	391976
Contig ID	28928_1.R1084
5'-most EST	uC-osflcyp045h09b1
Method	BLASTX
NCBI GI	g3860323
BLAST score	156
E value	6.0e-10
Match length	41
% identity	80
NCBI Description	(AJ012688) hypothetical protein [Cicer arietinum]

Seq. No.	391977
Contig ID	28929_1.R1084
5'-most EST	uC-osflcyp008d12b1
Method	BLASTX
NCBI GI	g2499931
BLAST score	352
E value	4.0e-33
Match length	92
% identity	73
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT) >gi_2129534_pir__S71272 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_1321681_emb_CAA65609_ (X96866) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_5902383_gb_AAD55485.1_AC009322_25 (AC009322) adenine phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	391978
Contig ID	28932_1.R1084
5'-most EST	uC-osflcyp037d02b1
Method	BLASTX
NCBI GI	g1839188
BLAST score	407
E value	2.0e-39
Match length	121
% identity	61

NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No.	391979
Contig ID	28935_1.R1084
5'-most EST	uC-osflcyp171g03b1

Seq. No.	391980
Contig ID	28960_1.R1084
5'-most EST	uC-osflcyp009e06b1

Seq. No.	391981
Contig ID	28965_1.R1084
5'-most EST	uC-osflcyp086d04b1

Seq. No.	391982
Contig ID	28965_2.R1084
5'-most EST	uC-osflcyp106d03b1

Seq. No.	391983
Contig ID	28966_1.R1084
5'-most EST	uC-osflcyp173c07b1

Seq. No.	391984
Contig ID	28975_1.R1084
5'-most EST	uC-osflM202052h04b1
Method	BLASTX
NCBI GI	g2262165
BLAST score	515
E value	4.0e-52
Match length	151
% identity	66
NCBI Description	(AC002329) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	391985
Contig ID	28981_1.R1084
5'-most EST	uC-osflcyp009h06b1
Method	BLASTX
NCBI GI	g5668770
BLAST score	612
E value	2.0e-63
Match length	170
% identity	69
NCBI Description	(AC005916) T17H3.9 [Arabidopsis thaliana]

Seq. No.	391986
Contig ID	28984_1.R1084
5'-most EST	uC-osflM202049h02b1

Seq. No.	391987
Contig ID	28994_1.R1084
5'-most EST	uC-osflcyp010e10b1

Seq. No.	391988
Contig ID	28997_1.R1084
5'-most EST	uC-osflM202092a08b1
Method	BLASTX

NCBI GI	g1076486
BLAST score	266
E value	4.0e-23
Match length	63
% identity	75
NCBI Description	cim1 protein - soybean >gi_555616 (U03860) cytokinin induced message [Glycine max]

Seq. No.	391989
Contig ID	29015_1.R1084
5'-most EST	uC-osrocyp006d08b1
Method	BLASTX
NCBI GI	g5080764
BLAST score	334
E value	5.0e-31
Match length	112
% identity	56
NCBI Description	(AC007203) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	391990
Contig ID	29016_1.R1084
5'-most EST	uC-osflcyp023h11b1

Seq. No.	391991
Contig ID	29025_1.R1084
5'-most EST	uC-osflcyp011d06b1

Seq. No.	391992
Contig ID	29028_1.R1084
5'-most EST	uC-osflcyp030h12b1
Method	BLASTX
NCBI GI	g1001708
BLAST score	444
E value	5.0e-44
Match length	160
% identity	57
NCBI Description	(D64004) NifS [Synechocystis sp.]

Seq. No.	391993
Contig ID	29032_1.R1084
5'-most EST	uC-osflcyp011e01b1
Method	BLASTX
NCBI GI	g5902376
BLAST score	297
E value	1.0e-26
Match length	171
% identity	42
NCBI Description	(AC009322) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	391994
Contig ID	29034_1.R1084
5'-most EST	uC-osflcyp011e03b1
Method	BLASTX
NCBI GI	g4759280
BLAST score	567
E value	8.0e-62
Match length	168

% identity	70
NCBI Description	U5 snRNP-specific protein, 116 kD >gi_434759_dbj_BAA04699_ (D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]

Seq. No.	391995
Contig ID	29040_1.R1084
5'-most EST	uC-osflcyp173d07b1
Method	BLASTX
NCBI GI	g3785989
BLAST score	615
E value	5.0e-64
Match length	146
% identity	78
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	391996
Contig ID	29041_1.R1084
5'-most EST	uC-osflM202062h12b1

Seq. No.	391997
Contig ID	29045_1.R1084
5'-most EST	g2310673

Seq. No.	391998
Contig ID	29047_1.R1084
5'-most EST	g571588
Method	BLASTX
NCBI GI	g2764574
BLAST score	258
E value	3.0e-22
Match length	139
% identity	41
NCBI Description	(AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

Seq. No.	391999
Contig ID	29049_1.R1084
5'-most EST	g2427626

Seq. No.	392000
Contig ID	29055_1.R1084
5'-most EST	g701727
Method	BLASTX
NCBI GI	g4512671
BLAST score	106
E value	9.0e-11
Match length	96
% identity	44
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4929128_gb_AAD33868.1_AF141375_1 (AF141375) protodermal factor 1 [Arabidopsis thaliana] >gi_4929130_gb_AAD33869.1_AF141376_1 (AF141376) protodermal factor 1 [Arabidopsis thaliana]

Seq. No.	392001
Contig ID	29057_1.R1084
5'-most EST	g700112

Method	BLASTX
NCBI GI	g1778093
BLAST score	368
E value	9.0e-39
Match length	113
% identity	76
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	392002
Contig ID	29058_1.R1084
5'-most EST	g2800956
Method	BLASTX
NCBI GI	g4309728
BLAST score	324
E value	5.0e-30
Match length	74
% identity	82
NCBI Description	(AC006439) putative ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	392003
Contig ID	29059_1.R1084
5'-most EST	uC-osroM202028c11b1
Method	BLASTX
NCBI GI	g2492636
BLAST score	644
E value	2.0e-67
Match length	156
% identity	81
NCBI Description	ACONITASE (ACONITATE HYDRATASE) (CITRATE HYDRO-LYASE) >gi_1084317_pir__S49849 aconitate hydratase (EC 4.2.1.3) - muskmelon (fragment) >gi_599723_emb_CAA58047_ (X82840) aconitase [Cucumis melo]

Seq. No.	392004
Contig ID	29061_1.R1084
5'-most EST	uC-osflcyp011h07b1

Seq. No.	392005
Contig ID	29075_1.R1084
5'-most EST	uC-osflcyp012b06b1
Method	BLASTX
NCBI GI	g5032015
BLAST score	180
E value	7.0e-13
Match length	202
% identity	13
NCBI Description	Rab9 effector p40 >gi_2217970_emb_CAB09808_ (Z97074) p40 [Homo sapiens]

Seq. No.	392006
Contig ID	29076_1.R1084
5'-most EST	uC-osflcyp012b08b1

Seq. No. 392007

Contig ID	29079_1.R1084
5'-most EST	g2309854
Method	BLASTN
NCBI GI	g4160401
BLAST score	39
E value	2.0e-12
Match length	156
% identity	86
NCBI Description	Zea mays eIF-5 gene, exons 1-2

Seq. No.	392008
Contig ID	29079_2.R1084
5'-most EST	g2310915
Method	BLASTX
NCBI GI	g4160402
BLAST score	223
E value	5.0e-18
Match length	45
% identity	96
NCBI Description	(AJ132240) eukaryotic translation initiation factor 5 [Zea mays]

Seq. No.	392009
Contig ID	29080_1.R1084
5'-most EST	g2801045

Seq. No.	392010
Contig ID	29082_1.R1084
5'-most EST	uC-osflcyp142b05b1

Seq. No.	392011
Contig ID	29082_2.R1084
5'-most EST	uC-osflcyp012c08b1

Seq. No.	392012
Contig ID	29092_2.R1084
5'-most EST	uC-osflM202054h03b1
Method	BLASTX
NCBI GI	g2145356
BLAST score	306
E value	1.0e-27
Match length	87
% identity	67
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	392013
Contig ID	29094_1.R1084
5'-most EST	uC-osflcyp012e07b1
Method	BLASTX
NCBI GI	g719291
BLAST score	360
E value	4.0e-34
Match length	183
% identity	52
NCBI Description	(U19134) unknown [Arabidopsis thaliana] >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]

Seq. No.	392014
Contig ID	29099_1.R1084
5'-most EST	uC-osrocyp025e02a1
Method	BLASTX
NCBI GI	g4567203
BLAST score	250
E value	3.0e-21
Match length	55
% identity	87
NCBI Description	(AC007168) putative beta-hydroxyacyl-ACP dehydratase [Arabidopsis thaliana]

Seq. No.	392015
Contig ID	29103_1.R1084
5'-most EST	uC-osflcyp012f11b1
Method	BLASTX
NCBI GI	g4586058
BLAST score	177
E value	1.0e-12
Match length	102
% identity	39
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	392016
Contig ID	29104_1.R1084
5'-most EST	uC-osflcyp012g01b1

Seq. No.	392017
Contig ID	29104_2.R1084
5'-most EST	uC-osflcyp086b05b1

Seq. No.	392018
Contig ID	29109_1.R1084
5'-most EST	uC-osflcyp035b08b1
Method	BLASTX
NCBI GI	g3386614
BLAST score	637
E value	3.0e-66
Match length	169
% identity	67
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	392019
Contig ID	29109_2.R1084
5'-most EST	g5003536
Method	BLASTX
NCBI GI	g2213632
BLAST score	326
E value	6.0e-30
Match length	127
% identity	50
NCBI Description	(AC000103) F21J9.24 [Arabidopsis thaliana]

Seq. No.	392020
Contig ID	29113_1.R1084

5'-most EST	uC-osflcyp012g12b1
Seq. No.	392021
Contig ID	29115_1.R1084
5'-most EST	uC-osflcyp012h03b1
Seq. No.	392022
Contig ID	29116_1.R1084
5'-most EST	uC-osflcyp012h05b1
Method	BLASTX
NCBI GI	g4512671
BLAST score	255
E value	2.0e-21
Match length	174
% identity	39
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4929128_gb_AAD33868.1_AF141375_1 (AF141375) protodermal factor 1 [Arabidopsis thaliana] >gi_4929130_gb_AAD33869.1_AF141376_1 (AF141376) protodermal factor 1 [Arabidopsis thaliana]
Seq. No.	392023
Contig ID	29119_1.R1084
5'-most EST	uC-osflm202102a11b1
Method	BLASTX
NCBI GI	g5733874
BLAST score	543
E value	4.0e-92
Match length	473
% identity	45
NCBI Description	(AC007932) F11A17.8 [Arabidopsis thaliana]
Seq. No.	392024
Contig ID	29130_1.R1084
5'-most EST	g2428212
Method	BLASTX
NCBI GI	g3297809
BLAST score	246
E value	9.0e-21
Match length	153
% identity	41
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]
Seq. No.	392025
Contig ID	29150_1.R1084
5'-most EST	uC-osflcyp024c07b1
Method	BLASTX
NCBI GI	g3033401
BLAST score	634
E value	3.0e-66
Match length	183
% identity	66
NCBI Description	(AC004238) putative potassium transporter [Arabidopsis thaliana]
Seq. No.	392026
Contig ID	29164_1.R1084

5'-most EST	g3763300
Method	BLASTN
NCBI GI	g2052354
BLAST score	54
E value	4.0e-21
Match length	106
% identity	92
NCBI Description	Human uncoupling protein homolog (UCPH) mRNA, complete cds

Seq. No.	392027
Contig ID	29164_2.R1084
5'-most EST	uC-osf1M202052f01b1
Method	BLASTX
NCBI GI	g1708236
BLAST score	667
E value	1.0e-105
Match length	280
% identity	66
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	392028
Contig ID	29167_1.R1084
5'-most EST	uC-osroM202036h01b1
Method	BLASTX
NCBI GI	g3451072
BLAST score	374
E value	2.0e-35
Match length	91
% identity	75
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	392029
Contig ID	29167_2.R1084
5'-most EST	g2310999
Method	BLASTX
NCBI GI	g3451072
BLAST score	511
E value	2.0e-58
Match length	154
% identity	70
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	392030
Contig ID	29168_1.R1084
5'-most EST	uC-osrocyp037g12b1

Seq. No.	392031
Contig ID	29184_1.R1084
5'-most EST	uC-osflcyp014a11b1
Method	BLASTX

NCBI GI g5733877
BLAST score 483
E value 3.0e-48
Match length 164
% identity 57
NCBI Description (AC007932) F11A17.13 [Arabidopsis thaliana]

Seq. No. 392032
Contig ID 29185_1.R1084
5'-most EST uC-osflcyp014a12b1

Seq. No. 392033
Contig ID 29193_1.R1084
5'-most EST uC-osflcyp156f02b1

Seq. No. 392034
Contig ID 29199_1.R1084
5'-most EST g2312884
Method BLASTX
NCBI GI g4567226
BLAST score 192
E value 2.0e-14
Match length 66
% identity 62
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 392035
Contig ID 29199_2.R1084
5'-most EST g2801185
Method BLASTX
NCBI GI g4567226
BLAST score 188
E value 9.0e-14
Match length 80
% identity 53
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 392036
Contig ID 29201_1.R1084
5'-most EST uC-osflcyp078c09a1
Method BLASTX
NCBI GI g550452
BLAST score 259
E value 3.0e-22
Match length 72
% identity 69
NCBI Description (U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]

Seq. No. 392037
Contig ID 29203_1.R1084
5'-most EST uC-osflcyp057c01b1
Method BLASTX
NCBI GI g4538939
BLAST score 694
E value 4.0e-80
Match length 162

% identity	87
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	392038
Contig ID	29211_1.R1084
5'-most EST	uC-osflcyp014e01b1
Method	BLASTX
NCBI GI	g2317901
BLAST score	628
E value	1.0e-65
Match length	158
% identity	72
NCBI Description	(U89959) Similar to vesicle transport protein, PIR Accession Number A55931 [Arabidopsis thaliana]

Seq. No.	392039
Contig ID	29217_1.R1084
5'-most EST	uC-osflcyp014e12b1

Seq. No.	392040
Contig ID	29228_1.R1084
5'-most EST	g2427893
Method	BLASTX
NCBI GI	g3668069
BLAST score	1001
E value	1.0e-134
Match length	347
% identity	71
NCBI Description	(U28007) Pto kinase interactor 1 [Lycopersicon esculentum]

Seq. No.	392041
Contig ID	29229_1.R1084
5'-most EST	uC-osflcyp014g11b1
Method	BLASTX
NCBI GI	g2546988
BLAST score	444
E value	5.0e-53
Match length	146
% identity	73
NCBI Description	(Y15113) 2-dehydro-3-deoxyphosphoheptonate aldolase [Morinda citrifolia]

Seq. No.	392042
Contig ID	29233_1.R1084
5'-most EST	uC-osflcyp014h03b1

Seq. No.	392043
Contig ID	29234_1.R1084
5'-most EST	g4968977

Seq. No.	392044
Contig ID	29247_1.R1084
5'-most EST	uC-osflM202054a04b1
Method	BLASTX
NCBI GI	g5732069
BLAST score	890

E value	9.0e-96
Match length	388
% identity	65
NCBI Description	(AF147263) contains similarity to Pfam family PF00036 - EF hand; score=11.7, E=0.66,N=1 [Arabidopsis thaliana]

Seq. No.	392045
Contig ID	29258_1.R1084
5'-most EST	uC-osflcyp017h04b1
Method	BLASTX
NCBI GI	g5668806
BLAST score	723
E value	1.0e-76
Match length	168
% identity	80
NCBI Description	(AC007519) Strong similarity to F16N3.17 from Arabidopsis thalian BAC gb_AC007519. [Arabidopsis thaliana]

Seq. No.	392046
Contig ID	29261_1.R1084
5'-most EST	uC-osflcyp023h07b1
Method	BLASTX
NCBI GI	g3386607
BLAST score	211
E value	1.0e-16
Match length	125
% identity	42
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392047
Contig ID	29264_1.R1084
5'-most EST	uC-osflcyp034f04b1

Seq. No.	392048
Contig ID	29266_1.R1084
5'-most EST	uC-osflcyp053h11b1
Method	BLASTX
NCBI GI	g1706082
BLAST score	665
E value	2.0e-69
Match length	308
% identity	46
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478.1_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	392049
Contig ID	29272_1.R1084
5'-most EST	uC-osrocyp017h08b1

Seq. No.	392050
Contig ID	29273_1.R1084
5'-most EST	uC-osflM202123f08b1

Method	BLASTX
NCBI GI	g4455287
BLAST score	238
E value	2.0e-35
Match length	125
% identity	63
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	392051
Contig ID	29278_1.R1084
5'-most EST	uC-osroM202032g08b1
Method	BLASTX
NCBI GI	g3758859
BLAST score	201
E value	3.0e-15
Match length	114
% identity	32
NCBI Description	(Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w), Hypothetical protein, len: 222 aa [Plasmodium falciparum]

Seq. No.	392052
Contig ID	29282_1.R1084
5'-most EST	uC-osf1cyp017e02b1
Method	BLASTX
NCBI GI	g2739376
BLAST score	436
E value	5.0e-43
Match length	122
% identity	65
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	392053
Contig ID	29285_1.R1084
5'-most EST	g5701690
Method	BLASTX
NCBI GI	g6094021
BLAST score	433
E value	7.0e-71
Match length	181
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_3021348_emb_CAA06246_ (AJ004961) ribosomal protein L18 [Cicer arietinum]

Seq. No.	392054
Contig ID	29287_1.R1084
5'-most EST	uC-osf1cyp052c01b1
Method	BLASTX
NCBI GI	g1084427
BLAST score	310
E value	3.0e-28
Match length	65
% identity	74
NCBI Description	gip1 protein - garden petunia >gi_825524_emb_CAA60677_ (X87225) gip1 [Petunia x hybrida]

Seq. No.	392055
Contig ID	29288_1.R1084

5'-most EST	g286279
Method	BLASTX
NCBI GI	g3096931
BLAST score	304
E value	2.0e-27
Match length	81
% identity	67
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	392056
Contig ID	29288_2.R1084
5'-most EST	uC-osflcyp017e11b1

Seq. No.	392057
Contig ID	29288_3.R1084
5'-most EST	g3763121
Method	BLASTX
NCBI GI	g3096931
BLAST score	290
E value	9.0e-26
Match length	81
% identity	63
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	392058
Contig ID	29299_1.R1084
5'-most EST	uC-osroM202028g01b1
Method	BLASTX
NCBI GI	g480450
BLAST score	430
E value	2.0e-42
Match length	95
% identity	89
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	392059
Contig ID	29301_1.R1084
5'-most EST	uC-osflcyp017h01b1

Seq. No.	392060
Contig ID	29305_1.R1084
5'-most EST	uC-osflcyp017h05b1
Method	BLASTX
NCBI GI	g3149952
BLAST score	1179
E value	1.0e-130
Match length	291
% identity	77
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana] >gi_6016713_gb_AAF01539.1_AC009325_9 (AC009325) RNA helicase, DRH1 [Arabidopsis thaliana]

Seq. No. 392061

Contig ID	29309_1.R1084
5'-most EST	uC-osflcyp081e12b1
Method	BLASTX
NCBI GI	g3885343
BLAST score	179
E value	7.0e-13
Match length	77
% identity	48
NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392062
Contig ID	29310_1.R1084
5'-most EST	uC-osflcyp018g02b1
Method	BLASTN
NCBI GI	g5091597
BLAST score	533
E value	0.0e+00
Match length	549
% identity	99
NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No.	392063
Contig ID	29314_1.R1084
5'-most EST	uC-osflcyp019a07b1

Seq. No.	392064
Contig ID	29315_1.R1084
5'-most EST	uC-osflcyp019a09b1

Seq. No.	392065
Contig ID	29317_1.R1084
5'-most EST	uC-osflcyp144b05b1

Seq. No.	392066
Contig ID	29320_1.R1084
5'-most EST	uC-osflcyp111f08b1

Seq. No.	392067
Contig ID	29326_1.R1084
5'-most EST	uC-osflcyp019b10b1
Method	BLASTX
NCBI GI	g4586255
BLAST score	539
E value	6.0e-55
Match length	147
% identity	73
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	392068
Contig ID	29328_1.R1084
5'-most EST	uC-osflcyp043f01b1
Method	BLASTX
NCBI GI	g3820531
BLAST score	713
E value	3.0e-75
Match length	250
% identity	54

NCBI Description	(AF072736) beta-glucosidase [Pinus contorta]
Seq. No.	392069
Contig ID	29329_1.R1084
5'-most EST	uC-osflcyp156e08b1
Seq. No.	392070
Contig ID	29330_1.R1084
5'-most EST	uC-osflm202101h09b1
Method	BLASTX
NCBI GI	g126386
BLAST score	183
E value	3.0e-13
Match length	67
% identity	48
NCBI Description	POLLEN ALLERGEN LOL P 2-A (LOL P II-A) >gi_82449_pir__A34291 pollen allergen Lol p IIA - perennial ryegrass
Seq. No.	392071
Contig ID	29331_1.R1084
5'-most EST	uC-osflcyp019c06b1
Method	BLASTX
NCBI GI	g5921933
BLAST score	613
E value	8.0e-64
Match length	153
% identity	72
NCBI Description	CYTOCHROME P450 85 (DWARF PROTEIN) >gi_1421741 (U54770) cytochrome P450 homolog [Lycopersicon esculentum]
Seq. No.	392072
Contig ID	29338_1.R1084
5'-most EST	uC-osflM202095e02b1
Method	BLASTX
NCBI GI	g322854
BLAST score	759
E value	1.0e-80
Match length	157
% identity	96
NCBI Description	pollen-specific protein - rice >gi_20310_emb_CAA78897_ (Z16402) pollen specific gene [Oryza sativa]
Seq. No.	392073
Contig ID	29344_1.R1084
5'-most EST	uC-osflcyp019e01b1
Seq. No.	392074
Contig ID	29345_1.R1084
5'-most EST	uC-osflcyp051h11b1
Seq. No.	392075
Contig ID	29347_1.R1084
5'-most EST	uC-osflcyp019e04b1
Seq. No.	392076
Contig ID	29350_1.R1084

5'-most EST	g700960
Method	BLASTX
NCBI GI	g2244786
BLAST score	252
E value	2.0e-21
Match length	87
% identity	37
NCBI Description	(Z97335) ribonucleoprotein like protein [Arabidopsis thaliana]

Seq. No.	392077
Contig ID	29355_1.R1084
5'-most EST	uC-osflm202101g04b1
Method	BLASTX
NCBI GI	g2117937
BLAST score	850
E value	1.0e-147
Match length	308
% identity	86
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No.	392078
Contig ID	29362_1.R1084
5'-most EST	uC-osflcyp055f09b1
Method	BLASTX
NCBI GI	g2880043
BLAST score	332
E value	1.0e-30
Match length	108
% identity	60
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	392079
Contig ID	29362_2.R1084
5'-most EST	g569712

Seq. No.	392080
Contig ID	29364_1.R1084
5'-most EST	uC-osflcyp019g10b1
Method	BLASTX
NCBI GI	g2760323
BLAST score	344
E value	6.0e-32
Match length	109
% identity	25
NCBI Description	(AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No.	392081
Contig ID	29365_1.R1084
5'-most EST	uC-osflcyp111e01b1
Method	BLASTX
NCBI GI	g3281853
BLAST score	187
E value	9.0e-14

Match length	122
% identity	53
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	392082
Contig ID	29369_1.R1084
5'-most EST	uC-osflcyp019h05b1

Seq. No.	392083
Contig ID	29375_1.R1084
5'-most EST	g428092
Method	BLASTX
NCBI GI	g2239091
BLAST score	285
E value	2.0e-25
Match length	130
% identity	49
NCBI Description	(Z84571) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	392084
Contig ID	29380_1.R1084
5'-most EST	uC-osflcyp174b02b1
Method	BLASTX
NCBI GI	g2498586
BLAST score	642
E value	4.0e-67
Match length	146
% identity	79
NCBI Description	MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]

Seq. No.	392085
Contig ID	29396_1.R1084
5'-most EST	uC-osflm202113e09b1
Method	BLASTX
NCBI GI	g1054843
BLAST score	408
E value	1.0e-39
Match length	131
% identity	58
NCBI Description	(X92847) D12 oleate desaturase [Solanum commersonii]

Seq. No.	392086
Contig ID	29396_2.R1084
5'-most EST	uC-osflcyp024e11b1
Method	BLASTX
NCBI GI	g1054843
BLAST score	213
E value	2.0e-33
Match length	120
% identity	60
NCBI Description	(X92847) D12 oleate desaturase [Solanum commersonii]

Seq. No.	392087
Contig ID	29398_1.R1084
5'-most EST	uC-osflcyp021c01b1

Method	BLASTX
NCBI GI	g417360
BLAST score	231
E value	5.0e-19
Match length	68
% identity	66
NCBI Description	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2 >gi_2131280_pir__S67767 high mobility group-like protein NHP2 - yeast (Saccharomyces cerevisiae) >gi_666101_emb_CAA40885_ (X57714) high mobility group-like nuclear protein 2 [Saccharomyces cerevisiae] >gi_1429348_emb_CAA67483_ (X99000) high-mobility-group-like protein [Saccharomyces cerevisiae] >gi_1431346_emb_CAA98786_ (Z74256) ORF YDL208w [Saccharomyces cerevisiae]

Seq. No.	392088
Contig ID	29401_1.R1084
5'-most EST	uC-osflcyp101f07b1

Seq. No.	392089
Contig ID	29403_1.R1084
5'-most EST	uC-osflcyp139e02b1
Method	BLASTX
NCBI GI	g231509
BLAST score	530
E value	4.0e-54
Match length	119
% identity	84
NCBI Description	ACTIN DEPOLYMERIZING FACTOR (ADF) >gi_419809_pir__S30935 actin-depolymerizing factor - trumpet lily >gi_22748_emb_CAA78483_ (Z14110) actin depolymerizing factor [Lilium longiflorum]

Seq. No.	392090
Contig ID	29411_1.R1084
5'-most EST	uC-osflcyp021d08b1

Seq. No.	392091
Contig ID	29419_1.R1084
5'-most EST	uC-osflcyp021e05b1

Seq. No.	392092
Contig ID	29435_1.R1084
5'-most EST	g2310064
Method	BLASTX
NCBI GI	g4337195
BLAST score	569
E value	1.0e-112
Match length	360
% identity	58
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	392093
Contig ID	29437_1.R1084
5'-most EST	uC-osflcyp152h12b1

Seq. No.	392094
Contig ID	29447_1.R1084
5'-most EST	uC-osflM202082a05b1

Seq. No.	392095
Contig ID	29451_1.R1084
5'-most EST	g3760275
Method	BLASTX
NCBI GI	g4531444
BLAST score	173
E value	6.0e-12
Match length	40
% identity	78
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	392096
Contig ID	29461_1.R1084
5'-most EST	uC-osflcyp048b11b1

Seq. No.	392097
Contig ID	29462_1.R1084
5'-most EST	uC-osflcyp031e07b1
Method	BLASTX
NCBI GI	g4490706
BLAST score	258
E value	5.0e-22
Match length	76
% identity	62
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	392098
Contig ID	29463_1.R1084
5'-most EST	uC-osflcyp022c01b1

Seq. No.	392099
Contig ID	29463_2.R1084
5'-most EST	g571774

Seq. No.	392100
Contig ID	29491_1.R1084
5'-most EST	uC-osflcyp022g09b1

Seq. No.	392101
Contig ID	29496_1.R1084
5'-most EST	uC-osflcyp022h11b1

Seq. No.	392102
Contig ID	29500_1.R1084
5'-most EST	uC-osroM202004c09a2
Method	BLASTX
NCBI GI	g5921189
BLAST score	435
E value	8.0e-43
Match length	205
% identity	49
NCBI Description	CYTOCHROME P450 71C4 >gi_550542_emb_CAA57425_ (X81831) cytochrome P450 [Zea mays] >gi_1850903_emb_CAA72196_

(Y11368) cytochrome p450 [Zea mays]

Seq. No.	392103
Contig ID	29501_1.R1084
5'-most EST	g701564
Method	BLASTX
NCBI GI	g282994
BLAST score	497
E value	4.0e-50
Match length	103
% identity	90
NCBI Description	Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No.	392104
Contig ID	29509_1.R1084
5'-most EST	uC-osflcyp029e07b1
Method	BLASTX
NCBI GI	g3702665
BLAST score	155
E value	3.0e-10
Match length	77
% identity	42
NCBI Description	(AJ007349) pathogenisis-related protein 1.2 [Triticum aestivum]

Seq. No.	392105
Contig ID	29518_1.R1084
5'-most EST	uC-osflm202101a09b1
Method	BLASTX
NCBI GI	g967125
BLAST score	299
E value	6.0e-27
Match length	71
% identity	77
NCBI Description	(U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No.	392106
Contig ID	29536_1.R1084
5'-most EST	g4879559
Method	BLASTX
NCBI GI	g3513744
BLAST score	260
E value	3.0e-22
Match length	89
% identity	32
NCBI Description	(AF080118) contains similarity to Medicago truncatula MtN3 (GB:Y08726) [Arabidopsis thaliana]

Seq. No.	392107
Contig ID	29537_1.R1084
5'-most EST	uC-osflcyp006h05b1
Method	BLASTX
NCBI GI	g4586031
BLAST score	274
E value	4.0e-24
Match length	64

% identity	81
NCBI Description	(AC007109) unknown protein [Arabidopsis thaliana]

Seq. No.	392108
Contig ID	29542_1.R1084
5'-most EST	uC-osflcyp023h03b1
Method	BLASTX
NCBI GI	g3287683
BLAST score	454
E value	1.0e-46
Match length	147
% identity	23
NCBI Description	(AC003979) Similar to apoptosis protein MA-3 gb_D50465 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	392109
Contig ID	29544_1.R1084
5'-most EST	g701708
Method	BLASTX
NCBI GI	g2239083
BLAST score	266
E value	5.0e-23
Match length	136
% identity	47
NCBI Description	(Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	392110
Contig ID	29546_1.R1084
5'-most EST	uC-osflcyp023h09b1
Method	BLASTX
NCBI GI	g3894383
BLAST score	287
E value	3.0e-25
Match length	263
% identity	4
NCBI Description	(AF053993) disease resistance protein [Lycopersicon esculentum]

Seq. No.	392111
Contig ID	29552_1.R1084
5'-most EST	g3061152
Method	BLASTX
NCBI GI	g547712
BLAST score	488
E value	4.0e-49
Match length	98
% identity	95
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No.	392112
Contig ID	29565_1.R1084

5'-most EST	uC-osflcyp024b12b1
Method	BLASTX
NCBI GI	g3298443
BLAST score	213
E value	5.0e-17
Match length	109
% identity	50
NCBI Description	(AB010880) chloroplast ribosomal protein L17 [Nicotiana tabacum]

Seq. No.	392113
Contig ID	29574_1.R1084
5'-most EST	g3762112
Method	BLASTX
NCBI GI	g3236248
BLAST score	1063
E value	1.0e-116
Match length	261
% identity	78
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	392114
Contig ID	29575_2.R1084
5'-most EST	uC-osflcyp024c12b1

Seq. No.	392115
Contig ID	29582_1.R1084
5'-most EST	uC-osflcyp107h02b1
Method	BLASTX
NCBI GI	g2385410
BLAST score	251
E value	3.0e-21
Match length	150
% identity	35
NCBI Description	(AB001372) TFIID subunit taf72p [Schizosaccharomyces pombe] >gi_3859081_emb_CAA21958_ (AL033406) tfiid subunit taf72p. [Schizosaccharomyces pombe]

Seq. No.	392116
Contig ID	29585_1.R1084
5'-most EST	uC-osflcyp057c03b1
Method	BLASTX
NCBI GI	g2055230
BLAST score	222
E value	2.0e-17
Match length	137
% identity	40
NCBI Description	(AB000130) SRC2 [Glycine max]

Seq. No.	392117
Contig ID	29585_2.R1084
5'-most EST	uC-osflcyp179f04b1
Method	BLASTN
NCBI GI	g6041757
BLAST score	314
E value	1.0e-176
Match length	406

% identity	95
NCBI Description	Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence

Seq. No.	392118
Contig ID	29591_1.R1084
5'-most EST	uC-osflcyp024f11b1
Method	BLASTX
NCBI GI	g5262169
BLAST score	686
E value	2.0e-72
Match length	156
% identity	84
NCBI Description	(AL080253) UDP-glucose 4-epimerase-like protein [Arabidopsis thaliana]

Seq. No.	392119
Contig ID	29594_1.R1084
5'-most EST	uC-osflcyp024g02b1
Method	BLASTX
NCBI GI	g2146741
BLAST score	854
E value	1.0e-102
Match length	226
% identity	81
NCBI Description	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) - Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Arabidopsis thaliana]

Seq. No.	392120
Contig ID	29596_1.R1084
5'-most EST	uC-osflcyp121d08b1

Seq. No.	392121
Contig ID	29605_1.R1084
5'-most EST	uC-osflcyp024h09b1
Method	BLASTX
NCBI GI	g4309759
BLAST score	499
E value	3.0e-50
Match length	195
% identity	61
NCBI Description	(AC006217) unknown protein with Src homology 3 (SH3) domain profile (PDOC50002) [Arabidopsis thaliana]

Seq. No.	392122
Contig ID	29608_1.R1084
5'-most EST	g4714193
Method	BLASTX
NCBI GI	g3551247
BLAST score	740
E value	1.0e-78
Match length	147
% identity	96
NCBI Description	(AB012703) 181 [Daucus carota]

Seq. No.	392123
Contig ID	29615_1.R1084
5'-most EST	uC-osflcyp172d05b1
Method	BLASTX
NCBI GI	g5823020
BLAST score	310
E value	3.0e-28
Match length	119
% identity	54
NCBI Description	(AF089849) senescence-specific cysteine protease [Brassica napus]

Seq. No.	392124
Contig ID	29619_1.R1084
5'-most EST	g4715905
Method	BLASTX
NCBI GI	g6006801
BLAST score	161
E value	2.0e-10
Match length	204
% identity	36
NCBI Description	(AF156783) apyrase [Arabidopsis thaliana]

Seq. No.	392125
Contig ID	29634_1.R1084
5'-most EST	uC-osflcyp026c03b1
Method	BLASTX
NCBI GI	g2160166
BLAST score	199
E value	4.0e-35
Match length	151
% identity	59
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	392126
Contig ID	29644_1.R1084
5'-most EST	uC-osflm202109e03b1
Method	BLASTX
NCBI GI	g3236246
BLAST score	382
E value	1.0e-36
Match length	109
% identity	59
NCBI Description	(AC004684) putative expansin protein [Arabidopsis thaliana]

Seq. No.	392127
Contig ID	29645_1.R1084
5'-most EST	g428039
Method	BLASTX
NCBI GI	g3193292
BLAST score	558
E value	3.0e-57
Match length	167
% identity	66
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	392128
Contig ID	29653_1.R1084
5'-most EST	uC-osflcyp140e04b1

Seq. No.	392129
Contig ID	29655_1.R1084
5'-most EST	uC-osflcyp026f01b1

Seq. No.	392130
Contig ID	29656_1.R1084
5'-most EST	g2431231
Method	BLASTX
NCBI GI	g3776578
BLAST score	253
E value	2.0e-21
Match length	128
% identity	37
NCBI Description	(AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No.	392131
Contig ID	29659_1.R1084
5'-most EST	uC-osflcyp026g07b1

Seq. No.	392132
Contig ID	29661_1.R1084
5'-most EST	g569301
Method	BLASTX
NCBI GI	g5734634
BLAST score	198
E value	2.0e-15
Match length	82
% identity	54
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No.	392133
Contig ID	29662_1.R1084
5'-most EST	g5607600
Method	BLASTX
NCBI GI	g4490313
BLAST score	423
E value	2.0e-41
Match length	121
% identity	64
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	392134
Contig ID	29663_1.R1084
5'-most EST	g3090627
Method	BLASTX
NCBI GI	g3281853
BLAST score	250
E value	3.0e-21
Match length	90
% identity	62

NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	392135
Contig ID	29667_1.R1084
5'-most EST	uC-osroM202022g08b1
Method	BLASTX
NCBI GI	g4455338
BLAST score	182
E value	5.0e-13
Match length	168
% identity	30
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	392136
Contig ID	29669_1.R1084
5'-most EST	uC-osflcyp117f01a1

Seq. No.	392137
Contig ID	29679_1.R1084
5'-most EST	uC-osflm202111b01b1
Method	BLASTX
NCBI GI	g4415916
BLAST score	221
E value	4.0e-25
Match length	274
% identity	28
NCBI Description	(AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	392138
Contig ID	29679_2.R1084
5'-most EST	g3761597

Seq. No.	392139
Contig ID	29681_1.R1084
5'-most EST	uC-osflcyp027b05b1
Method	BLASTX
NCBI GI	g5902387
BLAST score	191
E value	7.0e-21
Match length	123
% identity	46
NCBI Description	(AC009322) Similar to polygalacturonases [Arabidopsis thaliana]

Seq. No.	392140
Contig ID	29683_1.R1084
5'-most EST	uC-osflcyp027b08b1
Method	BLASTX
NCBI GI	g3183274
BLAST score	263
E value	1.0e-22
Match length	88
% identity	58
NCBI Description	HYPOTHETICAL 26.5 KD PROTEIN C15A10.05C IN CHROMOSOME I >gi_2239182_emb_CAB10102.1_ (Z97208) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	392141
Contig ID	29693_1.R1084
5'-most EST	uC-osflcyp035e03b1
Method	BLASTX
NCBI GI	g4680207
BLAST score	147
E value	7.0e-09
Match length	119
% identity	36
NCBI Description	(AF114171) disease resistance protein RPM1 homolog [Sorghum bicolor]

Seq. No.	392142
Contig ID	29695_1.R1084
5'-most EST	g1632462

Seq. No.	392143
Contig ID	29696_1.R1084
5'-most EST	uC-osflcyp027d05b1
Method	BLASTX
NCBI GI	g2244973
BLAST score	161
E value	1.0e-10
Match length	171
% identity	30
NCBI Description	(Z97340) transcription factor like protein [Arabidopsis thaliana]

Seq. No.	392144
Contig ID	29700_1.R1084
5'-most EST	uC-osflcyp027d11b1
Method	BLASTX
NCBI GI	g4895241
BLAST score	476
E value	1.0e-47
Match length	167
% identity	53
NCBI Description	(AC007659) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392145
Contig ID	29704_1.R1084
5'-most EST	uC-osflcyp075c03b1
Method	BLASTX
NCBI GI	g2342676
BLAST score	771
E value	6.0e-82
Match length	208
% identity	69
NCBI Description	(AC000106) Strong similarity to Oryza NADPH oxidase (gb_X93301). [Arabidopsis thaliana]

Seq. No.	392146
Contig ID	29705_1.R1084
5'-most EST	uC-osflcyp027e04b1

Seq. No.	392147

Contig ID 29713_1.R1084
5'-most EST g428392

Seq. No. 392148
Contig ID 29715_1.R1084
5'-most EST uC-osflcyp042e11b1
Method BLASTX
NCBI GI g1076809
BLAST score 2090
E value 0.0e+00
Match length 585
% identity 81
NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase [Zea mays]

Seq. No. 392149
Contig ID 29724_1.R1084
5'-most EST uC-osflcyp027g04b1

Seq. No. 392150
Contig ID 29725_1.R1084
5'-most EST uC-osflcyp027g05b1

Seq. No. 392151
Contig ID 29728_1.R1084
5'-most EST uC-osflcyp027g11b1
Method BLASTX
NCBI GI g2960364
BLAST score 419
E value 3.0e-52
Match length 169
% identity 63
NCBI Description (AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No. 392152
Contig ID 29740_1.R1084
5'-most EST uC-osflcyp028a12b1
Method BLASTX
NCBI GI g4895186
BLAST score 438
E value 3.0e-50
Match length 155
% identity 63
NCBI Description (AC007661) putative growth regulator protein [Arabidopsis thaliana]

Seq. No. 392153
Contig ID 29741_1.R1084
5'-most EST uC-osflM202098d09b1

Seq. No. 392154
Contig ID 29744_1.R1084
5'-most EST g3761390
Method BLASTX
NCBI GI g4678935

BLAST score 205
E value 9.0e-16
Match length 90
% identity 49
NCBI Description (AL049711) putative protein [Arabidopsis thaliana]

Seq. No. 392155
Contig ID 29749_1.R1084
5'-most EST g286666

Seq. No. 392156
Contig ID 29767_1.R1084
5'-most EST uC-osflcyp159c01b1

Seq. No. 392157
Contig ID 29773_1.R1084
5'-most EST uC-osflm202102h05b1
Method BLASTX
NCBI GI g4836892
BLAST score 771
E value 4.0e-82
Match length 225
% identity 34
NCBI Description (AC007369) Putative RNA helicase [Arabidopsis thaliana]

Seq. No. 392158
Contig ID 29775_1.R1084
5'-most EST g2310619

Seq. No. 392159
Contig ID 29781_1.R1084
5'-most EST uC-osflcyp142c01b1

Seq. No. 392160
Contig ID 29782_1.R1084
5'-most EST uC-osflcyp028g11b1
Method BLASTX
NCBI GI g5821406
BLAST score 472
E value 5.0e-47
Match length 248
% identity 41
NCBI Description (AB025531) 24 kDa vacuolar protein VP24 [Ipomoea batatas]

Seq. No. 392161
Contig ID 29789_1.R1084
5'-most EST uC-osflcyp028h10b1

Seq. No. 392162
Contig ID 29792_1.R1084
5'-most EST uC-osflm202110b02b1
Method BLASTX
NCBI GI g5002521
BLAST score 193
E value 3.0e-14
Match length 78
% identity 50

NCBI Description	(AL078606) putative protein [Arabidopsis thaliana]
Seq. No.	392163
Contig ID	29794_2.R1084
5'-most EST	uC-osflcyp093c04b1
Seq. No.	392164
Contig ID	29810_1.R1084
5'-most EST	g2312596
Seq. No.	392165
Contig ID	29813_1.R1084
5'-most EST	uC-osflcyp029c11b1
Method	BLASTX
NCBI GI	g6016720
BLAST score	323
E value	1.0e-29
Match length	100
% identity	56
NCBI Description	(AC009325) hypothetical protein [Arabidopsis thaliana]
Seq. No.	392166
Contig ID	29815_1.R1084
5'-most EST	g3445018
Method	BLASTX
NCBI GI	g2618689
BLAST score	370
E value	5.0e-45
Match length	147
% identity	66
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.	392167
Contig ID	29815_2.R1084
5'-most EST	g3761023
Method	BLASTN
NCBI GI	g4097943
BLAST score	210
E value	1.0e-114
Match length	210
% identity	100
NCBI Description	Oryza sativa beta-1,3-glucanase precursor (Gns7) gene, complete cds
Seq. No.	392168
Contig ID	29822_1.R1084
5'-most EST	uC-osflcyp029d10b1
Method	BLASTX
NCBI GI	g5430760
BLAST score	344
E value	5.0e-32
Match length	77
% identity	82
NCBI Description	(AC007504) Putative ribosomal protein [Arabidopsis thaliana]
Seq. No.	392169

Contig ID	29823_1.R1084
5'-most EST	uC-osflcyp029d11b1
Method	BLASTX
NCBI GI	g3297818
BLAST score	255
E value	1.0e-21
Match length	87
% identity	46
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	392170
Contig ID	29830_1.R1084
5'-most EST	g4716715
Method	BLASTX
NCBI GI	g3914212
BLAST score	271
E value	1.0e-23
Match length	108
% identity	49
NCBI Description	5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE) >gi_1732065 (U70825) 5-oxo-L-prolinase [Rattus norvegicus]

Seq. No.	392171
Contig ID	29836_1.R1084
5'-most EST	uC-osflM202051c09b1
Method	BLASTX
NCBI GI	g5091498
BLAST score	685
E value	4.0e-83
Match length	186
% identity	90
NCBI Description	(AB023482) ESTs AU058067(E20733), AAU058070(E20873) correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase mRNA, complete cds.(U27116) [Oryza sativa]

Seq. No.	392172
Contig ID	29850_1.R1084
5'-most EST	g3090628

Seq. No.	392173
Contig ID	29879_1.R1084
5'-most EST	g2428537

Seq. No.	392174
Contig ID	29886_1.R1084
5'-most EST	uC-osflcyp030e12b1

Seq. No.	392175
Contig ID	29895_1.R1084
5'-most EST	uC-osflcyp030g03b1

Seq. No.	392176
Contig ID	29900_1.R1084
5'-most EST	uC-osflcyp057g01b1
Method	BLASTX

NCBI GI	g4263771
BLAST score	250
E value	5.0e-21
Match length	86
% identity	50
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana] >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	392177
Contig ID	29902_1.R1084
5'-most EST	uC-osflcyp090e12b1
Method	BLASTX
NCBI GI	g3080420
BLAST score	285
E value	5.0e-31
Match length	114
% identity	65
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	392178
Contig ID	29903_1.R1084
5'-most EST	uC-osflcyp030h04b1
Method	BLASTX
NCBI GI	g3582333
BLAST score	168
E value	1.0e-15
Match length	119
% identity	44
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392179
Contig ID	29906_1.R1084
5'-most EST	uC-osflcyp030h09b1
Method	BLASTX
NCBI GI	g3386614
BLAST score	497
E value	3.0e-50
Match length	137
% identity	43
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	392180
Contig ID	29916_1.R1084
5'-most EST	uC-osflcyp031b03b1
Method	BLASTX
NCBI GI	g4314378
BLAST score	475
E value	2.0e-65
Match length	337
% identity	42
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana] >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative

lipase [Arabidopsis thaliana]

Seq. No.	392181
Contig ID	29917_1.R1084
5'-most EST	uC-osflcyp031b04b1

Seq. No.	392182
Contig ID	29918_1.R1084
5'-most EST	uC-osflcyp031b07b1

Seq. No.	392183
Contig ID	29920_1.R1084
5'-most EST	uC-osflcyp031b10b1

Seq. No.	392184
Contig ID	29931_1.R1084
5'-most EST	uC-osflcyp031d06b1
Method	BLASTX
NCBI GI	g6005904
BLAST score	202
E value	1.0e-15
Match length	149
% identity	20
NCBI Description	TATA element modulatory factor 1 >gi_423112_pir__A47212 transcription factor TMF, TATA element modulatory factor - human >gi_5870866_gb_AAD54608.1_ (L01042) TATA element modulatory factor [Homo sapiens]

Seq. No.	392185
Contig ID	29944_1.R1084
5'-most EST	g4715308
Method	BLASTX
NCBI GI	g4335752
BLAST score	248
E value	8.0e-21
Match length	82
% identity	56
NCBI Description	(AC006284) putative myb transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	392186
Contig ID	29952_1.R1084
5'-most EST	g700467
Method	BLASTX
NCBI GI	g5051771
BLAST score	768
E value	1.0e-81
Match length	217
% identity	70
NCBI Description	(AL078637) putative protein [Arabidopsis thaliana]

Seq. No.	392187
Contig ID	29962_1.R1084
5'-most EST	g2427432

Seq. No.	392188
Contig ID	29965_1.R1084

5'-most EST	uC-osflcyp032a01b1
Seq. No.	392189
Contig ID	29968_1.R1084
5'-most EST	uC-osflcyp032a06b1
Seq. No.	392190
Contig ID	29969_1.R1084
5'-most EST	uC-osflcyp002g04b1
Method	BLASTX
NCBI GI	g4538913
BLAST score	293
E value	4.0e-26
Match length	139
% identity	48
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]
Seq. No.	392191
Contig ID	29971_1.R1084
5'-most EST	uC-osflcyp041e03b1
Method	BLASTX
NCBI GI	g2088647
BLAST score	309
E value	1.0e-28
Match length	124
% identity	52
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]
Seq. No.	392192
Contig ID	29986_1.R1084
5'-most EST	g2428731
Seq. No.	392193
Contig ID	29988_1.R1084
5'-most EST	g5002773
Method	BLASTX
NCBI GI	g2149127
BLAST score	130
E value	1.0e-12
Match length	131
% identity	40
NCBI Description	(U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]
Seq. No.	392194
Contig ID	29989_1.R1084
5'-most EST	g2800410
Seq. No.	392195
Contig ID	29990_1.R1084
5'-most EST	uC-osflcyp032c12b1
Seq. No.	392196
Contig ID	29994_1.R1084
5'-most EST	uC-osflcyp032d04b1

Method	BLASTX
NCBI GI	g2829887
BLAST score	428
E value	9.0e-42
Match length	182
% identity	56
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	392197
Contig ID	29997_1.R1084
5'-most EST	uC-osflcyp176a10b1
Method	BLASTX
NCBI GI	g2341032
BLAST score	200
E value	3.0e-15
Match length	115
% identity	44
NCBI Description	(AC000104) EST gb_ATTS0956 comes from this gene. [Arabidopsis thaliana]

Seq. No.	392198
Contig ID	30008_1.R1084
5'-most EST	uC-osflcyp032e10b1

Seq. No.	392199
Contig ID	30014_1.R1084
5'-most EST	g700542
Method	BLASTX
NCBI GI	g4586054
BLAST score	202
E value	1.0e-15
Match length	77
% identity	51
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	392200
Contig ID	30021_1.R1084
5'-most EST	uC-osflcyp032g10b1
Method	BLASTX
NCBI GI	g2252860
BLAST score	173
E value	6.0e-12
Match length	54
% identity	65
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	392201
Contig ID	30025_1.R1084
5'-most EST	uC-osflM202056b08a1

Seq. No.	392202
Contig ID	30028_1.R1084
5'-most EST	uC-osflcyp033a01b1
Method	BLASTX
NCBI GI	g3152568
BLAST score	700
E value	1.0e-73

Match length	267
% identity	54
NCBI Description	(AC002986) Similar to hypothetical protein product gb_Z97337 from A. thaliana. EST gb_H76597 comes from this gene. [Arabidopsis thaliana]

Seq. No.	392203
Contig ID	30033_1.R1084
5'-most EST	uC-osflM202068c02b1
Method	BLASTX
NCBI GI	g1449179
BLAST score	362
E value	3.0e-34
Match length	133
% identity	56
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	392204
Contig ID	30035_1.R1084
5'-most EST	g3106678

Seq. No.	392205
Contig ID	30050_1.R1084
5'-most EST	uC-osflcyp026f06b1

Seq. No.	392206
Contig ID	30060_1.R1084
5'-most EST	g2312428
Method	BLASTX
NCBI GI	g4757948
BLAST score	320
E value	4.0e-51
Match length	166
% identity	58
NCBI Description	cell division cycle 23, yeast homolog; CDC23 >gi_3283051 (AF053977) cell division cycle protein 23 [Homo sapiens] >gi_4519431_dbj_BAA75628.1_ (AB011472) CDC23 [Homo sapiens]

Seq. No.	392207
Contig ID	30079_1.R1084
5'-most EST	uC-osflM202068d09b1
Method	BLASTX
NCBI GI	g5042461
BLAST score	538
E value	6.0e-55
Match length	128
% identity	82
NCBI Description	(AC007789) putative oxalate oxidase (germin protein) [Oryza sativa]

Seq. No.	392208
Contig ID	30085_1.R1084
5'-most EST	uC-osflM202046d09b1
Method	BLASTX
NCBI GI	g1946372
BLAST score	183

E value	2.0e-13
Match length	62
% identity	58
NCBI Description	(U93215) yeast hypothetical protein YDB1_SCHPO isolog [Arabidopsis thaliana]

Seq. No.	392209
Contig ID	30091_1.R1084
5'-most EST	uC-osflcyp034a03b1
Method	BLASTX
NCBI GI	g4584527
BLAST score	214
E value	8.0e-17
Match length	131
% identity	35
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	392210
Contig ID	30096_1.R1084
5'-most EST	g3760435

Seq. No.	392211
Contig ID	30097_1.R1084
5'-most EST	uC-osflcyp034b07b1
Method	BLASTX
NCBI GI	g1710805
BLAST score	147
E value	6.0e-09
Match length	168
% identity	5
NCBI Description	RTOA PROTEIN (RATIO-A) >gi_1206019 (U48298) rtoA gene product [Dictyostelium discoideum]

Seq. No.	392212
Contig ID	30101_1.R1084
5'-most EST	uC-osflcyp034b12b1

Seq. No.	392213
Contig ID	30104_1.R1084
5'-most EST	g702112

Seq. No.	392214
Contig ID	30106_1.R1084
5'-most EST	uC-osflM202043e02b1
Method	BLASTX
NCBI GI	g6018458
BLAST score	372
E value	2.0e-35
Match length	196
% identity	44
NCBI Description	(AJ243972) 6-phosphogluconolactonase [Homo sapiens]

Seq. No.	392215
Contig ID	30112_1.R1084
5'-most EST	uC-osroM202012c10a1

Seq. No.	392216

Contig ID	30112_2.R1084
5'-most EST	uC-osflcyp034e08b1
Seq. No.	392217
Contig ID	30118_1.R1084
5'-most EST	g4879958
Method	BLASTX
NCBI GI	g1402918
BLAST score	362
E value	2.0e-34
Match length	116
% identity	64
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]
Seq. No.	392218
Contig ID	30124_1.R1084
5'-most EST	g3758980
Method	BLASTX
NCBI GI	g2979563
BLAST score	399
E value	2.0e-38
Match length	97
% identity	76
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]
Seq. No.	392219
Contig ID	30131_1.R1084
5'-most EST	uC-osflcyp034h12b1
Method	BLASTX
NCBI GI	g5882731
BLAST score	804
E value	5.0e-86
Match length	220
% identity	61
NCBI Description	(AC008263) Similar to gb_AF000132 betaine aldehyde dehydrogenase from Amaranthus hypochondriacus. ESTs gb_T20662, gb_R90254, gb_AA651436 and gb_AA586226 come from this gene. [Arabidopsis thaliana]
Seq. No.	392220
Contig ID	30133_1.R1084
5'-most EST	g701784
Seq. No.	392221
Contig ID	30144_1.R1084
5'-most EST	g2312921
Seq. No.	392222
Contig ID	30145_1.R1084
5'-most EST	uC-osflcyp035c06b1
Method	BLASTX
NCBI GI	g1732411
BLAST score	352
E value	4.0e-33
Match length	175

% identity	29
NCBI Description	(U47924) isopeptidase T [Homo sapiens]

Seq. No.	392223
Contig ID	30151_1.R1084
5'-most EST	uC-osflcyp035d11b1
Method	BLASTX
NCBI GI	g4678297
BLAST score	538
E value	6.0e-55
Match length	180
% identity	59
NCBI Description	(AL049655) protein disulfide-isomerase-like protein [Arabidopsis thaliana]

Seq. No.	392224
Contig ID	30152_1.R1084
5'-most EST	uC-osflcyp035d01b1
Method	BLASTX
NCBI GI	g4538920
BLAST score	354
E value	8.0e-38
Match length	154
% identity	60
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	392225
Contig ID	30154_1.R1084
5'-most EST	g5003560
Method	BLASTX
NCBI GI	g5689236
BLAST score	363
E value	2.0e-34
Match length	83
% identity	89
NCBI Description	(AB024291) ZmRR2 [Zea mays] >gi_6009897_dbj_BAA85113.1_ (AB031012) response regulator 2 [Zea mays]

Seq. No.	392226
Contig ID	30157_1.R1084
5'-most EST	uC-osflcyp035d09b1
Method	BLASTX
NCBI GI	g6065749
BLAST score	216
E value	6.0e-36
Match length	178
% identity	46
NCBI Description	(AJ250341) beta-amylase enzyme [Arabidopsis thaliana]

Seq. No.	392227
Contig ID	30170_1.R1084
5'-most EST	uC-osflcyp035f04b1
Method	BLASTX
NCBI GI	g126386
BLAST score	193
E value	2.0e-14

Match length	90
% identity	43
NCBI Description	POLLEN ALLERGEN LOL P 2-A (LOL P II-A) >gi_82449_pir__A34291 pollen allergen Lol p IIA - perennial ryegrass

Seq. No.	392228
Contig ID	30171_1.R1084
5'-most EST	uC-osflcyp035f06b1

Seq. No.	392229
Contig ID	30173_1.R1084
5'-most EST	uC-osflcyp035f09b1
Method	BLASTX
NCBI GI	g4417283
BLAST score	408
E value	1.0e-39
Match length	169
% identity	46
NCBI Description	(AC007019) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	392230
Contig ID	30174_1.R1084
5'-most EST	uC-osrocyp029a10a1
Method	BLASTX
NCBI GI	g2160182
BLAST score	111
E value	2.0e-10
Match length	87
% identity	44
NCBI Description	(AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	392231
Contig ID	30175_1.R1084
5'-most EST	uC-osflM202037e05b1

Seq. No.	392232
Contig ID	30180_1.R1084
5'-most EST	uC-osflcyp071h09b1
Method	BLASTX
NCBI GI	g1777312
BLAST score	211
E value	1.0e-16
Match length	98
% identity	48
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	392233
Contig ID	30182_1.R1084
5'-most EST	g2427915
Method	BLASTX
NCBI GI	g6016691
BLAST score	487
E value	6.0e-49
Match length	147

% identity	62
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	392234
Contig ID	30185_1.R1084
5'-most EST	uC-osflcyp035h01b1
Method	BLASTX
NCBI GI	g4581164
BLAST score	285
E value	2.0e-25
Match length	145
% identity	46
NCBI Description	(AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No.	392235
Contig ID	30187_1.R1084
5'-most EST	uC-osflcyp088d02b1
Method	BLASTX
NCBI GI	g3746903
BLAST score	503
E value	1.0e-95
Match length	248
% identity	78
NCBI Description	(AF089724) signal recognition particle 54 kDa subunit precursor [Pisum sativum]

Seq. No.	392236
Contig ID	30188_1.R1084
5'-most EST	g426002
Method	BLASTX
NCBI GI	g2648032
BLAST score	832
E value	2.0e-89
Match length	206
% identity	74
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	392237
Contig ID	30190_1.R1084
5'-most EST	g702226

Seq. No.	392238
Contig ID	30192_1.R1084
5'-most EST	uC-osflM202016f02b1
Method	BLASTX
NCBI GI	g3702327
BLAST score	474
E value	5.0e-47
Match length	244
% identity	50
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	392239
Contig ID	30195_1.R1084
5'-most EST	uC-osflM202068c09b1
Method	BLASTX
NCBI GI	g431154

BLAST score	260
E value	7.0e-35
Match length	121
% identity	63
NCBI Description	(D21813) ORF [Lilium longiflorum]

Seq. No.	392240
Contig ID	30197_1.R1084
5'-most EST	uC-osflcyp036e02b1
Method	BLASTX
NCBI GI	g5430747
BLAST score	790
E value	2.0e-84
Match length	206
% identity	40
NCBI Description	(AC007504) Hypothetical Protein [Arabidopsis thaliana]

Seq. No.	392241
Contig ID	30207_1.R1084
5'-most EST	uC-osflcyp037a11b1
Method	BLASTX
NCBI GI	g4835793
BLAST score	555
E value	6.0e-57
Match length	182
% identity	62
NCBI Description	(AC007296) Similar to gb_U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF_00076 RNA recognition motif domains. ESTs gb_T44278, gb_R65195, gb_N65904, gb_H37499, gb_R90487, gb_N95952, gb_T4427

Seq. No.	392242
Contig ID	30209_1.R1084
5'-most EST	uC-osroM202019g10b1

Seq. No.	392243
Contig ID	30212_1.R1084
5'-most EST	uC-osroM202012g08b1
Method	BLASTX
NCBI GI	g2224915
BLAST score	362
E value	2.0e-34
Match length	105
% identity	58
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	392244
Contig ID	30223_1.R1084
5'-most EST	uC-osflcyp157h01b1
Method	BLASTX
NCBI GI	g4455270
BLAST score	156
E value	2.0e-10
Match length	71
% identity	48
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	392245
Contig ID	30226_1.R1084
5'-most EST	g2427897

Seq. No.	392246
Contig ID	30229_1.R1084
5'-most EST	uC-osroM202033a02b1

Seq. No.	392247
Contig ID	30230_1.R1084
5'-most EST	uC-osflcyp037d08b1
Method	BLASTX
NCBI GI	g3482919
BLAST score	151
E value	2.0e-09
Match length	46
% identity	67
NCBI Description	(AC003970) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	392248
Contig ID	30231_1.R1084
5'-most EST	g699741
Method	BLASTX
NCBI GI	g3360291
BLAST score	944
E value	1.0e-102
Match length	244
% identity	72
NCBI Description	(AF023165) leucine-rich repeat transmembrane protein kinase 2 [Zea mays]

Seq. No.	392249
Contig ID	30241_1.R1084
5'-most EST	uC-osrocyp037f04b1

Seq. No.	392250
Contig ID	30243_1.R1084
5'-most EST	uC-osflcyp111c03b1
Method	BLASTX
NCBI GI	g2275210
BLAST score	94
E value	3.0e-09
Match length	94
% identity	45
NCBI Description	(AC002337) peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No.	392251
Contig ID	30248_1.R1084
5'-most EST	uC-osflcyp037g04b1
Method	BLASTX
NCBI GI	g549061
BLAST score	573
E value	7.0e-59
Match length	224
% identity	55
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)

(CCT-ZETA-1) >gi_631655_pir__S43063 CCT (chaperonin containing TCP-1) zeta chain - mouse >gi_468554_emb_CAA83432_ (Z31557) CCT (chaperonin containing TCP-1) zeta subunit [Mus musculus] >gi_5295933_dbj_BAA81877.1_ (AB022159) chaperonin containing TCP-1 zeta-1 subunit [Mus musculus]

Seq. No.	392252
Contig ID	30263_1.R1084
5'-most EST	g3767386
Method	BLASTX
NCBI GI	g2274859
BLAST score	392
E value	1.0e-37
Match length	73
% identity	96
NCBI Description	(AJ000016) Cks1 protein [Arabidopsis thaliana] >gi_4510420_gb_AAD21506.1_ (AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana]

Seq. No.	392253
Contig ID	30264_1.R1084
5'-most EST	uC-osflcyp035b09b1
Method	BLASTX
NCBI GI	g3258575
BLAST score	898
E value	9.0e-97
Match length	273
% identity	68
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	392254
Contig ID	30264_2.R1084
5'-most EST	uC-osflM202092b01b1
Method	BLASTX
NCBI GI	g3258575
BLAST score	164
E value	2.0e-15
Match length	95
% identity	53
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	392255
Contig ID	30269_1.R1084
5'-most EST	g2310027
Method	BLASTX
NCBI GI	g4115377
BLAST score	829
E value	3.0e-91
Match length	244
% identity	70
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	392256
Contig ID	30270_1.R1084
5'-most EST	g2431204

Method	BLASTX
NCBI GI	g4587584
BLAST score	243
E value	2.0e-20
Match length	76
% identity	58
NCBI Description	(AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	392257
Contig ID	30294_1.R1084
5'-most EST	uC-osflcyp039h09b1

Seq. No.	392258
Contig ID	30294_2.R1084
5'-most EST	g3761574

Seq. No.	392259
Contig ID	30308_1.R1084
5'-most EST	uC-osflcyp042b07b1
Method	BLASTX
NCBI GI	g2507455
BLAST score	490
E value	7.0e-88
Match length	231
% identity	75
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	392260
Contig ID	30310_1.R1084
5'-most EST	uC-osflcyp171f07b1
Method	BLASTX
NCBI GI	g548493
BLAST score	367
E value	9.0e-35
Match length	122
% identity	53
NCBI Description	EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi_629854_pir__S30067 polygalacturonase - maize >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea mays]

Seq. No.	392261
Contig ID	30312_1.R1084
5'-most EST	uC-osflcyp122g02b1
Method	BLASTX
NCBI GI	g3415117
BLAST score	521
E value	1.0e-52
Match length	182
% identity	40
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	392262
Contig ID	30312_2.R1084
5'-most EST	uC-osflcyp042g03b1
Method	BLASTX
NCBI GI	g5880464
BLAST score	608
E value	3.0e-63
Match length	164
% identity	38
NCBI Description	(AF088901) actin bundling protein ABP135 [Lilium longiflorum]

Seq. No.	392263
Contig ID	30313_1.R1084
5'-most EST	g286821
Method	BLASTX
NCBI GI	g6103623
BLAST score	1080
E value	1.0e-118
Match length	209
% identity	98
NCBI Description	(AF172094) actin [Picea rubens]

Seq. No.	392264
Contig ID	30324_1.R1084
5'-most EST	uC-osflcyp154f08b1

Seq. No.	392265
Contig ID	30332_1.R1084
5'-most EST	g2280730
Method	BLASTX
NCBI GI	g3033398
BLAST score	914
E value	9.0e-99
Match length	229
% identity	76
NCBI Description	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No.	392266
Contig ID	30343_1.R1084
5'-most EST	uC-osflm202101h02b1
Method	BLASTX
NCBI GI	g4097831
BLAST score	170
E value	8.0e-12
Match length	93
% identity	42
NCBI Description	(U70048) zeta-crystallin [Bos taurus]

Seq. No.	392267
Contig ID	30347_1.R1084
5'-most EST	uC-osflcyp047b03b1
Method	BLASTX
NCBI GI	g3395938
BLAST score	484
E value	2.0e-48

Match length	147
% identity	40
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	392268
Contig ID	30354_1.R1084
5'-most EST	g4880039
Method	BLASTX
NCBI GI	g3913952
BLAST score	456
E value	7.0e-45
Match length	198
% identity	39
NCBI Description	ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi_2351578 (U82330) adenylate kinase homolog [Prunus armeniaca]

Seq. No.	392269
Contig ID	30356_1.R1084
5'-most EST	uC-osroM202041e01b1
Method	BLASTX
NCBI GI	g4006882
BLAST score	478
E value	2.0e-50
Match length	163
% identity	61
NCBI Description	(Z99707) UDP-glucuronyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	392270
Contig ID	30365_1.R1084
5'-most EST	g428389

Seq. No.	392271
Contig ID	30369_1.R1084
5'-most EST	g4715529
Method	BLASTX
NCBI GI	g4582488
BLAST score	750
E value	2.0e-79
Match length	257
% identity	66
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	392272
Contig ID	30379_1.R1084
5'-most EST	uC-osflcyp101g06b1
Method	BLASTX
NCBI GI	g5679838
BLAST score	309
E value	1.0e-27
Match length	133
% identity	44
NCBI Description	(AJ243961) has similarity to Arabidopsis thaliana gi_3068705 [Oryza sativa]

Seq. No.	392273

Contig ID	30390_1.R1084
5'-most EST	uC-osflm202107a10b1
Seq. No.	392274
Contig ID	30391_1.R1084
5'-most EST	uC-osflcyp050a06b1
Method	BLASTX
NCBI GI	g3878351
BLAST score	147
E value	2.0e-13
Match length	76
% identity	53
NCBI Description	(Z81098) Similarity to Entamoeba elongation factor 1-alpha (SW:EF1A_ENTHI); cDNA EST EMBL:M89117 comes from this gene; cDNA EST yk430d7.3 comes from this gene; cDNA EST yk430d7.5 comes from this gene; cDNA EST yk667b7.3 comes
Seq. No.	392275
Contig ID	30400_1.R1084
5'-most EST	g2442384
Seq. No.	392276
Contig ID	30403_1.R1084
5'-most EST	uC-osrocyp006f06b1
Method	BLASTX
NCBI GI	g1841468
BLAST score	338
E value	5.0e-37
Match length	105
% identity	69
NCBI Description	(Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]
Seq. No.	392277
Contig ID	30410_1.R1084
5'-most EST	uC-osflcyp170b07b1
Seq. No.	392278
Contig ID	30412_1.R1084
5'-most EST	g2427261
Method	BLASTX
NCBI GI	g4753658
BLAST score	985
E value	1.0e-107
Match length	287
% identity	66
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]
Seq. No.	392279
Contig ID	30416_1.R1084
5'-most EST	uC-osflcyp050f11b1
Seq. No.	392280
Contig ID	30419_1.R1084
5'-most EST	uC-osflcyp171a03b1
Method	BLASTX
NCBI GI	g4455323
BLAST score	221

E value	8.0e-18
Match length	78
% identity	55
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	392281
Contig ID	30420_1.R1084
5'-most EST	uC-osflcyp050h10b1

Seq. No.	392282
Contig ID	30421_1.R1084
5'-most EST	g5005522

Seq. No.	392283
Contig ID	30423_1.R1084
5'-most EST	uC-osrocyp006c02b1

Seq. No.	392284
Contig ID	30433_1.R1084
5'-most EST	uC-osroM202040d11b1
Method	BLASTX
NCBI GI	g4559342
BLAST score	958
E value	1.0e-104
Match length	185
% identity	92
NCBI Description	(AC007087) putative copper methylamine oxidase [Arabidopsis thaliana]

Seq. No.	392285
Contig ID	30446_1.R1084
5'-most EST	uC-osflcyp144b06b1
Method	BLASTX
NCBI GI	g5708091
BLAST score	255
E value	8.0e-22
Match length	125
% identity	50
NCBI Description	(AL022198) ribosomal protein S11-like [Arabidopsis thaliana]

Seq. No.	392286
Contig ID	30447_1.R1084
5'-most EST	uC-osflM202053d06b1
Method	BLASTX
NCBI GI	g4886756
BLAST score	483
E value	1.0e-48
Match length	119
% identity	73
NCBI Description	(AF088917) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	392287
Contig ID	30467_1.R1084
5'-most EST	uC-osflcyp052a02b1

Method	BLASTX
NCBI GI	g4539006
BLAST score	591
E value	6.0e-61
Match length	166
% identity	67
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	392288
Contig ID	30482_1.R1084
5'-most EST	uC-osflcyp155g09b1
Method	BLASTX
NCBI GI	g5669924
BLAST score	886
E value	2.0e-95
Match length	192
% identity	85
NCBI Description	(AF149116) soluble inorganic pyrophosphatase [Populus tremula x Populus tremuloides]

Seq. No.	392289
Contig ID	30483_1.R1084
5'-most EST	uC-osrocyp028b12b1
Method	BLASTX
NCBI GI	g4218120
BLAST score	154
E value	5.0e-11
Match length	74
% identity	58
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	392290
Contig ID	30494_1.R1084
5'-most EST	g2310976
Method	BLASTX
NCBI GI	g4678923
BLAST score	192
E value	3.0e-14
Match length	72
% identity	46
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	392291
Contig ID	30501_1.R1084
5'-most EST	uC-osflcyp023c02b1
Method	BLASTX
NCBI GI	g4678386
BLAST score	234
E value	4.0e-19
Match length	79
% identity	54
NCBI Description	(AL049656) putative protein [Arabidopsis thaliana]

Seq. No.	392292
Contig ID	30521_1.R1084
5'-most EST	g2427212

Method	BLASTX
NCBI GI	g3297810
BLAST score	242
E value	3.0e-20
Match length	156
% identity	36
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	392293
Contig ID	30529_1.R1084
5'-most EST	uC-osroM202033b06b1
Method	BLASTX
NCBI GI	g4191782
BLAST score	613
E value	1.0e-63
Match length	133
% identity	85
NCBI Description	(AC005917) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	392294
Contig ID	30530_1.R1084
5'-most EST	g4878449
Method	BLASTX
NCBI GI	g6014904
BLAST score	430
E value	3.0e-42
Match length	136
% identity	62
NCBI Description	DAG PROTEIN, CHLOROPLAST PRECURSOR >gi_1200205_emb_CAA65064_ (X95753) DAG [Antirrhinum majus]

Seq. No.	392295
Contig ID	30534_1.R1084
5'-most EST	uC-osflcyp053e03b1
Method	BLASTX
NCBI GI	g5902360
BLAST score	556
E value	8.0e-57
Match length	151
% identity	70
NCBI Description	(AC009322) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	392296
Contig ID	30546_1.R1084
5'-most EST	uC-osflcyp053g04b1

Seq. No.	392297
Contig ID	30552_1.R1084
5'-most EST	g3761570
Method	BLASTX
NCBI GI	g2583108
BLAST score	168
E value	2.0e-11
Match length	161
% identity	30
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	392298
Contig ID	30564_1.R1084
5'-most EST	uC-osf1M202020e02b1
Method	BLASTX
NCBI GI	g2982469
BLAST score	188
E value	5.0e-14
Match length	48
% identity	73
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	392299
Contig ID	30573_1.R1084
5'-most EST	g569859

Seq. No.	392300
Contig ID	30579_1.R1084
5'-most EST	uC-osf1cyp172h01b1

Seq. No.	392301
Contig ID	30587_1.R1084
5'-most EST	uC-osf1m202100b08b1

Seq. No.	392302
Contig ID	30591_1.R1084
5'-most EST	uC-osf1cyp055e06b1
Method	BLASTX
NCBI GI	g3702352
BLAST score	502
E value	8.0e-51
Match length	134
% identity	43
NCBI Description	(AC005397) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	392303
Contig ID	30598_1.R1084
5'-most EST	uC-osf1cyp055f08b1

Seq. No.	392304
Contig ID	30602_1.R1084
5'-most EST	uC-osf1cyp055g04b1

Seq. No.	392305
Contig ID	30606_1.R1084
5'-most EST	uC-osf1M202083a06b1
Method	BLASTX
NCBI GI	g134102
BLAST score	774
E value	2.0e-82
Match length	183
% identity	86
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_72959_pir__HHWTBA ribulose-bisphosphate carboxylase subunit-binding protein alpha chain - wheat (fragment) >gi_1345582_emb_CAA30699_ (X07851) rubisco subunit

	binding-protein alpha subunit (543 AA) [Triticum aestivum]
Seq. No.	392306
Contig ID	30612_1.R1084
5'-most EST	uC-osflcyp055h08b1
Method	BLASTX
NCBI GI	g2642213
BLAST score	168
E value	1.0e-16
Match length	84
% identity	56
NCBI Description	(AF030385) nitrate-induced NOI protein [Zea mays] >gi_2895781 (AF045033) nitrate-induced NOI protein [Zea mays]
Seq. No.	392307
Contig ID	30613_1.R1084
5'-most EST	uC-osflcyp055h10b1
Seq. No.	392308
Contig ID	30625_1.R1084
5'-most EST	g699720
Method	BLASTX
NCBI GI	g4235430
BLAST score	348
E value	5.0e-48
Match length	130
% identity	74
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.	392309
Contig ID	30626_1.R1084
5'-most EST	uC-osflcyp057d01b1
Seq. No.	392310
Contig ID	30629_1.R1084
5'-most EST	g4878125
Method	BLASTX
NCBI GI	g2980794
BLAST score	254
E value	3.0e-38
Match length	102
% identity	62
NCBI Description	(AL022197) myb-like protein [Arabidopsis thaliana]
Seq. No.	392311
Contig ID	30630_1.R1084
5'-most EST	g1632376
Seq. No.	392312
Contig ID	30636_1.R1084
5'-most EST	uC-osflcyp081a08b1
Method	BLASTX
NCBI GI	g2129552
BLAST score	235
E value	3.0e-19

Match length	69
% identity	61
NCBI Description	calcium-dependent protein kinase 19 - Arabidopsis thaliana (fragment)

Seq. No.	392313
Contig ID	30638_1.R1084
5'-most EST	g5803580
Method	BLASTX
NCBI GI	g4206114
BLAST score	787
E value	3.0e-84
Match length	166
% identity	89
NCBI Description	(AF097663) cytoplasmic glucose-6-phosphate 1-dehydrogenase [Mesembryanthemum crystallinum]

Seq. No.	392314
Contig ID	30676_1.R1084
5'-most EST	uC-osflcyp058g08b1
Method	BLASTX
NCBI GI	g2507281
BLAST score	538
E value	5.0e-55
Match length	126
% identity	81
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	392315
Contig ID	30682_1.R1084
5'-most EST	uC-osflcyp061a05b1

Seq. No.	392316
Contig ID	30689_1.R1084
5'-most EST	uC-osflcyp061b05b1

Seq. No.	392317
Contig ID	30707_1.R1084
5'-most EST	uC-osflcyp061f02b1
Method	BLASTX
NCBI GI	g3805765
BLAST score	658
E value	8.0e-69
Match length	207
% identity	66
NCBI Description	(AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No.	392318
Contig ID	30708_1.R1084
5'-most EST	g4880897
Method	BLASTX
NCBI GI	g2688830
BLAST score	410
E value	3.0e-61
Match length	164
% identity	76

NCBI Description	(AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No.	392319
Contig ID	30722_1.R1084
5'-most EST	uC-osflcyp061g12b1
Method	BLASTX
NCBI GI	g4678935
BLAST score	344
E value	5.0e-32
Match length	90
% identity	67
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	392320
Contig ID	30723_1.R1084
5'-most EST	uC-osflcyp061h02b1
Method	BLASTX
NCBI GI	g5499713
BLAST score	228
E value	1.0e-18
Match length	121
% identity	48
NCBI Description	(U78762) receptor-like kinase ARK1AS [Triticum aestivum]

Seq. No.	392321
Contig ID	30730_1.R1084
5'-most EST	g3768865

Seq. No.	392322
Contig ID	30745_1.R1084
5'-most EST	uC-osflcyp064b04b1
Method	BLASTX
NCBI GI	g3413700
BLAST score	809
E value	7.0e-90
Match length	222
% identity	79
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No.	392323
Contig ID	30747_1.R1084
5'-most EST	g2428081
Method	BLASTX
NCBI GI	g2832641
BLAST score	476
E value	1.0e-47
Match length	155
% identity	58
NCBI Description	(AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]

Seq. No.	392324
Contig ID	30766_1.R1084
5'-most EST	uC-osflcyp064d11b1

Seq. No.	392325
Contig ID	30772_1.R1084

5'-most EST	uC-osflcyp064e08b1
Method	BLASTN
NCBI GI	g4680189
BLAST score	35
E value	8.0e-10
Match length	51
% identity	92
NCBI Description	Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds

Seq. No.	392326
Contig ID	30773_1.R1084
5'-most EST	uC-osflcyp064e09b1
Method	BLASTX
NCBI GI	g4582436
BLAST score	771
E value	3.0e-82
Match length	200
% identity	76
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	392327
Contig ID	30775_1.R1084
5'-most EST	uC-osflcyp064e11b1
Method	BLASTX
NCBI GI	g3004565
BLAST score	709
E value	7.0e-75
Match length	234
% identity	59
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	392328
Contig ID	30779_1.R1084
5'-most EST	uC-osflcyp064f07b1

Seq. No.	392329
Contig ID	30785_1.R1084
5'-most EST	g4880336

Seq. No.	392330
Contig ID	30792_1.R1084
5'-most EST	uC-osroM202041e08b1
Method	BLASTX
NCBI GI	g2980774
BLAST score	165
E value	5.0e-25
Match length	118
% identity	57
NCBI Description	(AL022198) leucyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	392331
Contig ID	30794_1.R1084
5'-most EST	g4969202

Method	BLASTX
NCBI GI	g4586249
BLAST score	365
E value	2.0e-34
Match length	210
% identity	40
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]

Seq. No.	392332
Contig ID	30795_1.R1084
5'-most EST	uC-osflcyp172d12b1
Method	BLASTX
NCBI GI	g1009234
BLAST score	492
E value	3.0e-49
Match length	161
% identity	63
NCBI Description	(L38829) SUP2 gene product [Nicotiana tabacum]

Seq. No.	392333
Contig ID	30797_1.R1084
5'-most EST	uC-osflM202020c05b1
Method	BLASTX
NCBI GI	g4689108
BLAST score	433
E value	2.0e-42
Match length	165
% identity	49
NCBI Description	(AF077030) hypothetical 43.2 kDa protein [Homo sapiens] >gi_4929577_gb_AAD34049.1_AF151812_1 (AF151812) CGI-54 protein [Homo sapiens]

Seq. No.	392334
Contig ID	30797_2.R1084
5'-most EST	uC-osrocyp030a09b1
Method	BLASTX
NCBI GI	g4689108
BLAST score	149
E value	3.0e-09
Match length	47
% identity	55
NCBI Description	(AF077030) hypothetical 43.2 kDa protein [Homo sapiens] >gi_4929577_gb_AAD34049.1_AF151812_1 (AF151812) CGI-54 protein [Homo sapiens]

Seq. No.	392335
Contig ID	30799_1.R1084
5'-most EST	g3768807
Method	BLASTX
NCBI GI	g1871192
BLAST score	837
E value	1.0e-89
Match length	265
% identity	62
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	392336
Contig ID	30800_1.R1084
5'-most EST	uC-osflcyp065a09b1
Method	BLASTX
NCBI GI	g4503609
BLAST score	267
E value	1.0e-23
Match length	84
% identity	62
NCBI Description	electron-transfer-flavoprotein, beta polypeptide >gi_585110_sp_P38117_ETFB_HUMAN ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) >gi_479194_pir__S32482 electron transfer flavoprotein beta chain - human >gi_2781203_pdb_1EFV_B Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution >gi_297902_emb_CAA50441_ (X71129) electron transfer flavoprotein beta subunit [Homo sapiens]

Seq. No.	392337
Contig ID	30804_1.R1084
5'-most EST	uC-osflcyp065b02b1

Seq. No.	392338
Contig ID	30811_1.R1084
5'-most EST	uC-osflcyp065c06b1

Seq. No.	392339
Contig ID	30823_1.R1084
5'-most EST	g702465
Method	BLASTX
NCBI GI	g4191791
BLAST score	259
E value	3.0e-22
Match length	128
% identity	46
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

Seq. No.	392340
Contig ID	30827_2.R1084
5'-most EST	g2428180
Method	BLASTX
NCBI GI	g6045135
BLAST score	317
E value	2.0e-38
Match length	152
% identity	55
NCBI Description	(AB033335) oxidosqualene cyclase [Luffa cylindrica]

Seq. No.	392341
Contig ID	30833_1.R1084
5'-most EST	g701171

Seq. No.	392342
Contig ID	30842_1.R1084
5'-most EST	uC-osflm202120c12b1

Method	BLASTX
NCBI GI	g4417304
BLAST score	723
E value	2.0e-76
Match length	246
% identity	56
NCBI Description	(AC006446) putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana]

Seq. No.	392343
Contig ID	30848_1.R1084
5'-most EST	uC-osflM202097h07b1
Method	BLASTX
NCBI GI	g483412
BLAST score	471
E value	5.0e-47
Match length	202
% identity	54
NCBI Description	(L01497) calmodulin-binding protein [Zea mays]

Seq. No.	392344
Contig ID	30855_1.R1084
5'-most EST	uC-osflcyp035b10b1

Seq. No.	392345
Contig ID	30856_1.R1084
5'-most EST	g286572
Method	BLASTX
NCBI GI	g3668097
BLAST score	559
E value	3.0e-57
Match length	143
% identity	71
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	392346
Contig ID	30857_1.R1084
5'-most EST	uC-osflcyp071a01b1
Method	BLASTX
NCBI GI	g3402711
BLAST score	164
E value	4.0e-11
Match length	81
% identity	41
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	392347
Contig ID	30883_1.R1084
5'-most EST	g2800915
Method	BLASTX
NCBI GI	g5263314
BLAST score	316
E value	6.0e-29
Match length	130

% identity	49
NCBI Description	(AC007727) Similar to gb_X84260 POS5 gene product from Saccharomyces cerevisiae. EST gb_W43879 comes from this gene. [Arabidopsis thaliana]

Seq. No.	392348
Contig ID	30884_1.R1084
5'-most EST	g3107726
Method	BLASTX
NCBI GI	g4539404
BLAST score	658
E value	7.0e-69
Match length	170
% identity	41
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	392349
Contig ID	30885_1.R1084
5'-most EST	g702990

Seq. No.	392350
Contig ID	30885_2.R1084
5'-most EST	g3767293

Seq. No.	392351
Contig ID	30885_3.R1084
5'-most EST	g700917
Method	BLASTX
NCBI GI	g1872521
BLAST score	188
E value	6.0e-14
Match length	71
% identity	27
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_5262161_emb_CAB45804.1_ (AL080253) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	392352
Contig ID	30885_5.R1084
5'-most EST	uC-osflcyp071e07b1
Method	BLASTX
NCBI GI	g1872521
BLAST score	320
E value	4.0e-29
Match length	122
% identity	55
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_5262161_emb_CAB45804.1_ (AL080253) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	392353
Contig ID	30885_6.R1084
5'-most EST	g4968940

Seq. No.	392354

Contig ID	30889_1.R1084
5'-most EST	g2798760
Method	BLASTX
NCBI GI	g477819
BLAST score	562
E value	1.0e-57
Match length	198
% identity	54
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	392355
Contig ID	30898_1.R1084
5'-most EST	uC-osf1M202083c02b1
Method	BLASTX
NCBI GI	g2739383
BLAST score	475
E value	2.0e-47
Match length	155
% identity	63
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	392356
Contig ID	30899_1.R1084
5'-most EST	uC-osflcyp071g12b1
Method	BLASTX
NCBI GI	g3046731
BLAST score	197
E value	2.0e-24
Match length	126
% identity	54
NCBI Description	(AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No.	392357
Contig ID	30910_1.R1084
5'-most EST	uC-osflcyp074a11b1
Method	BLASTX
NCBI GI	g3599491
BLAST score	420
E value	1.0e-75
Match length	184
% identity	77
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	392358
Contig ID	30918_1.R1084
5'-most EST	g568607
Method	BLASTX
NCBI GI	g5734748
BLAST score	240
E value	3.0e-20
Match length	79
% identity	57
NCBI Description	(AC007651) Unknown protein [Arabidopsis thaliana]

Seq. No.	392359
Contig ID	30928_1.R1084
5'-most EST	uC-osflM202071d04b1
Method	BLASTX
NCBI GI	g4895197
BLAST score	171
E value	1.0e-11
Match length	92
% identity	38
NCBI Description	(AC007661) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392360
Contig ID	30942_1.R1084
5'-most EST	uC-osflcyp110d08a1
Method	BLASTX
NCBI GI	g3297808
BLAST score	367
E value	9.0e-35
Match length	128
% identity	34
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	392361
Contig ID	30956_1.R1084
5'-most EST	uC-osroM202037b05b1
Method	BLASTX
NCBI GI	g6049841
BLAST score	591
E value	4.0e-61
Match length	159
% identity	71
NCBI Description	(AF190728) asparagine synthetase [Helianthus annuus]

Seq. No.	392362
Contig ID	30964_1.R1084
5'-most EST	uC-osflcyp074e09b1

Seq. No.	392363
Contig ID	30966_1.R1084
5'-most EST	uC-osflcyp074e05b1
Method	BLASTX
NCBI GI	g4218151
BLAST score	191
E value	4.0e-14
Match length	86
% identity	44
NCBI Description	(AJ132705) hypothetical protein [Anabaena variabilis]

Seq. No.	392364
Contig ID	30970_1.R1084
5'-most EST	uC-osflcyp017h06b1

Seq. No.	392365
Contig ID	30971_1.R1084
5'-most EST	uC-osflcyp111c10b1

Seq. No.	392366
Contig ID	30978_1.R1084
5'-most EST	g2796694

Seq. No.	392367
Contig ID	30983_1.R1084
5'-most EST	uC-osflcyp074h12b1
Method	BLASTX
NCBI GI	g6041819
BLAST score	185
E value	4.0e-22
Match length	109
% identity	46
NCBI Description	(AC009918) unknown protein [Arabidopsis thaliana]

Seq. No.	392368
Contig ID	31010_1.R1084
5'-most EST	g5003515
Method	BLASTX
NCBI GI	g629592
BLAST score	477
E value	1.0e-47
Match length	177
% identity	51
NCBI Description	hypothetical protein - rape >gi_6065752_emb_CAB58175.1_ (X74225) putative pod-specific dehydrogenase SAC25 [Brassica napus]

Seq. No.	392369
Contig ID	31011_1.R1084
5'-most EST	g2801266

Seq. No.	392370
Contig ID	31021_1.R1084
5'-most EST	uC-osflcyp078c04b1

Seq. No.	392371
Contig ID	31030_1.R1084
5'-most EST	uC-osflcyp078d05b1

Seq. No.	392372
Contig ID	31031_1.R1084
5'-most EST	uC-osflM2020117f04a1

Seq. No.	392373
Contig ID	31034_1.R1084
5'-most EST	uC-osflcyp078d11b1
Method	BLASTX
NCBI GI	g3395938
BLAST score	266
E value	2.0e-38
Match length	106
% identity	78
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No. 392374

Contig ID	31035_1.R1084
5'-most EST	uC-osflcyp078d12b1
Method	BLASTX
NCBI GI	g2827702
BLAST score	346
E value	9.0e-56
Match length	169
% identity	61
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	392375
Contig ID	31038_1.R1084
5'-most EST	uC-osflcyp126e02b1

Seq. No.	392376
Contig ID	31041_1.R1084
5'-most EST	g3766947
Method	BLASTX
NCBI GI	g3193284
BLAST score	338
E value	1.0e-52
Match length	230
% identity	50
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	392377
Contig ID	31046_1.R1084
5'-most EST	uC-osflcyp078f05b1

Seq. No.	392378
Contig ID	31046_2.R1084
5'-most EST	g5003553

Seq. No.	392379
Contig ID	31047_1.R1084
5'-most EST	uC-osflcyp078f06b1
Method	BLASTX
NCBI GI	g4185143
BLAST score	651
E value	8.0e-68
Match length	189
% identity	66
NCBI Description	(AC005724) putative signal recognition particle receptor beta subunit [Arabidopsis thaliana]

Seq. No.	392380
Contig ID	31066_1.R1084
5'-most EST	uC-osflcyp078h11b1

Seq. No.	392381
Contig ID	31068_1.R1084
5'-most EST	uC-osflcyp080a02b1
Method	BLASTX
NCBI GI	g5453694
BLAST score	191
E value	4.0e-14
Match length	94

% identity	41
NCBI Description	cell cycle-regulated factor (78 kDa) >gi_3201964 (AF068007) cell cycle-regulated factor p78 [Homo sapiens]
Seq. No.	392382
Contig ID	31069_1.R1084
5'-most EST	uC-osflcyp080a03a1
Seq. No.	392383
Contig ID	31070_1.R1084
5'-most EST	uC-osflcyp080a04b1
Method	BLASTX
NCBI GI	g1086586
BLAST score	259
E value	5.0e-22
Match length	190
% identity	31
NCBI Description	(U41007) similar to G beta repeats (PROSITE:PS00670) [Caenorhabditis elegans]
Seq. No.	392384
Contig ID	31075_1.R1084
5'-most EST	uC-osflcyp080a10b1
Method	BLASTX
NCBI GI	g5690010
BLAST score	293
E value	3.0e-26
Match length	120
% identity	51
NCBI Description	(AJ132472) Family 3 Glycoside Hydrolase [Ruminococcus flavefaciens]
Seq. No.	392385
Contig ID	31091_1.R1084
5'-most EST	uC-osflcyp080d02b1
Method	BLASTX
NCBI GI	g5107819
BLAST score	500
E value	3.0e-50
Match length	144
% identity	65
NCBI Description	(AF149413) contains similarity to arabinosidase [Arabidopsis thaliana]
Seq. No.	392386
Contig ID	31096_1.R1084
5'-most EST	g2428054
Seq. No.	392387
Contig ID	31121_1.R1084
5'-most EST	g2428639
Seq. No.	392388
Contig ID	31129_1.R1084
5'-most EST	g4715322
Method	BLASTX
NCBI GI	g3880625

BLAST score	305
E value	3.0e-27
Match length	150
% identity	49
NCBI Description	(Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this

Seq. No.	392389
Contig ID	31132_1.R1084
5'-most EST	uC-osf1M202066f11b1

Seq. No.	392390
Contig ID	31134_1.R1084
5'-most EST	uC-osf1cyp081c04b1
Method	BLASTX
NCBI GI	g1172635
BLAST score	344
E value	3.0e-51
Match length	117
% identity	91
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	392391
Contig ID	31135_1.R1084
5'-most EST	uC-osf1cyp081c05b1

Seq. No.	392392
Contig ID	31138_1.R1084
5'-most EST	uC-osf1cyp081c12b1
Method	BLASTX
NCBI GI	g4544438
BLAST score	165
E value	2.0e-11
Match length	79
% identity	46
NCBI Description	(AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392393
Contig ID	31150_1.R1084
5'-most EST	uC-osf1cyp081e07b1
Method	BLASTX
NCBI GI	g4539335
BLAST score	506
E value	1.0e-103
Match length	243
% identity	71
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	392394
Contig ID	31151_2.R1084
5'-most EST	g4716324
Method	BLASTX
NCBI GI	g4877775

BLAST score 147
E value 4.0e-09
Match length 39
% identity 56
NCBI Description (AF126531) putative DNA-directed RNA polymerase III C11 subunit [Homo sapiens]

Seq. No. 392395
Contig ID 31155_1.R1084
5'-most EST g568011
Method BLASTX
NCBI GI g4959461
BLAST score 618
E value 4.0e-64
Match length 156
% identity 81
NCBI Description (AF126053) RACB small GTP binding protein [Zea mays]

Seq. No. 392396
Contig ID 31157_1.R1084
5'-most EST g2309743
Method BLASTX
NCBI GI g3023713
BLAST score 905
E value 7.0e-98
Match length 186
% identity 94
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372 (U09450) enolase [Oryza sativa]

Seq. No. 392397
Contig ID 31161_1.R1084
5'-most EST uC-osflcyp081f11b1
Method BLASTX
NCBI GI g639722
BLAST score 649
E value 8.0e-68
Match length 151
% identity 83
NCBI Description (L27484) calcium-dependent protein kinase [Zea mays]

Seq. No. 392398
Contig ID 31163_1.R1084
5'-most EST uC-osflcyp081g05b1

Seq. No. 392399
Contig ID 31166_1.R1084
5'-most EST uC-osroM202001h03b1
Method BLASTX
NCBI GI g1518540
BLAST score 893
E value 2.0e-97
Match length 203
% identity 88
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	392400
Contig ID	31168_1.R1084
5'-most EST	g2443157
Method	BLASTX
NCBI GI	g5306244
BLAST score	203
E value	2.0e-15
Match length	165
% identity	36
NCBI Description	(AC006438) unknown protein [Arabidopsis thaliana]

Seq. No.	392401
Contig ID	31168_3.R1084
5'-most EST	g3769043

Seq. No.	392402
Contig ID	31172_1.R1084
5'-most EST	uC-osflcyp081h07b1

Seq. No.	392403
Contig ID	31180_1.R1084
5'-most EST	uC-osroM202017b03b1
Method	BLASTX
NCBI GI	g4455364
BLAST score	223
E value	3.0e-18
Match length	85
% identity	52
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	392404
Contig ID	31188_1.R1084
5'-most EST	uC-osflcyp153f05a1

Seq. No.	392405
Contig ID	31201_1.R1084
5'-most EST	uC-osflcyp082e09b1
Method	BLASTX
NCBI GI	g4115925
BLAST score	484
E value	2.0e-48
Match length	151
% identity	38
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana] >gi_4959384_gb_AAD34325.1_ (AF109721) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	392406
Contig ID	31208_1.R1084
5'-most EST	uC-osflcyp082g10b1

Seq. No.	392407
Contig ID	31209_1.R1084
5'-most EST	g4879510

Seq. No.	392408
Contig ID	31213_1.R1084
5'-most EST	uC-osf1M202049g07b1

Seq. No.	392409
Contig ID	31217_1.R1084
5'-most EST	g2310471
Method	BLASTX
NCBI GI	g1781115
BLAST score	158
E value	2.0e-10
Match length	74
% identity	42
NCBI Description	(Z83864) glpQ1 [Mycobacterium tuberculosis]

Seq. No.	392410
Contig ID	31235_1.R1084
5'-most EST	uC-osf1cyp085c11b1

Seq. No.	392411
Contig ID	31243_1.R1084
5'-most EST	g2798990
Method	BLASTX
NCBI GI	g2499819
BLAST score	330
E value	6.0e-37
Match length	92
% identity	84
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No.	392412
Contig ID	31243_2.R1084
5'-most EST	g2799147
Method	BLASTX
NCBI GI	g1168536
BLAST score	279
E value	2.0e-24
Match length	112
% identity	55
NCBI Description	PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE) >gi_100567_pir__S19697 aspartic proteinase (EC 3.4.23.-) precursor - barley >gi_18904_emb_CAA39602_ (X56136) aspartic proteinase [Hordeum vulgare]

Seq. No.	392413
Contig ID	31243_3.R1084
5'-most EST	g2799538
Method	BLASTX
NCBI GI	g2499819
BLAST score	962
E value	1.0e-152
Match length	317

% identity	78
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]
Seq. No.	392414
Contig ID	31247_1.R1084
5'-most EST	uC-osflcyp157c10b1
Method	BLASTX
NCBI GI	g4539371
BLAST score	174
E value	3.0e-12
Match length	84
% identity	40
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]
Seq. No.	392415
Contig ID	31253_1.R1084
5'-most EST	uC-osflcyp085g01b1
Seq. No.	392416
Contig ID	31254_1.R1084
5'-most EST	uC-osflcyp085g02b1
Seq. No.	392417
Contig ID	31278_1.R1084
5'-most EST	g2799399
Method	BLASTX
NCBI GI	g3319353
BLAST score	189
E value	2.0e-23
Match length	94
% identity	53
NCBI Description	(AF077407) contains similarity to copper-binding proteins [Arabidopsis thaliana]
Seq. No.	392418
Contig ID	31280_1.R1084
5'-most EST	uC-osflcyp086b11b1
Method	BLASTX
NCBI GI	g5354158
BLAST score	599
E value	4.0e-62
Match length	156
% identity	69
NCBI Description	(AF149841) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_6041825_gb_AAF02140.1_AC009918_12 (AC009918) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
Seq. No.	392419
Contig ID	31291_1.R1084
5'-most EST	g4715089
Method	BLASTX

NCBI GI g5813796
BLAST score 200
E value 3.0e-15
Match length 112
% identity 39
NCBI Description (AF082862) unknown [Pisum sativum]

Seq. No. 392420
Contig ID 31294_2.R1084
5'-most EST uC-osflm202109e11b1
Method BLASTX
NCBI GI g4455274
BLAST score 173
E value 5.0e-12
Match length 94
% identity 43
NCBI Description (AL035527) spliceosome associated protein-like [Arabidopsis thaliana]

Seq. No. 392421
Contig ID 31297_1.R1084
5'-most EST uC-osflcyp086e06b1

Seq. No. 392422
Contig ID 31303_1.R1084
5'-most EST uC-osflM202014d08b1
Method BLASTX
NCBI GI g2117937
BLAST score 584
E value 2.0e-60
Match length 159
% identity 72
NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No. 392423
Contig ID 31322_1.R1084
5'-most EST uC-osflcyp086h12b1
Method BLASTX
NCBI GI g1491712
BLAST score 222
E value 9.0e-18
Match length 117
% identity 42
NCBI Description (X99961) unknown [Homo sapiens]

Seq. No. 392424
Contig ID 31351_1.R1084
5'-most EST g2799934

Seq. No. 392425
Contig ID 31364_1.R1084
5'-most EST uC-osflM202035d07b1
Method BLASTX
NCBI GI g3426041
BLAST score 664

E value 2.0e-69
Match length 198
% identity 59
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 392426
Contig ID 31373_1.R1084
5'-most EST uC-osflm202102b12b1
Method BLASTX
NCBI GI g2708741
BLAST score 978
E value 1.0e-106
Match length 241
% identity 76
NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No. 392427
Contig ID 31375_1.R1084
5'-most EST uC-osflcyp088h01b1
Method BLASTX
NCBI GI g4581164
BLAST score 335
E value 3.0e-31
Match length 168
% identity 41
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 392428
Contig ID 31400_1.R1084
5'-most EST g2280557
Method BLASTX
NCBI GI g3212854
BLAST score 254
E value 1.0e-21
Match length 157
% identity 38
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 392429
Contig ID 31405_1.R1084
5'-most EST uC-osflcyp089g01b1

Seq. No. 392430
Contig ID 31407_1.R1084
5'-most EST uC-osflcyp089g05b1
Method BLASTX
NCBI GI g3201627
BLAST score 540
E value 5.0e-55
Match length 122
% identity 77
NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 392431
Contig ID 31417_1.R1084
5'-most EST uC-osflcyp090a08b1
Method BLASTX

NCBI GI g3785978
BLAST score 293
E value 8.0e-28
Match length 121
% identity 56
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 392432
Contig ID 31424_1.R1084
5'-most EST g4969118
Method BLASTX
NCBI GI g6016877
BLAST score 166
E value 5.0e-11
Match length 47
% identity 62
NCBI Description (AP000570) ESTs AU077642(E30706),AU077641(E30706) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No. 392433
Contig ID 31442_1.R1084
5'-most EST uC-osflcyp091b05b1

Seq. No. 392434
Contig ID 31447_1.R1084
5'-most EST g4715143

Seq. No. 392435
Contig ID 31451_1.R1084
5'-most EST g2427633

Seq. No. 392436
Contig ID 31452_1.R1084
5'-most EST uC-osflM202068h11b1
Method BLASTX
NCBI GI g2244855
BLAST score 148
E value 5.0e-09
Match length 95
% identity 42
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 392437
Contig ID 31454_1.R1084
5'-most EST uC-osflm202104g02b1
Method BLASTX
NCBI GI g401237
BLAST score 1154
E value 1.0e-142
Match length 319
% identity 80
NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 2 >gi_170684 (M90663) ubiquitin activating enyme [Triticum aestivum]

Seq. No. 392438
Contig ID 31488_1.R1084

5'-most EST	uC-osflcyp106f11b1
Method	BLASTX
NCBI GI	g1495768
BLAST score	253
E value	7.0e-22
Match length	108
% identity	52
NCBI Description	(Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]

Seq. No.	392439
Contig ID	31495_1.R1084
5'-most EST	g2428559
Method	BLASTX
NCBI GI	g1353193
BLAST score	351
E value	4.0e-33
Match length	134
% identity	57
NCBI Description	O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No.	392440
Contig ID	31507_1.R1084
5'-most EST	g3761343

Seq. No.	392441
Contig ID	31509_1.R1084
5'-most EST	uC-osflcyp093e08b1
Method	BLASTX
NCBI GI	g3860262
BLAST score	359
E value	3.0e-34
Match length	126
% identity	60
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	392442
Contig ID	31514_1.R1084
5'-most EST	g4881052
Method	BLASTX
NCBI GI	g2407617
BLAST score	314
E value	1.0e-62
Match length	224
% identity	58
NCBI Description	(AF017984) glutathione synthetase [Lycopersicon esculentum]

Seq. No.	392443
Contig ID	31520_1.R1084
5'-most EST	uC-osflcyp095a05b1

Seq. No.	392444
Contig ID	31524_1.R1084
5'-most EST	uC-osflM202095g05b1
Method	BLASTX

NCBI GI	g3790188
BLAST score	351
E value	4.0e-33
Match length	104
% identity	66
NCBI Description	(Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana tabacum]

Seq. No.	392445
Contig ID	31525_1.R1084
5'-most EST	g5003831

Seq. No.	392446
Contig ID	31542_1.R1084
5'-most EST	uC-osf1M202053g09b1
Method	BLASTX
NCBI GI	g4455232
BLAST score	663
E value	1.0e-69
Match length	150
% identity	76
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	392447
Contig ID	31555_1.R1084
5'-most EST	uC-osroM202039b09b1
Method	BLASTX
NCBI GI	g4914414
BLAST score	462
E value	4.0e-46
Match length	148
% identity	66
NCBI Description	(AL050352) Ca2+-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No.	392448
Contig ID	31556_1.R1084
5'-most EST	uC-osf1M202098d05b1
Method	BLASTX
NCBI GI	g3785989
BLAST score	185
E value	9.0e-14
Match length	127
% identity	38
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	392449
Contig ID	31559_1.R1084
5'-most EST	g5004361
Method	BLASTX
NCBI GI	g3023945
BLAST score	620
E value	2.0e-81
Match length	187
% identity	84
NCBI Description	HISTONE DEACETYLASE (HD) >gi_2318131 (AF014824) histone deacetylase [Arabidopsis thaliana]

Seq. No.	392450
Contig ID	31559_2.R1084
5'-most EST	g5455382
Method	BLASTX
NCBI GI	g4467119
BLAST score	546
E value	5.0e-56
Match length	113
% identity	88
NCBI Description	(AL035538) Histone deacetylase [Arabidopsis thaliana]

Seq. No.	392451
Contig ID	31568_1.R1084
5'-most EST	uC-osflcyp096f01b1
Method	BLASTX
NCBI GI	g5478530
BLAST score	161
E value	2.0e-10
Match length	99
% identity	7
NCBI Description	(AF130441) UVB-resistance protein UVR8 [Arabidopsis thaliana]

Seq. No.	392452
Contig ID	31580_1.R1084
5'-most EST	uC-osflM202066b07b1
Method	BLASTX
NCBI GI	g134102
BLAST score	1030
E value	1.0e-149
Match length	459
% identity	76
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_72959_pir__HHWTBA ribulose-bisphosphate carboxylase subunit-binding protein alpha chain - wheat (fragment) >gi_1345582_emb_CAA30699_ (X07851) rubisco subunit binding-protein alpha subunit (543 AA) [Triticum aestivum]

Seq. No.	392453
Contig ID	31585_1.R1084
5'-most EST	g1632395

Seq. No.	392454
Contig ID	31585_2.R1084
5'-most EST	g5004025

Seq. No.	392455
Contig ID	31590_1.R1084
5'-most EST	uC-osflcyp097b06b1

Seq. No.	392456
Contig ID	31614_1.R1084
5'-most EST	uC-osflcyp097g09b1

Seq. No.	392457
Contig ID	31628_1.R1084
5'-most EST	uC-osflcyp126a11b1
Method	BLASTX
NCBI GI	g3859659
BLAST score	405
E value	2.0e-39
Match length	168
% identity	51
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No.	392458
Contig ID	31637_1.R1084
5'-most EST	uC-osflcyp098e01b1

Seq. No.	392459
Contig ID	31642_1.R1084
5'-most EST	g2796597
Method	BLASTX
NCBI GI	g1652084
BLAST score	168
E value	8.0e-12
Match length	89
% identity	40
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	392460
Contig ID	31646_1.R1084
5'-most EST	uC-osflcyp098g01b1

Seq. No.	392461
Contig ID	31648_1.R1084
5'-most EST	uC-osflM202049h10b1

Seq. No.	392462
Contig ID	31661_1.R1084
5'-most EST	g2800277

Seq. No.	392463
Contig ID	31667_1.R1084
5'-most EST	uC-osflm202002d10b1
Method	BLASTX
NCBI GI	g730290
BLAST score	625
E value	6.0e-65
Match length	227
% identity	54
NCBI Description	PECTATE LYASE PRECURSOR >gi_322883_pir__S29612 pectate lyase - trumpet lily >gi_19451_emb_CAA78976_ (Z17328) pectate lyase [Lilium longiflorum] >gi_308902 (L18911) pectate lyase [Lilium longiflorum]

Seq. No.	392464
Contig ID	31667_2.R1084
5'-most EST	uC-osflcyp126a02b1
Method	BLASTX

NCBI GI	g730290
BLAST score	150
E value	1.0e-09
Match length	61
% identity	51
NCBI Description	PECTATE LYASE PRECURSOR >gi_322883_pir__S29612 pectate lyase - trumpet lily >gi_19451_emb_CAA78976_ (Z17328) pectate lyase [Lilium longiflorum] >gi_308902 (L18911) pectate lyase [Lilium longiflorum]

Seq. No.	392465
Contig ID	31675_1.R1084
5'-most EST	uC-osflcyp099g01b1
Method	BLASTX
NCBI GI	g4585614
BLAST score	140
E value	4.0e-12
Match length	92
% identity	49
NCBI Description	(AL049628) L-aspartate oxidase [Streptomyces coelicolor]

Seq. No.	392466
Contig ID	31678_1.R1084
5'-most EST	uC-osflcyp099g06b1

Seq. No.	392467
Contig ID	31685_1.R1084
5'-most EST	uC-osflcyp005f07b1

Seq. No.	392468
Contig ID	31695_1.R1084
5'-most EST	uC-osroM202032f04b1
Method	BLASTX
NCBI GI	g4567250
BLAST score	224
E value	8.0e-18
Match length	115
% identity	45
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392469
Contig ID	31700_1.R1084
5'-most EST	uC-osflcyp101d05b1
Method	BLASTX
NCBI GI	g6005948
BLAST score	145
E value	6.0e-09
Match length	49
% identity	49
NCBI Description	WW domain binding protein 4 (formin binding protein 21) >gi_3550080 (AF071185) formin binding protein 21 [Homo sapiens]

Seq. No.	392470
Contig ID	31707_1.R1084
5'-most EST	uC-osflcyp101e09b1
Method	BLASTX

NCBI GI	g3150415
BLAST score	637
E value	2.0e-66
Match length	180
% identity	25
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	392471
Contig ID	31718_1.R1084
5'-most EST	uC-osflcyp101g09b1

Seq. No.	392472
Contig ID	31722_1.R1084
5'-most EST	g2428722

Seq. No.	392473
Contig ID	31724_1.R1084
5'-most EST	uC-osflcyp154e09b1
Method	BLASTX
NCBI GI	g4558552
BLAST score	299
E value	7.0e-27
Match length	73
% identity	41
NCBI Description	(AC007138) putative P-glycoprotein-like protein [Arabidopsis thaliana]

Seq. No.	392474
Contig ID	31736_1.R1084
5'-most EST	g3462538
Method	BLASTX
NCBI GI	g5103807
BLAST score	802
E value	1.0e-85
Match length	200
% identity	71
NCBI Description	(AC007591) Contains similarity to gb_AF014403 type-2 phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo sapiens. ESTs gb_T88254 and gb_AA394650 come from this gene. [Arabidopsis thaliana]

Seq. No.	392475
Contig ID	31743_1.R1084
5'-most EST	uC-osflm202113h11b1
Method	BLASTX
NCBI GI	g3063468
BLAST score	158
E value	5.0e-16
Match length	72
% identity	69
NCBI Description	(AC003981) F22O13.30 [Arabidopsis thaliana]

Seq. No.	392476
Contig ID	31747_1.R1084
5'-most EST	g4714103

Method	BLASTX
NCBI GI	g5091498
BLAST score	289
E value	6.0e-26
Match length	54
% identity	100
NCBI Description	(AB023482) ESTs AU058067(E20733), AAU058070(E20873) correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase mRNA, complete cds.(U27116) [Oryza sativa]

Seq. No.	392477
Contig ID	31756_1.R1084
5'-most EST	uC-osrocyp031h11b1

Seq. No.	392478
Contig ID	31764_1.R1084
5'-most EST	uC-osflcyp106g09b1

Seq. No.	392479
Contig ID	31765_1.R1084
5'-most EST	uC-osflcyp156g04b1

Seq. No.	392480
Contig ID	31775_1.R1084
5'-most EST	g4714785

Seq. No.	392481
Contig ID	31783_1.R1084
5'-most EST	uC-osflcyp107b06b1

Seq. No.	392482
Contig ID	31784_1.R1084
5'-most EST	uC-osflcyp107b08b1
Method	BLASTX
NCBI GI	g1877397
BLAST score	716
E value	2.0e-75
Match length	147
% identity	88
NCBI Description	(Y11591) shaggy-like kinase [Ricinus communis]

Seq. No.	392483
Contig ID	31789_1.R1084
5'-most EST	g2312179
Method	BLASTX
NCBI GI	g1168518
BLAST score	265
E value	5.0e-23
Match length	84
% identity	56
NCBI Description	APURINIC ENDONUCLEASE-REDOX PROTEIN (DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE) >gi_472869_emb_CAA54234_ (X76912) ARP protein [Arabidopsis thaliana]

Seq. No.	392484
Contig ID	31792_1.R1084

5'-most EST	g5003490
Method	BLASTX
NCBI GI	g5738362
BLAST score	484
E value	3.0e-50
Match length	243
% identity	52
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	392485
Contig ID	31807_1.R1084
5'-most EST	uC-osflcyp107g02b1
Method	BLASTX
NCBI GI	g1730560
BLAST score	788
E value	4.0e-84
Match length	189
% identity	75
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba]

Seq. No.	392486
Contig ID	31820_1.R1084
5'-most EST	uC-osflcyp107h11b1

Seq. No.	392487
Contig ID	31827_1.R1084
5'-most EST	g4715806

Seq. No.	392488
Contig ID	31845_1.R1084
5'-most EST	uC-osflcyp108f03b1
Method	BLASTX
NCBI GI	g5091520
BLAST score	716
E value	8.0e-76
Match length	158
% identity	89
NCBI Description	(AB023482) ESTs AU058081(E30812),AU058365(E50679), AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome 37kD subunit.(X96974) [Oryza sativa]

Seq. No.	392489
Contig ID	31845_2.R1084
5'-most EST	g570166
Method	BLASTX
NCBI GI	g5091520
BLAST score	303
E value	1.0e-27
Match length	83
% identity	77
NCBI Description	(AB023482) ESTs AU058081(E30812),AU058365(E50679), AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome 37kD subunit.(X96974) [Oryza sativa]

Seq. No.	392490
Contig ID	31851_1.R1084
5'-most EST	uC-osflcyp108g04b1
Seq. No.	392491
Contig ID	31855_1.R1084
5'-most EST	uC-osflm202120e01b1
Seq. No.	392492
Contig ID	31877_1.R1084
5'-most EST	uC-osflcyp109d02b1
Seq. No.	392493
Contig ID	31884_1.R1084
5'-most EST	g286854
Seq. No.	392494
Contig ID	31887_1.R1084
5'-most EST	g2309997
Method	BLASTX
NCBI GI	g3212861
BLAST score	715
E value	3.0e-75
Match length	284
% identity	51
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	392495
Contig ID	31888_1.R1084
5'-most EST	uC-osflcyp109e10b1
Method	BLASTX
NCBI GI	g1747294
BLAST score	465
E value	2.0e-74
Match length	176
% identity	85
NCBI Description	(D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.	392496
Contig ID	31891_1.R1084
5'-most EST	uC-osflcyp109f05b1
Seq. No.	392497
Contig ID	31893_1.R1084
5'-most EST	uC-osflcyp109f09b1
Seq. No.	392498
Contig ID	31917_1.R1084
5'-most EST	uC-osflcyp110a05b1
Seq. No.	392499
Contig ID	31922_1.R1084
5'-most EST	uC-osflM202043d09b1
Method	BLASTX
NCBI GI	g6091746
BLAST score	1480

E value	1.0e-179
Match length	383
% identity	79
NCBI Description	(AC010797) putative sulfite oxidase [Arabidopsis thaliana]

Seq. No.	392500
Contig ID	31930_1.R1084
5'-most EST	g1438558

Seq. No.	392501
Contig ID	31932_1.R1084
5'-most EST	uC-osflcyp110b11b1

Seq. No.	392502
Contig ID	31950_1.R1084
5'-most EST	uC-osflcyp110d12b1
Method	BLASTX
NCBI GI	g3080391
BLAST score	183
E value	2.0e-13
Match length	117
% identity	41
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	392503
Contig ID	31954_1.R1084
5'-most EST	uC-osflcyp110e04b1
Method	BLASTX
NCBI GI	g4455174
BLAST score	152
E value	7.0e-22
Match length	84
% identity	65
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	392504
Contig ID	31959_1.R1084
5'-most EST	uC-osflcyp110e11b1
Method	BLASTX
NCBI GI	g3451068
BLAST score	438
E value	3.0e-43
Match length	141
% identity	65
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	392505
Contig ID	31962_1.R1084
5'-most EST	uC-osroM202040d04b1
Method	BLASTX
NCBI GI	g2150002
BLAST score	552
E value	1.0e-75
Match length	177
% identity	81
NCBI Description	(AF000940) ribonuclease [Hordeum vulgare]

Seq. No.	392506
Contig ID	31975_1.R1084
5'-most EST	uC-osflcyp110g09b1
Method	BLASTX
NCBI GI	g3540195
BLAST score	443
E value	9.0e-44
Match length	109
% identity	37
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	392507
Contig ID	31976_1.R1084
5'-most EST	uC-osflcyp110g10b1

Seq. No.	392508
Contig ID	31977_1.R1084
5'-most EST	g2280538
Method	BLASTX
NCBI GI	g1888357
BLAST score	323
E value	4.0e-56
Match length	235
% identity	52
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	392509
Contig ID	31987_1.R1084
5'-most EST	uC-osflcyp110h12b1
Method	BLASTX
NCBI GI	g3063469
BLAST score	289
E value	2.0e-25
Match length	173
% identity	41
NCBI Description	(AC003981) F22O13.31 [Arabidopsis thaliana]

Seq. No.	392510
Contig ID	31990_1.R1084
5'-most EST	uC-osflcyp111b04b1
Method	BLASTX
NCBI GI	g6102610
BLAST score	254
E value	1.0e-21
Match length	128
% identity	39
NCBI Description	(AF187317) CAF protein [Arabidopsis thaliana]

Seq. No.	392511
Contig ID	31993_1.R1084
5'-most EST	g4969140
Method	BLASTX
NCBI GI	g3047104
BLAST score	183
E value	2.0e-13

Match length	82
% identity	50
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	392512
Contig ID	31995_1.R1084
5'-most EST	uC-osflcyp111a12b1
Method	BLASTX
NCBI GI	g1806140
BLAST score	180
E value	9.0e-13
Match length	79
% identity	51
NCBI Description	(X97314) cdc2MsC [Medicago sativa]

Seq. No.	392513
Contig ID	31999_1.R1084
5'-most EST	uC-osflcyp111b05b1
Method	BLASTX
NCBI GI	g2499115
BLAST score	694
E value	1.0e-106
Match length	267
% identity	70
NCBI Description	VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi_1835788 (U86662) VPS41 [Lycopersicon esculentum]

Seq. No.	392514
Contig ID	32004_1.R1084
5'-most EST	uC-osflcyp111c02b1

Seq. No.	392515
Contig ID	32009_1.R1084
5'-most EST	uC-osflcyp111c12b1
Method	BLASTX
NCBI GI	g3806016
BLAST score	1121
E value	1.0e-123
Match length	281
% identity	78
NCBI Description	(AF053104) peroxisomal targeting signal 1 receptor; PTS1 receptor; Pex5p [Nicotiana tabacum]

Seq. No.	392516
Contig ID	32010_1.R1084
5'-most EST	uC-osflcyp111d03b1
Method	BLASTX
NCBI GI	g4406761
BLAST score	432
E value	2.0e-42
Match length	131
% identity	68
NCBI Description	(AC006836) putative ubiquinone biosynthesis protein [Arabidopsis thaliana]

Seq. No.	392517
Contig ID	32012_1.R1084

5'-most EST	uC-osflcyp111d05b1
Seq. No.	392518
Contig ID	32016_1.R1084
5'-most EST	g3763629
Seq. No.	392519
Contig ID	32029_1.R1084
5'-most EST	uC-osflcyp111g01b1
Method	BLASTX
NCBI GI	g4309726
BLAST score	158
E value	1.0e-10
Match length	127
% identity	34
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]
Seq. No.	392520
Contig ID	32034_1.R1084
5'-most EST	g428334
Method	BLASTX
NCBI GI	g1742959
BLAST score	472
E value	2.0e-47
Match length	117
% identity	75
NCBI Description	(Z71450) CLC-d chloride channel protein [Arabidopsis thaliana]
Seq. No.	392521
Contig ID	32041_1.R1084
5'-most EST	uC-osflcyp111h06b1
Method	BLASTX
NCBI GI	g1946368
BLAST score	371
E value	4.0e-35
Match length	194
% identity	48
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]
Seq. No.	392522
Contig ID	32059_1.R1084
5'-most EST	uC-osflcyp112c03b1
Seq. No.	392523
Contig ID	32069_1.R1084
5'-most EST	uC-osroM202032f04a1
Seq. No.	392524
Contig ID	32072_1.R1084
5'-most EST	uC-osflcyp161f09b1
Method	BLASTX
NCBI GI	g5731756
BLAST score	294
E value	7.0e-32
Match length	156
% identity	39

NCBI Description	(AL109819) putative protein [Arabidopsis thaliana]
Seq. No.	392525
Contig ID	32073_1.R1084
5'-most EST	g5003073
Method	BLASTX
NCBI GI	g4337174
BLAST score	282
E value	1.0e-24
Match length	94
% identity	59
NCBI Description	(AC006416) Similar to gi_1573829 HI0816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gb_U32764. [Arabidopsis thaliana]
Seq. No.	392526
Contig ID	32073_2.R1084
5'-most EST	uC-osflcyp112d10b1
Method	BLASTX
NCBI GI	g4337174
BLAST score	698
E value	2.0e-73
Match length	229
% identity	58
NCBI Description	(AC006416) Similar to gi_1573829 HI0816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gb_U32764. [Arabidopsis thaliana]
Seq. No.	392527
Contig ID	32075_1.R1084
5'-most EST	uC-osflcyp112e01b1
Seq. No.	392528
Contig ID	32106_1.R1084
5'-most EST	g3107179
Method	BLASTX
NCBI GI	g6041797
BLAST score	434
E value	1.0e-48
Match length	236
% identity	50
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.	392529
Contig ID	32124_1.R1084
5'-most EST	uC-osflcyp120d02b1
Seq. No.	392530
Contig ID	32125_1.R1084
5'-most EST	uC-osflM202097b12b1
Seq. No.	392531
Contig ID	32126_1.R1084
5'-most EST	uC-osflcyp120d04b1
Method	BLASTX
NCBI GI	g3250676
BLAST score	377

E value 4.0e-46
Match length 254
% identity 44
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 392532
Contig ID 32135_1.R1084
5'-most EST uC-osflcyp120e02b1

Seq. No. 392533
Contig ID 32139_1.R1084
5'-most EST g2427610
Method BLASTX
NCBI GI g4138732
BLAST score 143
E value 1.0e-08
Match length 97
% identity 5
NCBI Description (Y17332) proline-rich protein [Zea mays]

Seq. No. 392534
Contig ID 32142_1.R1084
5'-most EST g572012
Method BLASTX
NCBI GI g3914467
BLAST score 489
E value 4.0e-79
Match length 251
% identity 66
NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum]

Seq. No. 392535
Contig ID 32155_1.R1084
5'-most EST g2801209
Method BLASTX
NCBI GI g1946329
BLAST score 510
E value 1.0e-51
Match length 141
% identity 70
NCBI Description (U69154) prohibitin [Nicotiana tabacum]

Seq. No. 392536
Contig ID 32192_1.R1084
5'-most EST g2280752

Seq. No. 392537
Contig ID 32196_1.R1084
5'-most EST uC-osflcyp121d09b1

Seq. No. 392538
Contig ID 32197_1.R1084
5'-most EST uC-osflcyp121d10b1
Method BLASTN
NCBI GI g2149018

BLAST score 45
E value 7.0e-16
Match length 69
% identity 57
NCBI Description Oryza sativa putative ADP-glucose pyrophosphorylase subunit SH2 and putative NADPH-dependent reductase A1 genes, complete cds

Seq. No. 392539
Contig ID 32212_1.R1084
5'-most EST g2310256
Method BLASTX
NCBI GI g3819164
BLAST score 351
E value 4.0e-33
Match length 131
% identity 54
NCBI Description (AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]

Seq. No. 392540
Contig ID 32224_1.R1084
5'-most EST uC-osflcyp121h01b1
Method BLASTX
NCBI GI g3929333
BLAST score 192
E value 1.0e-14
Match length 63
% identity 60
NCBI Description CYTOCHROME P450 76B1 (7-ETHOXYCOUMARIN O-DEETHYLASE) (ECOD) (PHENYLUREA DEALKYLASE) >gi_2370230_emb_CAA71054_ (Y09920) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus]

Seq. No. 392541
Contig ID 32228_1.R1084
5'-most EST uC-osflcyp121h10b1
Method BLASTX
NCBI GI g3063471
BLAST score 318
E value 4.0e-29
Match length 93
% identity 62
NCBI Description (AC003981) F22O13.33 [Arabidopsis thaliana]

Seq. No. 392542
Contig ID 32234_1.R1084
5'-most EST uC-osflcyp122a09b1
Method BLASTX
NCBI GI g4126473
BLAST score 306
E value 8.0e-28
Match length 131
% identity 46
NCBI Description (AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No. 392543

Contig ID	32240_1.R1084
5'-most EST	uC-osf1M202090b04b1
Method	BLASTX
NCBI GI	g2497953
BLAST score	243
E value	2.0e-38
Match length	117
% identity	72
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No.	392544
Contig ID	32242_1.R1084
5'-most EST	uC-osrocyp013f10b1
Method	BLASTX
NCBI GI	g1076668
BLAST score	388
E value	3.0e-37
Match length	87
% identity	84
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	392545
Contig ID	32247_1.R1084
5'-most EST	uC-osf1cyp122c01b1
Method	BLASTX
NCBI GI	g4530585
BLAST score	315
E value	8.0e-29
Match length	85
% identity	68
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

Seq. No.	392546
Contig ID	32254_1.R1084
5'-most EST	uC-osroM202010h07b1
Method	BLASTX
NCBI GI	g3935181
BLAST score	441
E value	2.0e-43
Match length	98
% identity	80
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	392547
Contig ID	32277_1.R1084
5'-most EST	g702345
Method	BLASTX
NCBI GI	g2827143
BLAST score	550
E value	1.0e-112
Match length	276

% identity	76
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	392548
Contig ID	32278_1.R1084
5'-most EST	uC-osflM202123a06b1
Method	BLASTX
NCBI GI	g4263711
BLAST score	839
E value	7.0e-90
Match length	248
% identity	63
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	392549
Contig ID	32298_1.R1084
5'-most EST	uC-osflcyp123b12b1

Seq. No.	392550
Contig ID	32304_1.R1084
5'-most EST	uC-osflcyp162h12b1
Method	BLASTX
NCBI GI	g2208988
BLAST score	399
E value	2.0e-38
Match length	91
% identity	81
NCBI Description	(Y10117) signal recognition particle subunit 9 [Zea mays]

Seq. No.	392551
Contig ID	32305_1.R1084
5'-most EST	uC-osflcyp123c04b1

Seq. No.	392552
Contig ID	32316_1.R1084
5'-most EST	uC-osroM202022d02b1
Method	BLASTX
NCBI GI	g2943792
BLAST score	557
E value	9.0e-92
Match length	195
% identity	81
NCBI Description	(AB006809) PV72 [Cucurbita sp.]

Seq. No.	392553
Contig ID	32320_1.R1084
5'-most EST	uC-osflcyp123e09b1

Seq. No.	392554
Contig ID	32326_1.R1084
5'-most EST	g427766
Method	BLASTX
NCBI GI	g940288
BLAST score	227
E value	2.0e-19

Match length	103
% identity	30
NCBI Description	(L43510) protein localized in the nucleoli of pea nuclei; ORF; putative [Pisum sativum]

Seq. No.	392555
Contig ID	32327_2.R1084
5'-most EST	g1631784
Method	BLASTX
NCBI GI	g6016437
BLAST score	217
E value	2.0e-22
Match length	168
% identity	39
NCBI Description	KINESIN HEAVY CHAIN >gi_1947184 (L47106) kinesin [Neurospora crassa]

Seq. No.	392556
Contig ID	32330_1.R1084
5'-most EST	g701963
Method	BLASTX
NCBI GI	g4581109
BLAST score	582
E value	6.0e-60
Match length	144
% identity	74
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	392557
Contig ID	32331_1.R1084
5'-most EST	g426828
Method	BLASTX
NCBI GI	g5730132
BLAST score	374
E value	1.0e-35
Match length	77
% identity	90
NCBI Description	(AL109796) snRNP Sm protein F-like [Arabidopsis thaliana]

Seq. No.	392558
Contig ID	32337_1.R1084
5'-most EST	uC-osflcyp153c02b1

Seq. No.	392559
Contig ID	32345_1.R1084
5'-most EST	g2800475

Seq. No.	392560
Contig ID	32357_1.R1084
5'-most EST	uC-osflcyp124d01b1
Method	BLASTX
NCBI GI	g5441893
BLAST score	502
E value	8.0e-51
Match length	139
% identity	55
NCBI Description	(AP000367) ESTs C99174(E10437),D22295(C10709) correspond to

	a region of the predicted gene.; Similar to Arabidopsis thaliana BAC genomic sequence. (AC005314) [Oryza sativa]
Seq. No.	392561
Contig ID	32362_1.R1084
5'-most EST	g4879769
Method	BLASTX
NCBI GI	g3367732
BLAST score	379
E value	2.0e-36
Match length	74
% identity	100
NCBI Description	(Y17835) p7 protein [Phleum pratense]
Seq. No.	392562
Contig ID	32367_1.R1084
5'-most EST	uC-osrocyp027b09b1
Method	BLASTX
NCBI GI	g3128186
BLAST score	251
E value	3.0e-21
Match length	74
% identity	68
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.	392563
Contig ID	32373_1.R1084
5'-most EST	g4715506
Seq. No.	392564
Contig ID	32381_1.R1084
5'-most EST	uC-osflcyp124g10b1
Method	BLASTX
NCBI GI	g2894378
BLAST score	392
E value	6.0e-38
Match length	104
% identity	79
NCBI Description	(Y14573) putative ribophorin I homologue [Hordeum vulgare]
Seq. No.	392565
Contig ID	32397_1.R1084
5'-most EST	uC-osroM202016d08b1
Method	BLASTX
NCBI GI	g4966344
BLAST score	463
E value	5.0e-46
Match length	167
% identity	56
NCBI Description	(AC006341) ESTs gb_F15498, gb_H37515, gb_T41906, gb_T22448, gb_W43356 and gb_T20739 come from this gene. [Arabidopsis thaliana]
Seq. No.	392566
Contig ID	32405_1.R1084
5'-most EST	uC-osflcyp125c02b1

Seq. No.	392567
Contig ID	32408_1.R1084
5'-most EST	uC-osflcyp125c05b1

Seq. No.	392568
Contig ID	32420_1.R1084
5'-most EST	uC-osflcyp125d07b1
Method	BLASTX
NCBI GI	g4835778
BLAST score	237
E value	1.0e-19
Match length	64
% identity	66
NCBI Description	(AC007296) F25C20.6 [Arabidopsis thaliana]

Seq. No.	392569
Contig ID	32423_1.R1084
5'-most EST	uC-osflcyp154d11b1
Method	BLASTX
NCBI GI	g1706956
BLAST score	471
E value	9.0e-66
Match length	172
% identity	75
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	392570
Contig ID	32425_1.R1084
5'-most EST	uC-osflM202089d11b1
Method	BLASTX
NCBI GI	g4220474
BLAST score	381
E value	2.0e-36
Match length	128
% identity	62
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	392571
Contig ID	32437_1.R1084
5'-most EST	uC-osflcyp125f09b1

Seq. No.	392572
Contig ID	32447_1.R1084
5'-most EST	g4879862

Seq. No.	392573
Contig ID	32447_2.R1084
5'-most EST	uC-osflcyp125g10b1

Seq. No.	392574
Contig ID	32457_1.R1084
5'-most EST	g2275998

Seq. No.	392575
Contig ID	32464_1.R1084
5'-most EST	uC-osflcyp126a12b1

Method	BLASTX
NCBI GI	g1841464
BLAST score	425
E value	9.0e-42
Match length	106
% identity	42
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum] >gi_5932420_gb_AAD56951.1_AF184886_1 (AF184886) LIM domain protein WLIM2 [Nicotiana tabacum]

Seq. No.	392576
Contig ID	32466_1.R1084
5'-most EST	uC-osflcyp126b02b1
Method	BLASTX
NCBI GI	g5731756
BLAST score	373
E value	1.0e-35
Match length	118
% identity	58
NCBI Description	(AL109819) putative protein [Arabidopsis thaliana]

Seq. No.	392577
Contig ID	32468_1.R1084
5'-most EST	uC-osflcyp126b04b1

Seq. No.	392578
Contig ID	32474_1.R1084
5'-most EST	uC-osflcyp126c03b1
Method	BLASTX
NCBI GI	g2224663
BLAST score	446
E value	5.0e-44
Match length	236
% identity	42
NCBI Description	(AB002359) KIAA0361 [Homo sapiens]

Seq. No.	392579
Contig ID	32484_1.R1084
5'-most EST	uC-osflcyp126d07b1

Seq. No.	392580
Contig ID	32487_1.R1084
5'-most EST	uC-osflcyp126d10b1
Method	BLASTX
NCBI GI	g6006894
BLAST score	265
E value	6.0e-23
Match length	168
% identity	43
NCBI Description	(AC008153) unknown protein [Arabidopsis thaliana]

Seq. No.	392581
Contig ID	32496_1.R1084
5'-most EST	uC-osrocyp010a06b1
Method	BLASTX
NCBI GI	g4469023
BLAST score	779

E value 7.0e-87
Match length 186
% identity 82
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 392582
Contig ID 32497_1.R1084
5'-most EST g426604
Method BLASTX
NCBI GI g1946366
BLAST score 172
E value 7.0e-12
Match length 91
% identity 49
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 392583
Contig ID 32509_1.R1084
5'-most EST uC-osflcyp126g11b1
Method BLASTX
NCBI GI g1353516
BLAST score 338
E value 1.0e-31
Match length 120
% identity 57
NCBI Description (U38651) sugar transporter [Medicago truncatula]

Seq. No. 392584
Contig ID 32522_1.R1084
5'-most EST g3107625

Seq. No. 392585
Contig ID 32526_1.R1084
5'-most EST uC-osflcyp139a09b1

Seq. No. 392586
Contig ID 32530_1.R1084
5'-most EST uC-osflcyp139b02b1

Seq. No. 392587
Contig ID 32534_1.R1084
5'-most EST uC-osflcyp139b09b1
Method BLASTX
NCBI GI g1794137
BLAST score 173
E value 3.0e-12
Match length 71
% identity 48
NCBI Description (AB000402) DMO25 [Drosophila melanogaster]

Seq. No. 392588
Contig ID 32537_1.R1084
5'-most EST uC-osflcyp139b12b1
Method BLASTX
NCBI GI g2341042
BLAST score 171
E value 1.0e-11

Match length	247
% identity	28
NCBI Description	(AC000104) F19P19.26 [Arabidopsis thaliana]

Seq. No.	392589
Contig ID	32543_1.R1084
5'-most EST	g5003990

Seq. No.	392590
Contig ID	32546_1.R1084
5'-most EST	uC-osflcyp139d03b1
Method	BLASTX
NCBI GI	g2154609
BLAST score	316
E value	5.0e-29
Match length	79
% identity	73
NCBI Description	(D63509) endoxyloglucan transferase related protein [Arabidopsis thaliana] >gi_4522010_gb_AAD21783.1_ (AC007069) endoxyloglucan transferase [Arabidopsis thaliana]

Seq. No.	392591
Contig ID	32554_1.R1084
5'-most EST	uC-osrocyp012b08b1
Method	BLASTX
NCBI GI	g2894607
BLAST score	477
E value	2.0e-47
Match length	135
% identity	63
NCBI Description	(AL021889) NAM (no apical meristem)-like protein [Arabidopsis thaliana]

Seq. No.	392592
Contig ID	32559_1.R1084
5'-most EST	uC-osrocyp031h12b1

Seq. No.	392593
Contig ID	32567_1.R1084
5'-most EST	g4881011
Method	BLASTX
NCBI GI	g5640155
BLAST score	323
E value	3.0e-44
Match length	239
% identity	54
NCBI Description	(AJ242530) gibberellin response modulator [Zea mays]

Seq. No.	392594
Contig ID	32589_1.R1084
5'-most EST	uC-osflcyp140a04b1

Seq. No.	392595
Contig ID	32592_1.R1084
5'-most EST	uC-osflcyp140a09b1

Seq. No.	392596
Contig ID	32604_1.R1084
5'-most EST	uC-osflcyp140c03b1
Method	BLASTX
NCBI GI	g1708236
BLAST score	522
E value	8.0e-61
Match length	192
% identity	63
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	392597
Contig ID	32606_1.R1084
5'-most EST	g569144

Seq. No.	392598
Contig ID	32619_1.R1084
5'-most EST	uC-osflcyp006h04b1
Method	BLASTX
NCBI GI	g5668762
BLAST score	304
E value	3.0e-27
Match length	289
% identity	34
NCBI Description	(AC005916) EST gb_N65787 comes from this gene. [Arabidopsis thaliana]

Seq. No.	392599
Contig ID	32624_1.R1084
5'-most EST	uC-osflcyp140f03b1
Method	BLASTX
NCBI GI	g2980788
BLAST score	203
E value	2.0e-15
Match length	100
% identity	45
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	392600
Contig ID	32625_1.R1084
5'-most EST	g2313015
Method	BLASTX
NCBI GI	g1213073
BLAST score	238
E value	6.0e-20
Match length	109
% identity	49
NCBI Description	(X75616) heat shock protein 17.8 [Oryza sativa]

Seq. No.	392601

Contig ID 32630_1.R1084
5'-most EST g426894

Seq. No. 392602
Contig ID 32650_1.R1084
5'-most EST uC-osflcyp141a09b1

Seq. No. 392603
Contig ID 32669_1.R1084
5'-most EST g4879477
Method BLASTX
NCBI GI g2723471
BLAST score 417
E value 1.0e-40
Match length 143
% identity 59
NCBI Description (D87819) sucrose transporter [Oryza sativa]

Seq. No. 392604
Contig ID 32671_1.R1084
5'-most EST uC-osflcyp141e01b1

Seq. No. 392605
Contig ID 32675_1.R1084
5'-most EST uC-osflcyp141e06b1

Seq. No. 392606
Contig ID 32682_1.R1084
5'-most EST g2310031

Seq. No. 392607
Contig ID 32689_1.R1084
5'-most EST uC-osflcyp141g05b1
Method BLASTX
NCBI GI g99809
BLAST score 1010
E value 1.0e-110
Match length 289
% identity 64
NCBI Description gene Bp10 protein - rape >gi_17795_emb_CAA47177_ (X66608) Bplo [Brassica napus]

Seq. No. 392608
Contig ID 32692_1.R1084
5'-most EST uC-osflcyp141g08b1

Seq. No. 392609
Contig ID 32697_1.R1084
5'-most EST g2311821

Seq. No. 392610
Contig ID 32697_2.R1084
5'-most EST g571793

Seq. No. 392611
Contig ID 32699_1.R1084
5'-most EST uC-osflcyp030a06b1

Seq. No.	392612
Contig ID	32701_1.R1084
5'-most EST	uC-osflcyp142a08b1
Method	BLASTX
NCBI GI	g4678342
BLAST score	304
E value	2.0e-27
Match length	139
% identity	41
NCBI Description	(AL049659) lipase-like protein [Arabidopsis thaliana]

Seq. No.	392613
Contig ID	32711_1.R1084
5'-most EST	uC-osflcyp142c05b1
Method	BLASTX
NCBI GI	g3258575
BLAST score	337
E value	4.0e-31
Match length	112
% identity	64
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	392614
Contig ID	32715_1.R1084
5'-most EST	g3762607

Seq. No.	392615
Contig ID	32720_1.R1084
5'-most EST	uC-osflcyp158d08b1

Seq. No.	392616
Contig ID	32725_1.R1084
5'-most EST	g5607371
Method	BLASTX
NCBI GI	g4982479
BLAST score	434
E value	5.0e-46
Match length	125
% identity	75
NCBI Description	(AF069441) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	392617
Contig ID	32731_1.R1084
5'-most EST	uC-osflcyp142f07b1
Method	BLASTX
NCBI GI	g5921933
BLAST score	356
E value	4.0e-33
Match length	168
% identity	36
NCBI Description	CYTOCHROME P450 85 (DWARF PROTEIN) >gi_1421741 (U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No.	392618
Contig ID	32739_1.R1084

5'-most EST	g702168
Method	BLASTX
NCBI GI	g3046731
BLAST score	306
E value	3.0e-52
Match length	133
% identity	83
NCBI Description	(AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No.	392619
Contig ID	32748_1.R1084
5'-most EST	uC-osrocyp013c11b1
Method	BLASTN
NCBI GI	g1212993
BLAST score	47
E value	4.0e-17
Match length	151
% identity	88
NCBI Description	H.vulgare mRNA for coproporphyrinogen oxidase

Seq. No.	392620
Contig ID	32749_1.R1084
5'-most EST	g2428302

Seq. No.	392621
Contig ID	32761_1.R1084
5'-most EST	uC-osflcyp143b09b1
Method	BLASTX
NCBI GI	g1651934
BLAST score	151
E value	6.0e-18
Match length	171
% identity	34
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	392622
Contig ID	32769_1.R1084
5'-most EST	g2427291

Seq. No.	392623
Contig ID	32774_1.R1084
5'-most EST	uC-osflcyp143d06b1

Seq. No.	392624
Contig ID	32780_1.R1084
5'-most EST	uC-osflcyp143e01b1
Method	BLASTX
NCBI GI	g2459429
BLAST score	278
E value	2.0e-24
Match length	73
% identity	67
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	392625
Contig ID	32788_1.R1084
5'-most EST	uC-osflcyp143f06b1

Method	BLASTX
NCBI GI	g3043426
BLAST score	417
E value	2.0e-40
Match length	125
% identity	62
NCBI Description	(AJ005345) hypothetical protein [Cicer arietinum]

Seq. No.	392626
Contig ID	32794_1.R1084
5'-most EST	uC-osflcyp143g03b1

Seq. No.	392627
Contig ID	32798_1.R1084
5'-most EST	uC-osflm202110e11b1

Seq. No.	392628
Contig ID	32808_1.R1084
5'-most EST	uC-osrocyp005d04b1

Seq. No.	392629
Contig ID	32823_1.R1084
5'-most EST	uC-osflcyp144c02b1

Seq. No.	392630
Contig ID	32824_1.R1084
5'-most EST	g2428347

Seq. No.	392631
Contig ID	32824_2.R1084
5'-most EST	uC-osflcyp156b05b1

Seq. No.	392632
Contig ID	32828_1.R1084
5'-most EST	uC-osflm202113h09b1

Seq. No.	392633
Contig ID	32844_1.R1084
5'-most EST	uC-osflcyp144f02b1
Method	BLASTX
NCBI GI	g2493494
BLAST score	491
E value	2.0e-64
Match length	159
% identity	81
NCBI Description	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase II-2 [Hordeum vulgare]

Seq. No.	392634
Contig ID	32856_1.R1084
5'-most EST	uC-osflcyp144g05b1

Seq. No.	392635
Contig ID	32858_1.R1084

5'-most EST	g428605
Method	BLASTX
NCBI GI	g4314390
BLAST score	461
E value	2.0e-45
Match length	177
% identity	53
NCBI Description	(AC006232) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	392636
Contig ID	32868_1.R1084
5'-most EST	uC-osflcyp144h11b1

Seq. No.	392637
Contig ID	32880_1.R1084
5'-most EST	g4969283
Method	BLASTX
NCBI GI	g4337175
BLAST score	267
E value	3.0e-23
Match length	84
% identity	58
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	392638
Contig ID	32881_1.R1084
5'-most EST	uC-osflcyp151c10b1
Method	BLASTX
NCBI GI	g1351222
BLAST score	640
E value	2.0e-93
Match length	215
% identity	83
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945087 (U31097) transcription factor TFIIB [Glycine max]

Seq. No.	392639
Contig ID	32888_1.R1084
5'-most EST	g4968772
Method	BLASTX
NCBI GI	g6094242
BLAST score	1315
E value	1.0e-145
Match length	297
% identity	78
NCBI Description	PUTATIVE SELENIUM-BINDING PROTEIN >gi_2244759_emb_CAB10182.1_ (Z97335) selenium-binding protein like [Arabidopsis thaliana]

Seq. No.	392640
Contig ID	32901_1.R1084
5'-most EST	uC-osflcyp151g01b1
Method	BLASTX

NCBI GI	g4514716
BLAST score	243
E value	3.0e-20
Match length	98
% identity	46
NCBI Description	(AB017533) EPc [Nicotiana tabacum]

Seq. No.	392641
Contig ID	32917_1.R1084
5'-most EST	uC-osflcyp152a06b1

Seq. No.	392642
Contig ID	32924_1.R1084
5'-most EST	uC-osflcyp152b01b1
Method	BLASTX
NCBI GI	g2462760
BLAST score	161
E value	1.0e-10
Match length	87
% identity	38
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	392643
Contig ID	32927_1.R1084
5'-most EST	uC-osflM202066e09b1
Method	BLASTX
NCBI GI	g4467157
BLAST score	376
E value	1.0e-35
Match length	158
% identity	50
NCBI Description	(AL035540) disease resistance response like protein [Arabidopsis thaliana]

Seq. No.	392644
Contig ID	32932_1.R1084
5'-most EST	g3759019

Seq. No.	392645
Contig ID	32935_1.R1084
5'-most EST	uC-osflcyp171b02b1
Method	BLASTX
NCBI GI	g4539383
BLAST score	282
E value	9.0e-25
Match length	182
% identity	38
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	392646
Contig ID	32946_1.R1084
5'-most EST	g2443067
Method	BLASTX
NCBI GI	g1354849
BLAST score	398
E value	2.0e-38

Match length 158
% identity 49
NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 392647
Contig ID 32948_1.R1084
5'-most EST uC-osrocyp010a10b1
Method BLASTX
NCBI GI g2262117
BLAST score 282
E value 1.0e-24
Match length 231
% identity 44
NCBI Description (AC002343) auxin inducible protein isolog [Arabidopsis thaliana]

Seq. No. 392648
Contig ID 32953_1.R1084
5'-most EST uC-osflcyp152e03b1

Seq. No. 392649
Contig ID 32958_1.R1084
5'-most EST uC-osflcyp152e12b1

Seq. No. 392650
Contig ID 32961_1.R1084
5'-most EST g3761830

Seq. No. 392651
Contig ID 32973_1.R1084
5'-most EST uC-osflcyp152g09b1
Method BLASTX
NCBI GI g4115916
BLAST score 155
E value 4.0e-10
Match length 50
% identity 54
NCBI Description (AF118222) F3H7.9 gene product [Arabidopsis thaliana] >gi_4539441_emb_CAB40029.1_ (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 392652
Contig ID 32975_1.R1084
5'-most EST uC-osflcyp152h03b1
Method BLASTX
NCBI GI g5354158
BLAST score 367
E value 7.0e-35
Match length 109
% identity 60
NCBI Description (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_6041825_gb_AAF02140.1_AC009918_12 (AC009918) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No. 392653

Contig ID	32981_1.R1084
5'-most EST	uC-osflcyp153a02b1
Method	BLASTX
NCBI GI	g559713
BLAST score	606
E value	6.0e-63
Match length	181
% identity	68
NCBI Description	(D38552) The ha1539 protein is related to cyclophilin. [Homo sapiens]

Seq. No.	392654
Contig ID	32984_1.R1084
5'-most EST	uC-osflcyp153a09b1

Seq. No.	392655
Contig ID	32997_1.R1084
5'-most EST	uC-osflcyp153c09b1
Method	BLASTX
NCBI GI	g2499819
BLAST score	477
E value	8.0e-49
Match length	157
% identity	64
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No.	392656
Contig ID	32998_1.R1084
5'-most EST	g428214

Seq. No.	392657
Contig ID	33013_1.R1084
5'-most EST	uC-osflcyp039g11b1

Seq. No.	392658
Contig ID	33014_1.R1084
5'-most EST	uC-osflcyp153f05b1

Seq. No.	392659
Contig ID	33017_1.R1084
5'-most EST	uC-osf1M202037f06b1
Method	BLASTX
NCBI GI	g3643603
BLAST score	564
E value	7.0e-58
Match length	214
% identity	53
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	392660
Contig ID	33020_1.R1084
5'-most EST	uC-osflcyp156b11b1
Method	BLASTX

NCBI GI g6091756
BLAST score 431
E value 2.0e-42
Match length 131
% identity 57
NCBI Description (AC009327) putative peroxidase [Arabidopsis thaliana]

Seq. No. 392661
Contig ID 33027_1.R1084
5'-most EST uC-osflM202062a06b1
Method BLASTX
NCBI GI g1731363
BLAST score 195
E value 1.0e-14
Match length 93
% identity 42
NCBI Description PUTATIVE SERINE CARBOXYPEPTIDASE F32A5.3 PRECURSOR >gi_669029 (U20864) similar to protective protein/cathepsin A and other serine carboxypeptidases [Caenorhabditis elegans]

Seq. No. 392662
Contig ID 33037_1.R1084
5'-most EST uC-osflM202046c12b1

Seq. No. 392663
Contig ID 33042_1.R1084
5'-most EST uC-osflcyp154a10b1
Method BLASTX
NCBI GI g6006892
BLAST score 561
E value 2.0e-57
Match length 126
% identity 83
NCBI Description (AC008153) unknown protein [Arabidopsis thaliana]

Seq. No. 392664
Contig ID 33051_1.R1084
5'-most EST uC-osflcyp158h06b1

Seq. No. 392665
Contig ID 33054_1.R1084
5'-most EST g2312696
Method BLASTX
NCBI GI g2760839
BLAST score 369
E value 4.0e-35
Match length 132
% identity 54
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 392666
Contig ID 33066_1.R1084
5'-most EST uC-osflcyp154e02b1

Seq. No. 392667
Contig ID 33069_1.R1084

5'-most EST	uC-osroM202018g05b1
Seq. No.	392668
Contig ID	33079_1.R1084
5'-most EST	uC-osrocyp011c10b1
Method	BLASTX
NCBI GI	g1174162
BLAST score	791
E value	2.0e-84
Match length	160
% identity	86
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
Seq. No.	392669
Contig ID	33083_1.R1084
5'-most EST	g426357
Method	BLASTX
NCBI GI	g3935168
BLAST score	427
E value	6.0e-42
Match length	185
% identity	53
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]
Seq. No.	392670
Contig ID	33094_1.R1084
5'-most EST	g2317312
Seq. No.	392671
Contig ID	33097_1.R1084
5'-most EST	uC-osflcyp155a02b1
Method	BLASTX
NCBI GI	g4204300
BLAST score	289
E value	9.0e-26
Match length	116
% identity	50
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]
Seq. No.	392672
Contig ID	33098_1.R1084
5'-most EST	uC-osflcyp155a03b1
Method	BLASTX
NCBI GI	g6006867
BLAST score	666
E value	7.0e-70
Match length	186
% identity	69
NCBI Description	(AC009540) unknown protein [Arabidopsis thaliana]
Seq. No.	392673
Contig ID	33100_1.R1084
5'-most EST	g428938
Method	BLASTX
NCBI GI	g129697

BLAST score	721
E value	1.0e-137
Match length	263
% identity	98
NCBI Description	PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN) >gi_100698_pir__S14415 proliferating cell nuclear antigen - rice >gi_20284_emb_CAA37979_ (X54046) proliferating cell nuclear antigen [Oryza sativa]

Seq. No.	392674
Contig ID	33105_1.R1084
5'-most EST	uC-osflcyp155b06b1
Method	BLASTX
NCBI GI	g4455159
BLAST score	960
E value	1.0e-104
Match length	220
% identity	78
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	392675
Contig ID	33112_1.R1084
5'-most EST	uC-osflcyp155c05b1
Method	BLASTX
NCBI GI	g1363051
BLAST score	270
E value	2.0e-23
Match length	114
% identity	48
NCBI Description	P58 protein - bovine >gi_468012 (U04631) PKR inhibitor P58 [Bos taurus]

Seq. No.	392676
Contig ID	33135_1.R1084
5'-most EST	uC-osflcyp161c09b1
Method	BLASTX
NCBI GI	g4539324
BLAST score	168
E value	5.0e-15
Match length	209
% identity	33
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	392677
Contig ID	33155_1.R1084
5'-most EST	g2312355
Method	BLASTX
NCBI GI	g4886522
BLAST score	200
E value	2.0e-15
Match length	84
% identity	52
NCBI Description	(AL050291) hypothetical protein [Homo sapiens]

Seq. No.	392678
Contig ID	33162_1.R1084
5'-most EST	g3761522

Method	BLASTX
NCBI GI	g3176717
BLAST score	156
E value	3.0e-10
Match length	61
% identity	49
NCBI Description	(AC002392) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	392679
Contig ID	33164_1.R1084
5'-most EST	uC-osflcyp156b10b1
Method	BLASTX
NCBI GI	g4262157
BLAST score	311
E value	2.0e-28
Match length	122
% identity	34
NCBI Description	(AC005275) putative calmodulin [Arabidopsis thaliana]

Seq. No.	392680
Contig ID	33171_1.R1084
5'-most EST	g2312643

Seq. No.	392681
Contig ID	33173_1.R1084
5'-most EST	g2427471
Method	BLASTX
NCBI GI	g5852098
BLAST score	459
E value	2.0e-69
Match length	226
% identity	79
NCBI Description	(AL117264) zwh21.1 [Oryza sativa]

Seq. No.	392682
Contig ID	33186_1.R1084
5'-most EST	g4715062

Seq. No.	392683
Contig ID	33187_1.R1084
5'-most EST	g3768173

Seq. No.	392684
Contig ID	33188_1.R1084
5'-most EST	g3768245
Method	BLASTX
NCBI GI	g4887020
BLAST score	122
E value	6.0e-11
Match length	44
% identity	86
NCBI Description	(AF123508) Nt-iaa28 deduced protein [Nicotiana tabacum]

Seq. No.	392685
Contig ID	33189_1.R1084
5'-most EST	uC-osflcyp156e06b1
Method	BLASTX

NCBI GI	g4103618
BLAST score	240
E value	2.0e-20
Match length	53
% identity	81
NCBI Description	(AF026382) HyPRP [Fragaria x ananassa]

Seq. No.	392686
Contig ID	33201_1.R1084
5'-most EST	g4878697
Method	BLASTX
NCBI GI	g3021357
BLAST score	694
E value	3.0e-73
Match length	158
% identity	81
NCBI Description	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	392687
Contig ID	33214_1.R1084
5'-most EST	g3760883
Method	BLASTX
NCBI GI	g4455172
BLAST score	480
E value	1.0e-50
Match length	164
% identity	62
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	392688
Contig ID	33217_1.R1084
5'-most EST	g4969173
Method	BLASTX
NCBI GI	g1488647
BLAST score	602
E value	2.0e-62
Match length	170
% identity	69
NCBI Description	(X99937) RNA helicase [Spinacia oleracea]

Seq. No.	392689
Contig ID	33240_1.R1084
5'-most EST	g2428155
Method	BLASTX
NCBI GI	g5579092
BLAST score	472
E value	4.0e-71
Match length	292
% identity	49
NCBI Description	(AF100954) gibberellin 2-oxidase-like protein [Pisum sativum]

Seq. No.	392690
Contig ID	33250_2.R1084
5'-most EST	uC-osflcyp157e01b1
Method	BLASTX

NCBI GI	g3915866
BLAST score	311
E value	3.0e-49
Match length	127
% identity	72
NCBI Description	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

Seq. No.	392691
Contig ID	33262_1.R1084
5'-most EST	uC-osflcyp157f10b1

Seq. No.	392692
Contig ID	33266_1.R1084
5'-most EST	g701237

Seq. No.	392693
Contig ID	33267_1.R1084
5'-most EST	uC-osflcyp157g06b1
Method	BLASTN
NCBI GI	g1504051
BLAST score	40
E value	7.0e-13
Match length	75
% identity	88
NCBI Description	Zea mays mRNA for Calcium-dependent protein kinase, complete cds

Seq. No.	392694
Contig ID	33274_1.R1084
5'-most EST	uC-osflcyp157h09b1

Seq. No.	392695
Contig ID	33283_1.R1084
5'-most EST	uC-osflcyp142c12b1
Method	BLASTX
NCBI GI	g2370253
BLAST score	608
E value	6.0e-63
Match length	223
% identity	55
NCBI Description	(Y13273) putative protein kinase [Lycopersicon esculentum] >gi_5669642_gb_AAD46406.1_AF096250_1 (AF096250) ethylene-responsive protein kinase TCTR1 [Lycopersicon esculentum]

Seq. No.	392696
Contig ID	33287_1.R1084
5'-most EST	uC-osroM202020d05b1

Seq. No.	392697
Contig ID	33296_1.R1084
5'-most EST	g572235
Method	BLASTX
NCBI GI	g4417283
BLAST score	236

E value	1.0e-19
Match length	114
% identity	38
NCBI Description	(AC007019) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	392698
Contig ID	33309_1.R1084
5'-most EST	g5004752
Method	BLASTX
NCBI GI	g2655008
BLAST score	185
E value	1.0e-13
Match length	80
% identity	47
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No.	392699
Contig ID	33317_1.R1084
5'-most EST	uC-osflcyp158f04b1

Seq. No.	392700
Contig ID	33332_1.R1084
5'-most EST	g4716003
Method	BLASTX
NCBI GI	g2749982
BLAST score	247
E value	2.0e-49
Match length	222
% identity	49
NCBI Description	(AF036705) Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. elegans cDNA yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded for by C. elegans cDNA yk303f4.5; coded for by C. elegans cDNA yk257d4.5;

Seq. No.	392701
Contig ID	33336_1.R1084
5'-most EST	uC-osflcyp158h02b1
Method	BLASTX
NCBI GI	g5080776
BLAST score	559
E value	3.0e-57
Match length	135
% identity	76
NCBI Description	(AC007576) Similar to protein kinases [Arabidopsis thaliana]

Seq. No.	392702
Contig ID	33342_1.R1084
5'-most EST	uC-osflcyp158h12b1

Seq. No.	392703
Contig ID	33343_1.R1084
5'-most EST	uC-osflm202110h04b1
Method	BLASTX
NCBI GI	g5803266

BLAST score	581
E value	1.0e-59
Match length	187
% identity	85
NCBI Description	(AP000399) ESTs AU078063(S15496),C97608(C60475), C28255(C60475) correspond to a region of the predicted gene; similar to plastid transketolase 2 (Y15782) [Oryza sativa]

Seq. No.	392704
Contig ID	33347_1.R1084
5'-most EST	uC-osflcyp159a10b1
Method	BLASTX
NCBI GI	g4512659
BLAST score	170
E value	9.0e-12
Match length	144
% identity	33
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	392705
Contig ID	33357_1.R1084
5'-most EST	uC-osflcyp159c04b1

Seq. No.	392706
Contig ID	33363_1.R1084
5'-most EST	g5002787

Seq. No.	392707
Contig ID	33365_1.R1084
5'-most EST	uC-osflcyp159d03b1
Method	BLASTX
NCBI GI	g4588003
BLAST score	468
E value	1.0e-46
Match length	160
% identity	63
NCBI Description	(AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana]

Seq. No.	392708
Contig ID	33368_1.R1084
5'-most EST	g2427232
Method	BLASTX
NCBI GI	g4580389
BLAST score	209
E value	8.0e-29
Match length	120
% identity	58
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	392709
Contig ID	33381_1.R1084
5'-most EST	g2800316

Seq. No. 392710

Contig ID	33385_1.R1084
5'-most EST	g428896
Method	BLASTX
NCBI GI	g3080437
BLAST score	145
E value	1.0e-08
Match length	223
% identity	29
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	392711
Contig ID	33390_1.R1084
5'-most EST	uC-osflcyp159g10b1

Seq. No.	392712
Contig ID	33390_2.R1084
5'-most EST	uC-osflM202088g12a1

Seq. No.	392713
Contig ID	33402_1.R1084
5'-most EST	g4715814
Method	BLASTX
NCBI GI	g3337356
BLAST score	562
E value	9.0e-68
Match length	153
% identity	89
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	392714
Contig ID	33402_2.R1084
5'-most EST	uC-osflcyp159h11b1
Method	BLASTX
NCBI GI	g3337356
BLAST score	598
E value	5.0e-62
Match length	122
% identity	96
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	392715
Contig ID	33403_1.R1084
5'-most EST	uC-osflm202107b08b1

Seq. No.	392716
Contig ID	33422_1.R1084
5'-most EST	uC-osflcyp161d11b1

Seq. No.	392717
Contig ID	33424_1.R1084
5'-most EST	uC-osroM202038d07b1

Seq. No.	392718
Contig ID	33435_1.R1084
5'-most EST	uC-osflcyp161g02b1

Seq. No.	392719
Contig ID	33440_1.R1084
5'-most EST	uC-osflcyp162a02b1

Seq. No.	392720
Contig ID	33464_1.R1084
5'-most EST	uC-osflcyp162d07b1

Seq. No.	392721
Contig ID	33471_1.R1084
5'-most EST	uC-osflcyp162e03b1
Method	BLASTX
NCBI GI	g3386614
BLAST score	251
E value	3.0e-21
Match length	55
% identity	38
NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No.	392722
Contig ID	33499_1.R1084
5'-most EST	uC-osflcyp162h08b1
Method	BLASTX
NCBI GI	g5302811
BLAST score	482
E value	4.0e-48
Match length	214
% identity	51
NCBI Description	(Z97342) putative serine protease-like protein [Arabidopsis thaliana]

Seq. No.	392723
Contig ID	33500_1.R1084
5'-most EST	uC-osflcyp156h07b1

Seq. No.	392724
Contig ID	33509_1.R1084
5'-most EST	g2310643
Method	BLASTX
NCBI GI	g1173073
BLAST score	278
E value	2.0e-24
Match length	109
% identity	56
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_1076787_pir__S54179 acidic ribosomal protein 60S - maize >gi_2130117_pir__S65781 acidic ribosomal protein P2 - maize >gi_790508_emb_CAA60251_ (X86553) 60S acidic ribosomal protein [Zea mays]

Seq. No.	392725
Contig ID	33510_1.R1084
5'-most EST	uC-osflcyp168b03b1
Method	BLASTX
NCBI GI	g3790188

BLAST score	382
E value	3.0e-39
Match length	100
% identity	84
NCBI Description	(Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana tabacum]

Seq. No.	392726
Contig ID	33511_1.R1084
5'-most EST	g4714790
Method	BLASTX
NCBI GI	g3549652
BLAST score	249
E value	2.0e-36
Match length	220
% identity	48
NCBI Description	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]

Seq. No.	392727
Contig ID	33524_1.R1084
5'-most EST	g2428377

Seq. No.	392728
Contig ID	33532_1.R1084
5'-most EST	uC-osf1M202089f05b1
Method	BLASTX
NCBI GI	g3201615
BLAST score	401
E value	6.0e-39
Match length	92
% identity	79
NCBI Description	(AC004669) unknown protein [Arabidopsis thaliana]

Seq. No.	392729
Contig ID	33542_1.R1084
5'-most EST	uC-osf1m202104b11b1
Method	BLASTX
NCBI GI	g510876
BLAST score	744
E value	1.0e-106
Match length	227
% identity	84
NCBI Description	(X80051) NADP dependent malic enzyme [Phaseolus vulgaris]

Seq. No.	392730
Contig ID	33564_1.R1084
5'-most EST	g428824
Method	BLASTX
NCBI GI	g5262191
BLAST score	824
E value	2.0e-88
Match length	207
% identity	73
NCBI Description	(AL080252) putative protein [Arabidopsis thaliana]

Seq. No.	392731

Contig ID 33579_1.R1084
5'-most EST uC-osflcyp169d09b1

Seq. No. 392732
Contig ID 33585_1.R1084
5'-most EST uC-osflcyp169e07b1

Seq. No. 392733
Contig ID 33605_1.R1084
5'-most EST uC-osflcyp169h05b1

Seq. No. 392734
Contig ID 33608_1.R1084
5'-most EST g428850
Method BLASTX
NCBI GI g3128203
BLAST score 501
E value 1.0e-50
Match length 127
% identity 72
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 392735
Contig ID 33609_1.R1084
5'-most EST uC-osflcyp154g02a1

Seq. No. 392736
Contig ID 33613_1.R1084
5'-most EST uC-osflcyp170a06b1

Seq. No. 392737
Contig ID 33625_1.R1084
5'-most EST uC-osflcyp005h09b1

Seq. No. 392738
Contig ID 33640_1.R1084
5'-most EST g5003673

Seq. No. 392739
Contig ID 33643_1.R1084
5'-most EST uC-osflcyp170g07b1

Seq. No. 392740
Contig ID 33646_1.R1084
5'-most EST uC-osflcyp170h03b1
Method BLASTX
NCBI GI g6016726
BLAST score 155
E value 2.0e-12
Match length 101
% identity 38
NCBI Description (AC009325) unknown protein [Arabidopsis thaliana]
>gi_6091713_gb_AAF03425.1_AC010797_1 (AC010797) unknown protein [Arabidopsis thaliana]

Seq. No. 392741
Contig ID 33668_1.R1084

5'-most EST	uC-osflcyp171c01b1
Seq. No.	392742
Contig ID	33672_1.R1084
5'-most EST	g428026
Method	BLASTX
NCBI GI	g4678328
BLAST score	321
E value	8.0e-35
Match length	129
% identity	60
NCBI Description	(AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana]
Seq. No.	392743
Contig ID	33680_1.R1084
5'-most EST	uC-osflcyp171d03b1
Seq. No.	392744
Contig ID	33683_1.R1084
5'-most EST	uC-osflcyp171d06b1
Seq. No.	392745
Contig ID	33691_1.R1084
5'-most EST	g2428330
Method	BLASTX
NCBI GI	g4587514
BLAST score	705
E value	2.0e-74
Match length	163
% identity	82
NCBI Description	(AC007060) Similar to WO8E3.3 gi_3880615 putative GTP-binding protein from C. elegans cosmid gb_Z92773. EST gb_AA597331 comes from this gene. [Arabidopsis thaliana]
Seq. No.	392746
Contig ID	33697_1.R1084
5'-most EST	uC-osflcyp171e12b1
Method	BLASTX
NCBI GI	g4572673
BLAST score	687
E value	4.0e-72
Match length	233
% identity	57
NCBI Description	(AC006954) putative sarcosine oxidase [Arabidopsis thaliana]
Seq. No.	392747
Contig ID	33699_1.R1084
5'-most EST	uC-osflcyp169c07a1
Seq. No.	392748
Contig ID	33705_1.R1084
5'-most EST	uC-osflcyp171f11b1
Seq. No.	392749
Contig ID	33713_1.R1084

5'-most EST	uC-osflcyp171g10b1
Method	BLASTX
NCBI GI	g3402684
BLAST score	334
E value	7.0e-31
Match length	98
% identity	66
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392750
Contig ID	33729_1.R1084
5'-most EST	uC-osflcyp172b01b1

Seq. No.	392751
Contig ID	33744_1.R1084
5'-most EST	g700484
Method	BLASTX
NCBI GI	g4731111
BLAST score	325
E value	4.0e-30
Match length	82
% identity	80
NCBI Description	(AF064707) exhydrolase II [Zea mays]

Seq. No.	392752
Contig ID	33756_1.R1084
5'-most EST	uC-osflcyp172e02b1

Seq. No.	392753
Contig ID	33757_1.R1084
5'-most EST	uC-osflcyp172e03b1

Seq. No.	392754
Contig ID	33758_1.R1084
5'-most EST	uC-osflcyp172e04b1
Method	BLASTX
NCBI GI	g4835789
BLAST score	633
E value	2.0e-82
Match length	277
% identity	58
NCBI Description	(AC007296) Strong similarity to gi_3367522 F8K4.9 from Arabidopsis thaliana BAC gb_AC004392. EST gb_W43487 comes from this gene

Seq. No.	392755
Contig ID	33774_1.R1084
5'-most EST	uC-osflcyp172g05b1

Seq. No.	392756
Contig ID	33779_1.R1084
5'-most EST	uC-osroM202025a10a1

Seq. No.	392757
Contig ID	33786_1.R1084
5'-most EST	uC-osflcyp173a03b1
Method	BLASTX

NCBI GI	g2829889
BLAST score	518
E value	2.0e-52
Match length	147
% identity	71
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	392758
Contig ID	33787_1.R1084
5'-most EST	uC-osflcyp173a06a1

Seq. No.	392759
Contig ID	33788_1.R1084
5'-most EST	uC-osflM202056f04a1

Seq. No.	392760
Contig ID	33791_1.R1084
5'-most EST	uC-osflM202095g12b1

Seq. No.	392761
Contig ID	33797_1.R1084
5'-most EST	uC-osflcyp173b07b1
Method	BLASTX
NCBI GI	g3643602
BLAST score	294
E value	3.0e-26
Match length	99
% identity	58
NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	392762
Contig ID	33800_1.R1084
5'-most EST	g2428367

Seq. No.	392763
Contig ID	33802_1.R1084
5'-most EST	g3762805
Method	BLASTX
NCBI GI	g4559353
BLAST score	737
E value	3.0e-78
Match length	172
% identity	80
NCBI Description	(AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]

Seq. No.	392764
Contig ID	33803_1.R1084
5'-most EST	uC-osflcyp173c02b1
Method	BLASTX
NCBI GI	g5679840
BLAST score	858
E value	1.0e-156
Match length	288
% identity	68
NCBI Description	(AJ243961) 11332.4 [Oryza sativa]

Seq. No.	392765
Contig ID	33804_1.R1084
5'-most EST	uC-osflcyp176f11b1
Method	BLASTX
NCBI GI	g3367523
BLAST score	263
E value	1.0e-22
Match length	88
% identity	57
NCBI Description	(AC004392) ESTs gb_AA728658 and gb_N95943 come from this gene. [Arabidopsis thaliana]

Seq. No.	392766
Contig ID	33805_1.R1084
5'-most EST	g4716178
Method	BLASTX
NCBI GI	g4220491
BLAST score	216
E value	4.0e-17
Match length	59
% identity	58
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392767
Contig ID	33806_1.R1084
5'-most EST	g428117
Method	BLASTX
NCBI GI	g575605
BLAST score	427
E value	3.0e-49
Match length	240
% identity	48
NCBI Description	(D42065) cationic peroxidase isozyme 40K precursor [Nicotiana tabacum]

Seq. No.	392768
Contig ID	33820_1.R1084
5'-most EST	uC-osflcyp173d11b1
Method	BLASTX
NCBI GI	g1652856
BLAST score	187
E value	2.0e-13
Match length	125
% identity	33
NCBI Description	(D90909) hypothetical protein [Synechocystis sp.]

Seq. No.	392769
Contig ID	33826_1.R1084
5'-most EST	g2311971
Method	BLASTX
NCBI GI	g5869967
BLAST score	1517
E value	1.0e-169
Match length	320
% identity	90
NCBI Description	(AJ010946) isovaleryl-CoA Dehydrogenase [Pisum sativum]

Seq. No.	392770
Contig ID	33839_1.R1084
5'-most EST	uC-osflcyp173g02b1
Method	BLASTX
NCBI GI	g4220472
BLAST score	479
E value	5.0e-48
Match length	120
% identity	80
NCBI Description	(AC006069) similar to yeast ccc1 protein [Arabidopsis thaliana]

Seq. No.	392771
Contig ID	33840_1.R1084
5'-most EST	uC-osflcyp173g03b1
Method	BLASTX
NCBI GI	g1546706
BLAST score	213
E value	7.0e-17
Match length	68
% identity	60
NCBI Description	(X98855) peroxidase ATP8a [Arabidopsis thaliana] >gi_5730127_emb_CAB52461.1_ (AL109796) peroxidase ATP8a [Arabidopsis thaliana]

Seq. No.	392772
Contig ID	33848_1.R1084
5'-most EST	uC-osflm202112h04b1

Seq. No.	392773
Contig ID	33851_1.R1084
5'-most EST	uC-osflcyp173h07b1
Method	BLASTX
NCBI GI	g3236238
BLAST score	360
E value	3.0e-45
Match length	127
% identity	70
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	392774
Contig ID	33852_1.R1084
5'-most EST	uC-osflcyp030a12b1

Seq. No.	392775
Contig ID	33855_1.R1084
5'-most EST	g5038676
Method	BLASTX
NCBI GI	g2842482
BLAST score	300
E value	6.0e-27
Match length	87
% identity	70
NCBI Description	(AL021749) protein phosphatase 2C-like protein [Arabidopsis

thaliana]

Seq. No.	392776
Contig ID	33857_1.R1084
5'-most EST	uC-osflcyp174a05b1
Method	BLASTX
NCBI GI	g4508073
BLAST score	258
E value	5.0e-22
Match length	121
% identity	48
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	392777
Contig ID	33858_1.R1084
5'-most EST	uC-osflcyp174a07b1
Method	BLASTX
NCBI GI	g5031793
BLAST score	290
E value	1.0e-25
Match length	79
% identity	61
NCBI Description	inhibitor of growth family, member 1 >gi_2183221 (AF001954) p33ING1 [Homo sapiens]

Seq. No.	392778
Contig ID	33862_1.R1084
5'-most EST	uC-osflcyp174a12a1

Seq. No.	392779
Contig ID	33878_1.R1084
5'-most EST	uC-osflcyp174c10b1

Seq. No.	392780
Contig ID	33883_1.R1084
5'-most EST	uC-osflcyp174d06b1
Method	BLASTX
NCBI GI	g4249409
BLAST score	413
E value	4.0e-40
Match length	132
% identity	55
NCBI Description	(AC006072) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	392781
Contig ID	33892_1.R1084
5'-most EST	uC-osflm202112g08b1
Method	BLASTX
NCBI GI	g4753658
BLAST score	590
E value	6.0e-61
Match length	207
% identity	61
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	392782

Contig ID 33901_1.R1084
5'-most EST uC-osrocyp016c11b1
Method BLASTX
NCBI GI g4262154
BLAST score 477
E value 2.0e-47
Match length 144
% identity 65
NCBI Description (AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]

Seq. No. 392783
Contig ID 33904_1.R1084
5'-most EST uC-osflm202107d07b1

Seq. No. 392784
Contig ID 33909_1.R1084
5'-most EST uC-osflcyp174g04b1

Seq. No. 392785
Contig ID 33921_1.R1084
5'-most EST g3762130
Method BLASTX
NCBI GI g5834248
BLAST score 1330
E value 1.0e-147
Match length 265
% identity 88
NCBI Description (AF175124) SINAH1 protein [Gossypium hirsutum]

Seq. No. 392786
Contig ID 33933_1.R1084
5'-most EST uC-osflcyp175a11b1
Method BLASTX
NCBI GI g6041837
BLAST score 198
E value 4.0e-15
Match length 49
% identity 69
NCBI Description (AC009853) hypothetical protein [Arabidopsis thaliana]

Seq. No. 392787
Contig ID 33934_1.R1084
5'-most EST uC-osflcyp175a12b1
Method BLASTX
NCBI GI g4432839
BLAST score 280
E value 1.0e-24
Match length 199
% identity 37
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 392788
Contig ID 33936_1.R1084
5'-most EST g3090629
Method BLASTX
NCBI GI g2244831

BLAST score 233
E value 1.0e-47
Match length 300
% identity 49
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 392789
Contig ID 33945_1.R1084
5'-most EST uC-osflcyp175c02b1
Method BLASTX
NCBI GI g2583133
BLAST score 240
E value 4.0e-27
Match length 215
% identity 36
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]

Seq. No. 392790
Contig ID 33955_1.R1084
5'-most EST uC-osflcyp096h05a1

Seq. No. 392791
Contig ID 33960_1.R1084
5'-most EST uC-osflcyp175e04b1

Seq. No. 392792
Contig ID 33970_1.R1084
5'-most EST uC-osflcyp175g05b1

Seq. No. 392793
Contig ID 33984_1.R1084
5'-most EST uC-osflcyp176a07b1

Seq. No. 392794
Contig ID 33988_1.R1084
5'-most EST uC-osflcyp176b01b1
Method BLASTX
NCBI GI g4512667
BLAST score 354
E value 3.0e-33
Match length 172
% identity 48
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 392795
Contig ID 33993_1.R1084
5'-most EST uC-osflcyp176b08b1
Method BLASTX
NCBI GI g3935138
BLAST score 593
E value 3.0e-61
Match length 217
% identity 53
NCBI Description (AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No. 392796
Contig ID 34010_1.R1084

5'-most EST	uC-osflcyp176d04b1
Method	BLASTX
NCBI GI	g2281633
BLAST score	269
E value	2.0e-24
Match length	113
% identity	56
NCBI Description	(AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No.	392797
Contig ID	34014_1.R1084
5'-most EST	uC-osflcyp176d11b1
Method	BLASTX
NCBI GI	g3511128
BLAST score	199
E value	5.0e-15
Match length	120
% identity	42
NCBI Description	(AF060858) unknown [Salmonella dublin]

Seq. No.	392798
Contig ID	34019_1.R1084
5'-most EST	uC-osflcyp176e07b1
Method	BLASTX
NCBI GI	g5880464
BLAST score	820
E value	1.0e-95
Match length	254
% identity	68
NCBI Description	(AF088901) actin bundling protein ABP135 [Lilium longiflorum]

Seq. No.	392799
Contig ID	34024_1.R1084
5'-most EST	uC-osflcyp025a09b1
Method	BLASTX
NCBI GI	g1197461
BLAST score	923
E value	1.0e-100
Match length	191
% identity	87
NCBI Description	(X78819) casein kinase I [Arabidopsis thaliana]

Seq. No.	392800
Contig ID	34039_1.R1084
5'-most EST	uC-osflcyp176h06b1
Method	BLASTX
NCBI GI	g4218120
BLAST score	405
E value	2.0e-39
Match length	99
% identity	79
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	392801

Contig ID 34053_1.R1084
5'-most EST uC-osflcyp177b05b1
Method BLASTX
NCBI GI g585349
BLAST score 737
E value 1.0e-111
Match length 223
% identity 87
NCBI Description CASEIN KINASE II, ALPHA CHAIN 1 (CK II) >gi_419752_pir__S31098 casein kinase II (EC 2.7.1.-) alpha-type chain (clone ATCKA1) - Arabidopsis thaliana >gi_391603_dbj_BAA01090_ (D10246) casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No. 392802
Contig ID 34069_1.R1084
5'-most EST g4969147
Method BLASTX
NCBI GI g5668770
BLAST score 211
E value 1.0e-31
Match length 214
% identity 45
NCBI Description (AC005916) T17H3.9 [Arabidopsis thaliana]

Seq. No. 392803
Contig ID 34081_1.R1084
5'-most EST uC-osflcyp177f03a1

Seq. No. 392804
Contig ID 34081_2.R1084
5'-most EST g2801135

Seq. No. 392805
Contig ID 34091_1.R1084
5'-most EST g699750
Method BLASTX
NCBI GI g4567201
BLAST score 374
E value 9.0e-36
Match length 102
% identity 70
NCBI Description (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]

Seq. No. 392806
Contig ID 34095_1.R1084
5'-most EST uC-osflcyp177h04b1

Seq. No. 392807
Contig ID 34098_1.R1084
5'-most EST uC-osflcyp177h09b1
Method BLASTX
NCBI GI g2160144
BLAST score 380
E value 3.0e-36
Match length 222

% identity	39
NCBI Description	(AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb_X77503). [Arabidopsis thaliana]

Seq. No.	392808
Contig ID	34101_1.R1084
5'-most EST	uC-osflM202050d07b1
Method	BLASTX
NCBI GI	g4539383
BLAST score	429
E value	6.0e-42
Match length	236
% identity	47
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	392809
Contig ID	34104_1.R1084
5'-most EST	uC-osflcyp178b05b1
Method	BLASTX
NCBI GI	g6091723
BLAST score	467
E value	1.0e-46
Match length	160
% identity	58
NCBI Description	(AC010797) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392810
Contig ID	34105_1.R1084
5'-most EST	uC-osflcyp178a08b1
Method	BLASTN
NCBI GI	g3341647
BLAST score	36
E value	2.0e-10
Match length	146
% identity	88
NCBI Description	Zea mays Ama gene encoding single-subunit RNA polymerase

Seq. No.	392811
Contig ID	34134_1.R1084
5'-most EST	uC-osflcyp178f06b1
Method	BLASTX
NCBI GI	g1350986
BLAST score	632
E value	4.0e-66
Match length	148
% identity	86
NCBI Description	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN) >gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No.	392812
Contig ID	34168_1.R1084
5'-most EST	g2428372

Seq. No.	392813
Contig ID	34174_1.R1084
5'-most EST	g2312422

Seq. No.	392814
Contig ID	34177_1.R1084
5'-most EST	g2310438
Method	BLASTX
NCBI GI	g5280991
BLAST score	555
E value	6.0e-57
Match length	111
% identity	88
NCBI Description	(Z97338) putative phosphocholine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	392815
Contig ID	34183_1.R1084
5'-most EST	uC-osflcyp179e09b1
Method	BLASTX
NCBI GI	g586021
BLAST score	178
E value	4.0e-15
Match length	94
% identity	45
NCBI Description	PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION PROTEIN C) >gi_2127242_pir__S66083 stage V sporulation protein - Bacillus subtilis >gi_467442_dbj_BAA05288_ (D26185) stage V sporulation [Bacillus subtilis] >gi_2632320_emb_CAB11829_ (Z99104) thermosensitive mutant blocks spore coat formation (stage V sporulation) [Bacillus subtilis]

Seq. No.	392816
Contig ID	34187_1.R1084
5'-most EST	uC-osflcyp179f06b1
Method	BLASTX
NCBI GI	g4558672
BLAST score	182
E value	3.0e-13
Match length	41
% identity	88
NCBI Description	(AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis thaliana]

Seq. No.	392817
Contig ID	34199_1.R1084
5'-most EST	g2442796

Seq. No.	392818
Contig ID	34205_1.R1084
5'-most EST	g4716700

Seq. No.	392819
Contig ID	34209_1.R1084
5'-most EST	g5004123

Seq. No.	392820
Contig ID	34211_1.R1084
5'-most EST	g4715776

Method	BLASTX
NCBI GI	g4455225
BLAST score	236
E value	1.0e-19
Match length	48
% identity	79
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	392821
Contig ID	34216_1.R1084
5'-most EST	uC-osflcyp079e11a1
Method	BLASTX
NCBI GI	g2266947
BLAST score	1444
E value	1.0e-161
Match length	324
% identity	84
NCBI Description	(AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium hirsutum]

Seq. No.	392822
Contig ID	34229_1.R1084
5'-most EST	uC-osflcyp002b07b2
Method	BLASTX
NCBI GI	g2702281
BLAST score	533
E value	3.0e-54
Match length	137
% identity	74
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	392823
Contig ID	34251_1.R1084
5'-most EST	uC-osflcyp003h05b1
Method	BLASTX
NCBI GI	g4704410
BLAST score	960
E value	1.0e-104
Match length	243
% identity	74
NCBI Description	(AF047046) translation initiation factor eIF6 [Mus musculus]

Seq. No.	392824
Contig ID	34257_1.R1084
5'-most EST	g569856

Seq. No.	392825
Contig ID	34258_1.R1084
5'-most EST	uC-osroM202004d06b1

Seq. No.	392826
Contig ID	34262_1.R1084
5'-most EST	g4879379
Method	BLASTX
NCBI GI	g5912424

BLAST score	509
E value	2.0e-51
Match length	155
% identity	66
NCBI Description	(AJ242970) BTF3b-like factor [Arabidopsis thaliana]

Seq. No.	392827
Contig ID	34263_1.R1084
5'-most EST	g2312412

Seq. No.	392828
Contig ID	34268_1.R1084
5'-most EST	uC-osflcyp037h10b1

Seq. No.	392829
Contig ID	34284_1.R1084
5'-most EST	g3766964
Method	BLASTX
NCBI GI	g1361983
BLAST score	642
E value	4.0e-67
Match length	182
% identity	71
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	392830
Contig ID	34285_1.R1084
5'-most EST	uC-osflcyp051c01b1

Seq. No.	392831
Contig ID	34297_1.R1084
5'-most EST	g572223

Seq. No.	392832
Contig ID	34300_1.R1084
5'-most EST	g568413

Seq. No.	392833
Contig ID	34308_1.R1084
5'-most EST	uC-osflcyp052c12b1
Method	BLASTX
NCBI GI	g4758356
BLAST score	447
E value	2.0e-44
Match length	139
% identity	64
NCBI Description	flap structure-specific endonuclease 1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN >gi_729475_sp_P39748_FEN1_HUMAN FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) >gi_1362788_pir__A56531 DNA structure-specific endonuclease FEN1 - human >gi_704377_bbs_157592 DNase IV=nuclear 42 kda 5' -> 3' exonuclease [human, HeLa cells, Peptide, 380 aa] >gi_642090 (L37374) endonuclease [Homo sapiens] >gi_3169155 (AC004770) FEN1_HUMAN; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN [Homo sapiens] >gi_3980293_emb_CAA54166_ (X76771) flap endonuclease-1 [Homo sapiens]

Seq. No.	392834
Contig ID	34313_1.R1084
5'-most EST	uC-osflcyp052d09b1

Seq. No.	392835
Contig ID	34328_1.R1084
5'-most EST	uC-osroM202022c11b1
Method	BLASTN
NCBI GI	g6063530
BLAST score	37
E value	5.0e-11
Match length	91
% identity	35
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	392836
Contig ID	34332_1.R1084
5'-most EST	uC-osflcyp053a01b1
Method	BLASTX
NCBI GI	g4584529
BLAST score	153
E value	6.0e-20
Match length	77
% identity	66
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	392837
Contig ID	34342_1.R1084
5'-most EST	uC-osflcyp053c06b1
Method	BLASTX
NCBI GI	g1491710
BLAST score	261
E value	2.0e-22
Match length	91
% identity	53
NCBI Description	(X96506) alpha subunit; forms heterodimer with NC2 alpha/Dr1 [Homo sapiens]

Seq. No.	392838
Contig ID	34347_1.R1084
5'-most EST	g4969389

Seq. No.	392839
Contig ID	34347_2.R1084
5'-most EST	g2280828

Seq. No.	392840
Contig ID	34370_1.R1084
5'-most EST	uC-osflcyp061b10b1
Method	BLASTX
NCBI GI	g4895189
BLAST score	145
E value	1.0e-08
Match length	70
% identity	43
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No. 392841
Contig ID 34397_1.R1084
5'-most EST uC-osflcyp070b02a1

Seq. No. 392842
Contig ID 34398_1.R1084
5'-most EST uC-osflcyp070b03a1

Seq. No. 392843
Contig ID 34400_1.R1084
5'-most EST uC-osflcyp116a06a1

Seq. No. 392844
Contig ID 34403_1.R1084
5'-most EST g4715282

Seq. No. 392845
Contig ID 34405_1.R1084
5'-most EST uC-osflcyp070c01a1

Seq. No. 392846
Contig ID 34410_1.R1084
5'-most EST uC-osflcyp070e12a1

Seq. No. 392847
Contig ID 34417_1.R1084
5'-most EST g3761741
Method BLASTX
NCBI GI g520544
BLAST score 201
E value 5.0e-17
Match length 77
% identity 65
NCBI Description (U12195) betaine aldehyde dehydrogenase [Sorghum bicolor]

Seq. No. 392848
Contig ID 34423_1.R1084
5'-most EST g2799368

Seq. No. 392849
Contig ID 34435_1.R1084
5'-most EST uC-osflm202120h04b1
Method BLASTX
NCBI GI g6093736
BLAST score 398
E value 1.0e-38
Match length 172
% identity 48
NCBI Description PECTINESTERASE 1 PRECURSOR (PECTIN METHYLESTERASE 1) (PE 1) >gi_1076365_pir__S51370 pectinesterase (EC 3.1.1.11) PME1 precursor - Arabidopsis thaliana >gi_2129666_pir__JC4778 pectinesterase (EC 3.1.1.11) 1 - Arabidopsis thaliana >gi_550306_emb_CAA57275_ (X81585) ATPME1 [Arabidopsis thaliana] >gi_903895 (U25649) ATPME1 precursor [Arabidopsis thaliana] >gi_6056393_gb_AAF02857.1_AC009324_6 (AC009324) Pectinesterase 1 [Arabidopsis thaliana]

Seq. No. 392850
Contig ID 34438_1.R1084
5'-most EST uC-osflcyp074d06b1

Seq. No. 392851
Contig ID 34445_1.R1084
5'-most EST uC-osflcyp074g09b1

Seq. No. 392852
Contig ID 34456_1.R1084
5'-most EST uC-osflcyp074g06b1

Seq. No. 392853
Contig ID 34488_1.R1084
5'-most EST uC-osroM202029h05a1
Method BLASTX
NCBI GI g2832660
BLAST score 360
E value 5.0e-34
Match length 135
% identity 51
NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]

Seq. No. 392854
Contig ID 34490_1.R1084
5'-most EST g5667632

Seq. No. 392855
Contig ID 34494_1.R1084
5'-most EST uC-osroM202028g01a1
Method BLASTX
NCBI GI g3452497
BLAST score 339
E value 2.0e-48
Match length 122
% identity 79
NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No. 392856
Contig ID 34498_1.R1084
5'-most EST g1854320

Seq. No. 392857
Contig ID 34503_1.R1084
5'-most EST uC-osflcyp132g09a1

Seq. No. 392858
Contig ID 34515_1.R1084
5'-most EST g2428784

Seq. No. 392859
Contig ID 34521_1.R1084
5'-most EST g1631612

Seq. No. 392860
Contig ID 34530_1.R1084

5'-most EST	uC-osflcyp170f10b1
Seq. No.	392861
Contig ID	34533_1.R1084
5'-most EST	g427117
Method	BLASTX
NCBI GI	g2245001
BLAST score	438
E value	4.0e-43
Match length	99
% identity	84
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.	392862
Contig ID	34540_1.R1084
5'-most EST	uC-osflcyp171h11a1
Method	BLASTX
NCBI GI	g548493
BLAST score	315
E value	7.0e-29
Match length	73
% identity	75
NCBI Description	EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi_629854_pir__S30067 polygalacturonase - maize >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea mays]
Seq. No.	392863
Contig ID	34542_1.R1084
5'-most EST	uC-osflcyp007a04b2
Seq. No.	392864
Contig ID	34587_1.R1084
5'-most EST	uC-osflcyp081a03b1
Method	BLASTX
NCBI GI	g5881784
BLAST score	297
E value	2.0e-26
Match length	62
% identity	85
NCBI Description	(AJ249442) putative AUX1-like permease [Arabidopsis thaliana]
Seq. No.	392865
Contig ID	34591_1.R1084
5'-most EST	g3768254
Seq. No.	392866
Contig ID	34607_1.R1084
5'-most EST	g3766755
Method	BLASTX
NCBI GI	g5306263
BLAST score	245
E value	2.0e-20
Match length	143
% identity	41

NCBI Description (AC006233) unknown protein [Arabidopsis thaliana]

Seq. No. 392867
Contig ID 34608_1.R1084
5'-most EST g5038665

Seq. No. 392868
Contig ID 34630_1.R1084
5'-most EST g3759904

Seq. No. 392869
Contig ID 34635_1.R1084
5'-most EST uC-osflcyp176b07b1

Seq. No. 392870
Contig ID 34645_1.R1084
5'-most EST uC-osflcyp002c07b1
Method BLASTX
NCBI GI g1171577
BLAST score 468
E value 9.0e-47
Match length 145
% identity 63
NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 392871
Contig ID 34649_1.R1084
5'-most EST g2280546

Seq. No. 392872
Contig ID 34651_1.R1084
5'-most EST uC-osflcyp173c11b1

Seq. No. 392873
Contig ID 34656_1.R1084
5'-most EST uC-osflcyp002f06b1

Seq. No. 392874
Contig ID 34661_1.R1084
5'-most EST uC-osflcyp002g03b1
Method BLASTX
NCBI GI g4584541
BLAST score 765
E value 3.0e-81
Match length 242
% identity 60
NCBI Description (AL049608) 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein [Arabidopsis thaliana]

Seq. No. 392875
Contig ID 34663_1.R1084
5'-most EST g569748
Method BLASTX
NCBI GI g6016561
BLAST score 396
E value 1.0e-68
Match length 142

% identity	88
NCBI Description	MAGO NASHI PROTEIN HOMOLOG >gi_3123515_emb_CAA70006_ (Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	392876
Contig ID	34683_1.R1084
5'-most EST	g700663
Method	BLASTX
NCBI GI	g2501555
BLAST score	183
E value	2.0e-13
Match length	74
% identity	51
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	392877
Contig ID	34690_1.R1084
5'-most EST	g3106770
Method	BLASTX
NCBI GI	g2980798
BLAST score	505
E value	2.0e-58
Match length	230
% identity	57
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	392878
Contig ID	34697_1.R1084
5'-most EST	g2442312

Seq. No.	392879
Contig ID	34708_1.R1084
5'-most EST	g2798163
Method	BLASTX
NCBI GI	g1498384
BLAST score	589
E value	1.0e-115
Match length	265
% identity	82
NCBI Description	(U60508) actin [Zea mays]

Seq. No.	392880
Contig ID	34727_1.R1084
5'-most EST	g2800561

Seq. No.	392881
Contig ID	34732_1.R1084
5'-most EST	uC-osflcyp018c11b2
Method	BLASTX
NCBI GI	g3877047
BLAST score	134
E value	1.0e-15
Match length	73
% identity	53
NCBI Description	(Z68116) Similarity to Human 3-oxo-5-alpha-steroid 4-dehydrogenase protein (PIR Acc. No. A35856)

[Caenorhabditis elegans]

Seq. No.	392882
Contig ID	34735_1.R1084
5'-most EST	g287213
Method	BLASTX
NCBI GI	g4582783
BLAST score	240
E value	5.0e-20
Match length	77
% identity	56
NCBI Description	(AJ006752) starch synthase, isoform V [Vigna unguiculata]

Seq. No.	392883
Contig ID	34744_1.R1084
5'-most EST	g2443146

Seq. No.	392884
Contig ID	34745_1.R1084
5'-most EST	uC-osflcyp018e07b2

Seq. No.	392885
Contig ID	34748_1.R1084
5'-most EST	g4714725

Seq. No.	392886
Contig ID	34750_1.R1084
5'-most EST	g3761482

Seq. No.	392887
Contig ID	34759_1.R1084
5'-most EST	g702004
Method	BLASTX
NCBI GI	g5921722
BLAST score	183
E value	5.0e-13
Match length	136
% identity	35
NCBI Description	CHALCONE--FLAVONONE ISOMERASE (CHALCONE ISOMERASE) >gi_3126969 (AF061808) chalcone isomerase [Elaeagnus umbellata]

Seq. No.	392888
Contig ID	34763_1.R1084
5'-most EST	g701703
Method	BLASTX
NCBI GI	g3738306
BLAST score	345
E value	4.0e-32
Match length	141
% identity	68
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	392889
Contig ID	34764_1.R1084
5'-most EST	uC-osflcyp019a08b1

Seq. No.	392890
Contig ID	34765_1.R1084
5'-most EST	uC-osflcyp019a10b1
Method	BLASTX
NCBI GI	g2252841
BLAST score	166
E value	1.0e-24
Match length	134
% identity	46
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana] >gi_6049883_gb_AAF02798.1_AF195115_18 (AF195115) No definition line found [Arabidopsis thaliana]

Seq. No.	392891
Contig ID	34776_1.R1084
5'-most EST	uC-osflcyp019f02b1
Method	BLASTX
NCBI GI	g2244833
BLAST score	155
E value	1.0e-09
Match length	297
% identity	22
NCBI Description	(Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No.	392892
Contig ID	34788_1.R1084
5'-most EST	uC-osflcyp023a07b1
Method	BLASTX
NCBI GI	g4097561
BLAST score	293
E value	3.0e-26
Match length	123
% identity	57
NCBI Description	(U64918) ATGP1 [Arabidopsis thaliana]

Seq. No.	392893
Contig ID	34790_1.R1084
5'-most EST	uC-osflm202120f09b1

Seq. No.	392894
Contig ID	34794_1.R1084
5'-most EST	uC-osflcyp005b09b1

Seq. No.	392895
Contig ID	34805_1.R1084
5'-most EST	uC-osflcyp023d08b1
Method	BLASTX
NCBI GI	g549010
BLAST score	747
E value	2.0e-79
Match length	160
% identity	86
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir__S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast

omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No.	392896
Contig ID	34812_1.R1084
5'-most EST	uC-osrocyp008c01b1

Seq. No.	392897
Contig ID	34813_1.R1084
5'-most EST	g4879708
Method	BLASTX
NCBI GI	g5668814
BLAST score	178
E value	1.0e-12
Match length	83
% identity	48
NCBI Description	(AC007519) ESTs gb_H36253 and gb_AA04251 come from this gene. [Arabidopsis thaliana]

Seq. No.	392898
Contig ID	34828_1.R1084
5'-most EST	uC-osflcyp047h11b1
Method	BLASTN
NCBI GI	g607894
BLAST score	417
E value	0.0e+00
Match length	630
% identity	99
NCBI Description	Oryza sativa IR54 anther specific (RTS2) gene, complete cds

Seq. No.	392899
Contig ID	34852_1.R1084
5'-most EST	uC-osflcyp034h01b1

Seq. No.	392900
Contig ID	34858_1.R1084
5'-most EST	uC-osflcyp035a08b1

Seq. No.	392901
Contig ID	34859_1.R1084
5'-most EST	uC-osflm202106d07b1

Seq. No.	392902
Contig ID	34866_1.R1084
5'-most EST	uC-osflcyp035d04b1

Seq. No.	392903
Contig ID	34873_1.R1084
5'-most EST	uC-osroM202037g08b1

Seq. No.	392904
Contig ID	34884_1.R1084
5'-most EST	g4879069
Method	BLASTX

NCBI GI g2271477
BLAST score 623
E value 1.0e-64
Match length 291
% identity 59
NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No. 392905
Contig ID 34888_2.R1084
5'-most EST uC-osflcyp082b05a1
Method BLASTX
NCBI GI g5262760
BLAST score 276
E value 3.0e-24
Match length 67
% identity 85
NCBI Description (AL080283) Beta-COP-like protein [Arabidopsis thaliana]

Seq. No. 392906
Contig ID 34891_1.R1084
5'-most EST g2309816
Method BLASTX
NCBI GI g4336205
BLAST score 316
E value 2.0e-55
Match length 137
% identity 82
NCBI Description (AF077372) cytochrome b5 reductase [Zea mays]

Seq. No. 392907
Contig ID 34892_1.R1084
5'-most EST uC-osflcyp082c09b1

Seq. No. 392908
Contig ID 34900_1.R1084
5'-most EST uC-osflcyp082e04b1
Method BLASTX
NCBI GI g2149640
BLAST score 595
E value 1.0e-92
Match length 242
% identity 75
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana] >gi_5733867_gb_AAD49755.1_AC007932_3 (AC007932) Identical to gb_U91995 Argonaute protein from Arabidopsis thaliana. ESTs gb_H76075, gb_AA720232, gb_N65911 and gb_AA651494 come from this gene

Seq. No. 392909
Contig ID 34914_1.R1084
5'-most EST uC-osflcyp083a03a1

Seq. No. 392910
Contig ID 34917_1.R1084
5'-most EST g2797350

Seq. No. 392911

Contig ID	34933_1.R1084
5'-most EST	uC-osflcyp083c06a1
Method	BLASTN
NCBI GI	g4959460
BLAST score	55
E value	7.0e-22
Match length	321
% identity	86
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	392912
Contig ID	34943_1.R1084
5'-most EST	uC-osflcyp083d08a1
Method	BLASTX
NCBI GI	g4582456
BLAST score	181
E value	4.0e-13
Match length	58
% identity	66
NCBI Description	(AC007071) putative trithorax protein [Arabidopsis thaliana]

Seq. No.	392913
Contig ID	34951_1.R1084
5'-most EST	uC-osflcyp083e11a1
Method	BLASTX
NCBI GI	g3056601
BLAST score	178
E value	4.0e-18
Match length	104
% identity	59
NCBI Description	(AC004255) T1F9.22 [Arabidopsis thaliana]

Seq. No.	392914
Contig ID	34956_1.R1084
5'-most EST	uC-osflcyp083e12a1

Seq. No.	392915
Contig ID	34991_1.R1084
5'-most EST	g3766694
Method	BLASTX
NCBI GI	g1890575
BLAST score	236
E value	2.0e-19
Match length	95
% identity	51
NCBI Description	(X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]

Seq. No.	392916
Contig ID	34996_1.R1084
5'-most EST	g5456491
Method	BLASTX
NCBI GI	g4467139
BLAST score	630
E value	1.0e-65
Match length	169

% identity	72
NCBI Description	(AL035540) putative protein phosphatase-2c [Arabidopsis thaliana]

Seq. No.	392917
Contig ID	35007_1.R1084
5'-most EST	g5003585

Seq. No.	392918
Contig ID	35008_1.R1084
5'-most EST	uC-osflcyp168c05a1

Seq. No.	392919
Contig ID	35014_1.R1084
5'-most EST	uC-osflcyp129d12a1
Method	BLASTX
NCBI GI	g3643596
BLAST score	273
E value	2.0e-40
Match length	120
% identity	72
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	392920
Contig ID	35017_1.R1084
5'-most EST	g2799019
Method	BLASTX
NCBI GI	g3885334
BLAST score	265
E value	1.0e-30
Match length	124
% identity	60
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	392921
Contig ID	35018_1.R1084
5'-most EST	uC-osflcyp129e04a1
Method	BLASTX
NCBI GI	g5091552
BLAST score	518
E value	1.0e-52
Match length	111
% identity	80
NCBI Description	(AC007067) T10O24.21 [Arabidopsis thaliana]

Seq. No.	392922
Contig ID	35044_1.R1084
5'-most EST	g3761845

Seq. No.	392923
Contig ID	35048_1.R1084
5'-most EST	uC-osflcyp117b08a1

Seq. No.	392924
Contig ID	35050_1.R1084
5'-most EST	uC-osflM202021h06a1

Seq. No.	392925
Contig ID	35064_1.R1084
5'-most EST	uC-osflcyp169f02a1
Method	BLASTX
NCBI GI	g2829892
BLAST score	174
E value	3.0e-12
Match length	60
% identity	55
NCBI Description	(AC002311) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	392926
Contig ID	35076_1.R1084
5'-most EST	uC-osflcyp130d11a1
Method	BLASTX
NCBI GI	g4586249
BLAST score	220
E value	9.0e-18
Match length	86
% identity	53
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]

Seq. No.	392927
Contig ID	35079_1.R1084
5'-most EST	uC-osflcyp130e04a1
Method	BLASTN
NCBI GI	g4680488
BLAST score	46
E value	3.0e-16
Match length	145
% identity	86
NCBI Description	Oryza sativa BAC clone 1.H19, complete sequence

Seq. No.	392928
Contig ID	35085_1.R1084
5'-most EST	g3766837

Seq. No.	392929
Contig ID	35090_1.R1084
5'-most EST	uC-osroM202013c11b1

Seq. No.	392930
Contig ID	35099_1.R1084
5'-most EST	g4715401

Seq. No.	392931
Contig ID	35110_1.R1084
5'-most EST	uC-osroM202035e02b1
Method	BLASTX
NCBI GI	g5081779
BLAST score	309
E value	7.0e-40
Match length	89
% identity	92
NCBI Description	(AF150630) cellulose synthase [Gossypium hirsutum]

Seq. No.	392932
Contig ID	35111_1.R1084
5'-most EST	g3762278
Method	BLASTX
NCBI GI	g3021344
BLAST score	177
E value	1.0e-12
Match length	80
% identity	45
NCBI Description	(AJ004959) hypothetical protein [Cicer arietinum]

Seq. No.	392933
Contig ID	35119_1.R1084
5'-most EST	uC-osflcyp155b12b1
Method	BLASTX
NCBI GI	g3901268
BLAST score	266
E value	5.0e-23
Match length	146
% identity	36
NCBI Description	(AF060173) SV2 related protein [Rattus norvegicus]

Seq. No.	392934
Contig ID	35126_1.R1084
5'-most EST	uC-osflcyp156b01b1

Seq. No.	392935
Contig ID	35127_1.R1084
5'-most EST	uC-osflcyp156b04b1
Method	BLASTX
NCBI GI	g4262152
BLAST score	431
E value	3.0e-42
Match length	110
% identity	70
NCBI Description	(AC005275) putative frataxin-like protein [Arabidopsis thaliana]

Seq. No.	392936
Contig ID	35133_1.R1084
5'-most EST	uC-osflcyp156d12b1

Seq. No.	392937
Contig ID	35137_1.R1084
5'-most EST	uC-osflcyp156f10b1

Seq. No.	392938
Contig ID	35138_1.R1084
5'-most EST	g2310679

Seq. No.	392939
Contig ID	35145_1.R1084
5'-most EST	g2427698

Seq. No.	392940
Contig ID	35153_1.R1084

5'-most EST	uC-osroM202005d06b1
Method	BLASTX
NCBI GI	g3522937
BLAST score	417
E value	2.0e-40
Match length	158
% identity	55
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	392941
Contig ID	35156_1.R1084
5'-most EST	uC-osflcyp157e08b1

Seq. No.	392942
Contig ID	35159_1.R1084
5'-most EST	g2312257
Method	BLASTX
NCBI GI	g1815664
BLAST score	282
E value	5.0e-25
Match length	113
% identity	54
NCBI Description	(U83671) low molecular mass heat shock protein Oshsp17.7 [Oryza sativa]

Seq. No.	392943
Contig ID	35170_1.R1084
5'-most EST	g5771060

Seq. No.	392944
Contig ID	35172_1.R1084
5'-most EST	uC-osrocyp016h02b1

Seq. No.	392945
Contig ID	35178_1.R1084
5'-most EST	g2428975

Seq. No.	392946
Contig ID	35187_1.R1084
5'-most EST	uC-osflcyp158f06b1
Method	BLASTX
NCBI GI	g5541672
BLAST score	129
E value	6.0e-11
Match length	97
% identity	47
NCBI Description	(AL096859) putative protein [Arabidopsis thaliana]

Seq. No.	392947
Contig ID	35189_1.R1084
5'-most EST	uC-osflcyp158g12b1

Seq. No.	392948
Contig ID	35197_1.R1084
5'-most EST	uC-osflM202016d02b1

Seq. No.	392949

Contig ID 35212_1.R1084
5'-most EST uC-osflcyp159g05b1

Seq. No. 392950
Contig ID 35223_1.R1084
5'-most EST g3768803
Method BLASTX
NCBI GI g4557587
BLAST score 399
E value 1.0e-38
Match length 112
% identity 62
NCBI Description fumarylacetoacetase >gi_119778_sp_P16930_FAAA_HUMAN FUMARYLACETOACETASE (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) >gi_106043_pir__A37926 fumarylacetoacetase (EC 3.7.1.2) - human >gi_182393 (M55150) fumarylacetoacetate hydrolase [Homo sapiens]

Seq. No. 392951
Contig ID 35235_1.R1084
5'-most EST uC-osflcyp160c09a1
Method BLASTX
NCBI GI g3183991
BLAST score 383
E value 2.0e-46
Match length 208
% identity 52
NCBI Description (AJ005173) P69F protein [Lycopersicon esculentum]

Seq. No. 392952
Contig ID 35244_1.R1084
5'-most EST uC-osflcyp160d09a1
Method BLASTX
NCBI GI g3790593
BLAST score 147
E value 4.0e-09
Match length 66
% identity 42
NCBI Description (AF079185) RING-H2 finger protein RHY1a [Arabidopsis thaliana]

Seq. No. 392953
Contig ID 35257_1.R1084
5'-most EST g5038902

Seq. No. 392954
Contig ID 35266_1.R1084
5'-most EST uC-osflcyp160g02a1

Seq. No. 392955
Contig ID 35271_1.R1084
5'-most EST g3761378

Seq. No. 392956
Contig ID 35290_1.R1084
5'-most EST uC-osflcyp161h05b1
Method BLASTX

NCBI GI	g4217999
BLAST score	186
E value	2.0e-14
Match length	87
% identity	54
NCBI Description	(AC006135) putative ubiquitin--protein ligase (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]

Seq. No.	392957
Contig ID	35294_1.R1084
5'-most EST	uC-osflcyp162a05b1
Method	BLASTX
NCBI GI	g2865394
BLAST score	219
E value	1.0e-17
Match length	158
% identity	45
NCBI Description	(AF036949) basic leucine zipper protein [Zea mays]

Seq. No.	392958
Contig ID	35300_1.R1084
5'-most EST	uC-osflM202094b06b1
Method	BLASTX
NCBI GI	g2880043
BLAST score	211
E value	1.0e-16
Match length	95
% identity	46
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	392959
Contig ID	35301_1.R1084
5'-most EST	uC-osflcyp162c12b1

Seq. No.	392960
Contig ID	35316_1.R1084
5'-most EST	g4968896
Method	BLASTX
NCBI GI	g4680211
BLAST score	480
E value	7.0e-48
Match length	130
% identity	75
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	392961
Contig ID	35332_1.R1084
5'-most EST	uC-osflm202101d06b1
Method	BLASTX
NCBI GI	g3367520
BLAST score	728
E value	5.0e-77
Match length	226
% identity	61
NCBI Description	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb_D12522 from A.

thaliana. [Arabidopsis thaliana]

Seq. No.	392962
Contig ID	35337_1.R1084
5'-most EST	uC-osflcyp174f01b1
Method	BLASTX
NCBI GI	g1213460
BLAST score	394
E value	3.0e-44
Match length	191
% identity	51
NCBI Description	(U03374) C subunit of V-ATPase [Amblyomma americanum]

Seq. No.	392963
Contig ID	35339_1.R1084
5'-most EST	uC-osflcyp174g07b1

Seq. No.	392964
Contig ID	35352_1.R1084
5'-most EST	g2801116

Seq. No.	392965
Contig ID	35354_1.R1084
5'-most EST	uC-osflm202104d04b1
Method	BLASTX
NCBI GI	g3287695
BLAST score	335
E value	3.0e-48
Match length	135
% identity	78
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	392966
Contig ID	35357_1.R1084
5'-most EST	g2431427
Method	BLASTX
NCBI GI	g2493318
BLAST score	203
E value	8.0e-26
Match length	84
% identity	68
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	392967
Contig ID	35419_1.R1084
5'-most EST	uC-osflcyp179e11b1

Seq. No.	392968
Contig ID	35424_1.R1084
5'-most EST	uC-osflcyp179h03b1

Seq. No.	392969
Contig ID	35425_1.R1084

5'-most EST	uC-osflcyp179h07b1
Seq. No.	392970
Contig ID	35428_1.R1084
5'-most EST	g427190
Seq. No.	392971
Contig ID	35432_1.R1084
5'-most EST	uC-osflcyp131d02a1
Seq. No.	392972
Contig ID	35442_1.R1084
5'-most EST	uC-osroM202030a03b1
Seq. No.	392973
Contig ID	35443_1.R1084
5'-most EST	g701987
Method	BLASTX
NCBI GI	g4309742
BLAST score	213
E value	2.0e-16
Match length	104
% identity	42
NCBI Description	(AC006439) putative Rer1 protein [Arabidopsis thaliana]
Seq. No.	392974
Contig ID	35453_1.R1084
5'-most EST	uC-osflcyp022b08b1
Seq. No.	392975
Contig ID	35458_1.R1084
5'-most EST	g2311707
Method	BLASTX
NCBI GI	g3868853
BLAST score	255
E value	1.0e-21
Match length	118
% identity	46
NCBI Description	(AB013853) GPI-anchored protein [Vigna radiata]
Seq. No.	392976
Contig ID	35461_1.R1084
5'-most EST	uC-osflcyp022e01b1
Method	BLASTX
NCBI GI	g4512624
BLAST score	434
E value	1.0e-84
Match length	234
% identity	75
NCBI Description	(AC004793) Strong similarity to gi_3033401 F19I3.29 putative potassium transporter from Arabidopsis thaliana BAC gb_AC004238
Seq. No.	392977
Contig ID	35463_1.R1084
5'-most EST	uC-osflcyp022e05b1

Seq. No.	392978
Contig ID	35468_1.R1084
5'-most EST	g700439
Seq. No.	392979
Contig ID	35473_1.R1084
5'-most EST	uC-osrocyp028c06b1
Method	BLASTX
NCBI GI	g1237250
BLAST score	641
E value	1.0e-128
Match length	350
% identity	67
NCBI Description	(X96784) cytochrome P450 [Nicotiana tabacum]
Seq. No.	392980
Contig ID	35475_1.R1084
5'-most EST	uC-osflcyp022a11b1
Method	BLASTX
NCBI GI	g4454484
BLAST score	302
E value	7.0e-55
Match length	196
% identity	60
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.	392981
Contig ID	35479_1.R1084
5'-most EST	uC-osflcyp029a01b1
Seq. No.	392982
Contig ID	35512_1.R1084
5'-most EST	uC-osflcyp030c03b1
Seq. No.	392983
Contig ID	35514_1.R1084
5'-most EST	uC-osflcyp030c08b1
Method	BLASTX
NCBI GI	g4538965
BLAST score	145
E value	1.0e-14
Match length	111
% identity	42
NCBI Description	(AL049488) hypothetical protein [Arabidopsis thaliana]
Seq. No.	392984
Contig ID	35533_1.R1084
5'-most EST	g4879085
Method	BLASTX
NCBI GI	g5302799
BLAST score	277
E value	2.0e-24
Match length	151
% identity	39
NCBI Description	(Z97341) gibberellin oxidase-like protein [Arabidopsis thaliana]

Seq. No.	392985
Contig ID	35542_1.R1084
5'-most EST	g2431481
Method	BLASTX
NCBI GI	g3617837
BLAST score	657
E value	1.0e-130
Match length	383
% identity	31
NCBI Description	(AF035820) gibberellin action negative regulator SPY [Hordeum vulgare]

Seq. No.	392986
Contig ID	35543_1.R1084
5'-most EST	uC-osflcyp031d04b1

Seq. No.	392987
Contig ID	35559_1.R1084
5'-most EST	uC-osflcyp032a08b1

Seq. No.	392988
Contig ID	35595_1.R1084
5'-most EST	uC-osflcyp033f07b1

Seq. No.	392989
Contig ID	35603_1.R1084
5'-most EST	uC-osflcyp039a04b1

Seq. No.	392990
Contig ID	35609_1.R1084
5'-most EST	g1631985

Seq. No.	392991
Contig ID	35622_1.R1084
5'-most EST	g3762463
Method	BLASTX
NCBI GI	g3298437
BLAST score	693
E value	7.0e-73
Match length	230
% identity	64
NCBI Description	(AB010877) chloroplast ribosomal protein L3 [Nicotiana tabacum]

Seq. No.	392992
Contig ID	35649_1.R1084
5'-most EST	g2798392

Seq. No.	392993
Contig ID	35654_1.R1084
5'-most EST	g699952
Method	BLASTX
NCBI GI	g2459443
BLAST score	469
E value	4.0e-47
Match length	130

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% identity	68
NCBI Description	(AC002332) putative NAD(P)-dependent cholesterol dehydrogenase [Arabidopsis thaliana]

Seq. No.	392994
Contig ID	35659_1.R1084
5'-most EST	uC-osf1M202054a02b1
Method	BLASTX
NCBI GI	g3821254
BLAST score	535
E value	9.0e-98
Match length	235
% identity	78
NCBI Description	(AJ007789) geranylgeranyl reductase [Nicotiana tabacum]

Seq. No.	392995
Contig ID	35688_1.R1084
5'-most EST	uC-osflcyp057e08b1

Seq. No.	392996
Contig ID	35691_1.R1084
5'-most EST	g2312114

Seq. No.	392997
Contig ID	35695_1.R1084
5'-most EST	g4715016
Method	BLASTN
NCBI GI	g5803242
BLAST score	267
E value	1.0e-148
Match length	449
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	392998
Contig ID	35696_1.R1084
5'-most EST	uC-osroM202004g09b1

Seq. No.	392999
Contig ID	35707_1.R1084
5'-most EST	g2442552

Seq. No.	393000
Contig ID	35725_1.R1084
5'-most EST	uC-osflcyp062b09a1
Method	BLASTX
NCBI GI	g2708744
BLAST score	148
E value	2.0e-09
Match length	52
% identity	62
NCBI Description	(AC003952) putative Bop-like zinc finger protein [Arabidopsis thaliana]

Seq. No.	393001
Contig ID	35739_1.R1084
5'-most EST	uC-osflcyp062d02a1

Method	BLASTX
NCBI GI	g2098709
BLAST score	171
E value	6.0e-12
Match length	68
% identity	47
NCBI Description	(U82975) pectinesterase [Citrus sinensis]

Seq. No.	393002
Contig ID	35760_1.R1084
5'-most EST	uC-osroM202037g03a1
Method	BLASTX
NCBI GI	g4510383
BLAST score	310
E value	2.0e-28
Match length	86
% identity	73
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	393003
Contig ID	35776_1.R1084
5'-most EST	uC-osflcyp064c02b1

Seq. No.	393004
Contig ID	35784_1.R1084
5'-most EST	uC-osflcyp064f01b1
Method	BLASTX
NCBI GI	g4490316
BLAST score	400
E value	8.0e-39
Match length	172
% identity	48
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	393005
Contig ID	35799_1.R1084
5'-most EST	g2312443
Method	BLASTX
NCBI GI	g3914935
BLAST score	220
E value	2.0e-17
Match length	62
% identity	71
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_3204099_emb_CAA07226.1_ (AJ006759) ribosome-associated protein p40 [Cicer arietinum]

Seq. No.	393006
Contig ID	35812_1.R1084
5'-most EST	g2311864
Method	BLASTX
NCBI GI	g2880048
BLAST score	529
E value	3.0e-68
Match length	157
% identity	77
NCBI Description	(AC002340) unknown protein [Arabidopsis thaliana]

Seq. No. 393007
Contig ID 35818_1.R1084
5'-most EST uC-osflM202014a09b1

Seq. No. 393008
Contig ID 35825_1.R1084
5'-most EST g5667555

Seq. No. 393009
Contig ID 35837_1.R1084
5'-most EST uC-osflcyp078c06b1

Seq. No. 393010
Contig ID 35841_1.R1084
5'-most EST uC-osflcyp078e05b1

Seq. No. 393011
Contig ID 35853_1.R1084
5'-most EST uC-osflcyp109a04b1
Method BLASTX
NCBI GI g3287693
BLAST score 259
E value 1.0e-26
Match length 83
% identity 68
NCBI Description (AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No. 393012
Contig ID 35863_1.R1084
5'-most EST uC-osflcyp109c04b1

Seq. No. 393013
Contig ID 35877_1.R1084
5'-most EST uC-osflcyp109f04b1
Method BLASTX
NCBI GI g3935184
BLAST score 388
E value 3.0e-37
Match length 223
% identity 42
NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]

Seq. No. 393014
Contig ID 35881_1.R1084
5'-most EST uC-osroM202022h09b1

Seq. No. 393015
Contig ID 35891_1.R1084
5'-most EST uC-osroM202020a11a1
Method BLASTX
NCBI GI g3393062
BLAST score 639
E value 9.0e-67
Match length 165

% identity	72
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]
Seq. No.	393016
Contig ID	35892_1.R1084
5'-most EST	uC-osflcyp111c05b1
Seq. No.	393017
Contig ID	35904_1.R1084
5'-most EST	uC-osflcyp111e08b1
Method	BLASTX
NCBI GI	g4827050
BLAST score	544
E value	2.0e-55
Match length	211
% identity	48
NCBI Description	ubiquitin specific protease 14 (tRNA-guanine transglycosylase) >gi_1729927_sp_P54578_TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi_940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]
Seq. No.	393018
Contig ID	35940_1.R1084
5'-most EST	g5038840
Method	BLASTN
NCBI GI	g5918186
BLAST score	138
E value	3.0e-71
Match length	446
% identity	83
NCBI Description	Hordeum vulgare mRNA for hordeum vulgare (barley) ribophorin I, partial
Seq. No.	393019
Contig ID	35955_1.R1084
5'-most EST	uC-osflcyp115c07a1
Seq. No.	393020
Contig ID	35961_1.R1084
5'-most EST	uC-osflM2020117e08a1
Seq. No.	393021
Contig ID	35962_1.R1084
5'-most EST	uC-osflcyp115c11a1
Method	BLASTX
NCBI GI	g5123546
BLAST score	143
E value	3.0e-14
Match length	75
% identity	57
NCBI Description	(AL079344) putative protein [Arabidopsis thaliana]
Seq. No.	393022
Contig ID	35968_1.R1084
5'-most EST	g2799810
Method	BLASTN

NCBI GI	g58066
BLAST score	53
E value	2.0e-20
Match length	137
% identity	91
NCBI Description	pBluescript SK(-) vector DNA, phagemid excised from lambda ZAP

Seq. No.	393023
Contig ID	35968_2.R1084
5'-most EST	g2800637

Seq. No.	393024
Contig ID	35968_3.R1084
5'-most EST	g2800835
Method	BLASTN
NCBI GI	g950081
BLAST score	52
E value	5.0e-20
Match length	52
% identity	100
NCBI Description	M.sativa mRNA for ASET2

Seq. No.	393025
Contig ID	35972_1.R1084
5'-most EST	g2312507

Seq. No.	393026
Contig ID	35977_1.R1084
5'-most EST	uC-osflcyp115e10a1

Seq. No.	393027
Contig ID	35982_1.R1084
5'-most EST	uC-osflcyp115f06a1

Seq. No.	393028
Contig ID	35996_1.R1084
5'-most EST	uC-osflcyp141a08a1

Seq. No.	393029
Contig ID	36002_1.R1084
5'-most EST	g5004062

Seq. No.	393030
Contig ID	36004_1.R1084
5'-most EST	uC-osflM202083c10b1

Seq. No.	393031
Contig ID	36025_1.R1084
5'-most EST	uC-osflM202064b12a1
Method	BLASTX
NCBI GI	g4512702
BLAST score	433
E value	2.0e-42
Match length	101
% identity	79
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393032
Contig ID 36037_1.R1084
5'-most EST uC-osflcyp156b11a1

Seq. No. 393033
Contig ID 36048_1.R1084
5'-most EST g4716195
Method BLASTX
NCBI GI g3746568
BLAST score 659
E value 1.0e-143
Match length 318
% identity 82
NCBI Description (AF061638) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]

Seq. No. 393034
Contig ID 36062_1.R1084
5'-most EST uC-osflcyp128c05a1

Seq. No. 393035
Contig ID 36063_1.R1084
5'-most EST uC-osflcyp127e07a1

Seq. No. 393036
Contig ID 36081_1.R1084
5'-most EST g3767344

Seq. No. 393037
Contig ID 36084_1.R1084
5'-most EST g3768159

Seq. No. 393038
Contig ID 36088_1.R1084
5'-most EST uC-osflcyp127h08a1

Seq. No. 393039
Contig ID 36100_1.R1084
5'-most EST g4716771
Method BLASTX
NCBI GI g3201615
BLAST score 422
E value 4.0e-64
Match length 284
% identity 48
NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 393040
Contig ID 36104_1.R1084
5'-most EST uC-osflcyp128b09a1
Method BLASTX
NCBI GI g5263310
BLAST score 214
E value 1.0e-16
Match length 76
% identity 55

NCBI Description	(AC007727) EST gb_N95925 comes from this gene. [Arabidopsis thaliana]

Seq. No.	393041
Contig ID	36105_1.R1084
5'-most EST	uC-osflcyp128b10a1
Method	BLASTX
NCBI GI	g2088643
BLAST score	369
E value	5.0e-35
Match length	112
% identity	44
NCBI Description	(AF002109) transcription factor SF3 isolog [Arabidopsis thaliana]

Seq. No.	393042
Contig ID	36109_1.R1084
5'-most EST	uC-osflcyp152g04a1

Seq. No.	393043
Contig ID	36114_1.R1084
5'-most EST	uC-osrocyp017b06a1
Method	BLASTX
NCBI GI	g5441894
BLAST score	158
E value	2.0e-10
Match length	99
% identity	39
NCBI Description	(AP000367) EST AU030111(E50640) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	393044
Contig ID	36115_1.R1084
5'-most EST	g3761571

Seq. No.	393045
Contig ID	36122_1.R1084
5'-most EST	uC-osflM202086b05a1
Method	BLASTX
NCBI GI	g1946300
BLAST score	226
E value	2.0e-18
Match length	78
% identity	31
NCBI Description	(Y12529) hypothetical protein [Silene latifolia]

Seq. No.	393046
Contig ID	36126_1.R1084
5'-most EST	uC-osflcyp118b06a1
Method	BLASTN
NCBI GI	g6016845
BLAST score	34
E value	3.0e-09
Match length	150
% identity	81
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	393047
Contig ID	36132_1.R1084
5'-most EST	g2799141
Method	BLASTX
NCBI GI	g5902382
BLAST score	234
E value	3.0e-19
Match length	76
% identity	61
NCBI Description	(AC009322) Unknown protein [Arabidopsis thaliana]

Seq. No.	393048
Contig ID	36132_2.R1084
5'-most EST	g3763534
Method	BLASTX
NCBI GI	g5902382
BLAST score	241
E value	1.0e-29
Match length	157
% identity	43
NCBI Description	(AC009322) Unknown protein [Arabidopsis thaliana]

Seq. No.	393049
Contig ID	36133_1.R1084
5'-most EST	uC-osflcyp128f04a1

Seq. No.	393050
Contig ID	36156_1.R1084
5'-most EST	uC-osflcyp017b09b2
Method	BLASTX
NCBI GI	g3341511
BLAST score	292
E value	3.0e-26
Match length	72
% identity	76
NCBI Description	(AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]

Seq. No.	393051
Contig ID	36172_1.R1084
5'-most EST	uC-osroM202028b03b1

Seq. No.	393052
Contig ID	36172_2.R1084
5'-most EST	uC-osflcyp151e01b1

Seq. No.	393053
Contig ID	36179_1.R1084
5'-most EST	uC-osflcyp151h06b1
Method	BLASTX
NCBI GI	g4314378
BLAST score	221
E value	9.0e-18
Match length	86
% identity	51
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana] >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative lipase [Arabidopsis thaliana]

Seq. No. 393054
Contig ID 36180_1.R1084
5'-most EST uC-osflcyp151h09b1

Seq. No. 393055
Contig ID 36188_1.R1084
5'-most EST uC-osflcyp089c10b1
Method BLASTX
NCBI GI g4585899
BLAST score 220
E value 1.0e-17
Match length 71
% identity 56
NCBI Description (AC007133) unknown protein [Arabidopsis thaliana]

Seq. No. 393056
Contig ID 36201_1.R1084
5'-most EST uC-osflcyp012a09b1
Method BLASTX
NCBI GI g5714658
BLAST score 620
E value 4.0e-72
Match length 170
% identity 85
NCBI Description (AF165095) Rab GTP-binding protein Rab11a [Gossypium hirsutum]

Seq. No. 393057
Contig ID 36220_1.R1084
5'-most EST uC-osflcyp012e09b1
Method BLASTX
NCBI GI g4678259
BLAST score 629
E value 1.0e-65
Match length 180
% identity 22
NCBI Description (AL049657) putative protein [Arabidopsis thaliana]

Seq. No. 393058
Contig ID 36232_1.R1084
5'-most EST uC-osflcyp013b10b1
Method BLASTX
NCBI GI g2737973
BLAST score 399
E value 2.0e-38
Match length 132
% identity 62
NCBI Description (U83625) protein kinase ZmMEK1 [Zea mays]

Seq. No. 393059
Contig ID 36237_1.R1084
5'-most EST uC-osflM202020b06b1
Method BLASTX
NCBI GI g1084442
BLAST score 318
E value 3.0e-29

Match length	72
% identity	79
NCBI Description	cellulase (EC 3.2.1.4) - European elder >gi_575404_emb_CAA52343_ (X74290) cellulase [Sambucus nigra]

Seq. No.	393060
Contig ID	36248_1.R1084
5'-most EST	g2428049
Method	BLASTX
NCBI GI	g3785989
BLAST score	483
E value	2.0e-48
Match length	168
% identity	59
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	393061
Contig ID	36259_1.R1084
5'-most EST	uC-osflcyp091b10b1

Seq. No.	393062
Contig ID	36269_1.R1084
5'-most EST	g4880898
Method	BLASTX
NCBI GI	g2495171
BLAST score	333
E value	7.0e-37
Match length	127
% identity	65
NCBI Description	DELTA-AMINOLEVULINIC ACID DEHYDRATASE PRECURSOR (PORPHOBILINOGEN SYNTHASE) (ALADH) >gi_1041423_emb_CAA63139_ (X92402) aminolevulinate dehydratase [Hordeum vulgare]

Seq. No.	393063
Contig ID	36280_1.R1084
5'-most EST	uC-osflcyp139c12b1
Method	BLASTX
NCBI GI	g5295971
BLAST score	764
E value	1.0e-81
Match length	149
% identity	98
NCBI Description	(AB026295) EST D24315(R1718) corresponds to a region of the predicted gene.; Similar to Tobacco DNA for retroviral-like transposon Tnt 1-94.(X13777) [Oryza sativa]

Seq. No.	393064
Contig ID	36294_1.R1084
5'-most EST	uC-osflcyp140a07b1
Method	BLASTX
NCBI GI	g4102600
BLAST score	416
E value	4.0e-42
Match length	160
% identity	61

NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.	393065
Contig ID	36296_1.R1084
5'-most EST	uC-osflcyp140a11b1
Method	BLASTX
NCBI GI	g3953465
BLAST score	306
E value	1.0e-27
Match length	107
% identity	50
NCBI Description	(AC002328) F20N2.10 [Arabidopsis thaliana]
Seq. No.	393066
Contig ID	36314_1.R1084
5'-most EST	g701837
Method	BLASTX
NCBI GI	g4760700
BLAST score	201
E value	2.0e-15
Match length	79
% identity	53
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]
Seq. No.	393067
Contig ID	36315_1.R1084
5'-most EST	uC-osflcyp140g07b1
Method	BLASTX
NCBI GI	g2832608
BLAST score	147
E value	5.0e-09
Match length	131
% identity	10
NCBI Description	(AL021637) leucine rich repeat-like protein (fragment) [Arabidopsis thaliana]
Seq. No.	393068
Contig ID	36349_1.R1084
5'-most EST	g2799013
Method	BLASTN
NCBI GI	g1698774
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	Filamentous phage display expression cloning vector pZGT5 with murine Ig kappa light chain fragment insert, complete sequence
Seq. No.	393069
Contig ID	36349_2.R1084
5'-most EST	uC-osrocyp036b08a1
Seq. No.	393070
Contig ID	36356_1.R1084
5'-most EST	g3768433

Seq. No.	393071
Contig ID	36372_1.R1084
5'-most EST	uC-osflcyp112c03a1

Seq. No.	393072
Contig ID	36398_1.R1084
5'-most EST	uC-osflcyp112g04a1
Method	BLASTX
NCBI GI	g1531756
BLAST score	209
E value	2.0e-16
Match length	41
% identity	93
NCBI Description	(X82413) proline-rich-like protein [Asparagus officinalis]

Seq. No.	393073
Contig ID	36404_1.R1084
5'-most EST	g3767873

Seq. No.	393074
Contig ID	36420_1.R1084
5'-most EST	uC-osflM202054h09b1
Method	BLASTX
NCBI GI	g2342682
BLAST score	745
E value	4.0e-79
Match length	194
% identity	71
NCBI Description	(AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No.	393075
Contig ID	36421_1.R1084
5'-most EST	g2427681
Method	BLASTX
NCBI GI	g3123745
BLAST score	373
E value	2.0e-35
Match length	174
% identity	45
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	393076
Contig ID	36428_1.R1084
5'-most EST	g3061100
Method	BLASTX
NCBI GI	g3643082
BLAST score	153
E value	8.0e-10
Match length	92
% identity	45
NCBI Description	(AF075579) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	393077
Contig ID	36430_1.R1084
5'-most EST	uC-osroM202040h06b1

Method	BLASTX
NCBI GI	g4531446
BLAST score	248
E value	9.0e-21
Match length	89
% identity	55
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393078
Contig ID	36441_1.R1084
5'-most EST	uC-osflcyp121c11b1

Seq. No.	393079
Contig ID	36453_1.R1084
5'-most EST	uC-osflcyp121h08b1
Method	BLASTX
NCBI GI	g1709128
BLAST score	450
E value	3.0e-58
Match length	150
% identity	78
NCBI Description	GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-2 >gi_481019_pir__S37643 protein kinase MSK-2 (EC 2.7.1.-) - alfalfa >gi_313146_emb_CAA48473_ (X68410) protein kinase [Medicago sativa]

Seq. No.	393080
Contig ID	36455_1.R1084
5'-most EST	uC-osflcyp122a01b1

Seq. No.	393081
Contig ID	36459_1.R1084
5'-most EST	uC-osflcyp122b05b1
Method	BLASTX
NCBI GI	g4544436
BLAST score	230
E value	9.0e-19
Match length	116
% identity	47
NCBI Description	(AC006592) anthocyanidin-3-glucoside rhamnosyltransferase, 3' partial [Arabidopsis thaliana]

Seq. No.	393082
Contig ID	36467_1.R1084
5'-most EST	uC-osflcyp122e03b1
Method	BLASTX
NCBI GI	g5689413
BLAST score	179
E value	6.0e-13
Match length	94
% identity	40
NCBI Description	(AB028961) KIAA1038 protein [Homo sapiens]

Seq. No.	393083
Contig ID	36476_1.R1084
5'-most EST	uC-osrocyp037h11b1

Seq. No.	393084
Contig ID	36477_1.R1084
5'-most EST	g2443135
Method	BLASTX
NCBI GI	g416583
BLAST score	177
E value	2.0e-12
Match length	137
% identity	36
NCBI Description	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME) >gi_396404 (U00006) acetyl-CoA sythetase [Escherichia coli] >gi_1790505 (AE000480) acetyl-CoA synthetase [Escherichia coli]

Seq. No.	393085
Contig ID	36485_1.R1084
5'-most EST	uC-osflcyp123b07b1

Seq. No.	393086
Contig ID	36505_1.R1084
5'-most EST	uC-osflcyp123g10b1

Seq. No.	393087
Contig ID	36511_1.R1084
5'-most EST	g5003546
Method	BLASTX
NCBI GI	g3738302
BLAST score	382
E value	2.0e-36
Match length	170
% identity	45
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	393088
Contig ID	36525_1.R1084
5'-most EST	uC-osflm202002e01b1
Method	BLASTX
NCBI GI	g1076511
BLAST score	494
E value	1.0e-49
Match length	125
% identity	79
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	393089
Contig ID	36544_1.R1084
5'-most EST	uC-osroM202013b07b1

Seq. No.	393090
Contig ID	36546_1.R1084
5'-most EST	uC-osflcyp125e08b1
Method	BLASTX
NCBI GI	g4585991

BLAST score	229
E value	2.0e-18
Match length	107
% identity	47
NCBI Description	(AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis thaliana]

Seq. No.	393091
Contig ID	36563_1.R1084
5'-most EST	g2317408
Method	BLASTX
NCBI GI	g4455158
BLAST score	1093
E value	1.0e-120
Match length	256
% identity	77
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No.	393092
Contig ID	36564_1.R1084
5'-most EST	uC-osflcyp126c09b1
Method	BLASTX
NCBI GI	g5262154
BLAST score	159
E value	3.0e-10
Match length	43
% identity	72
NCBI Description	(AL080237) putative protein [Arabidopsis thaliana]

Seq. No.	393093
Contig ID	36571_1.R1084
5'-most EST	uC-osflcyp154h09b1
Method	BLASTX
NCBI GI	g3193292
BLAST score	537
E value	8.0e-55
Match length	181
% identity	55
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	393094
Contig ID	36588_1.R1084
5'-most EST	g2311801
Method	BLASTN
NCBI GI	g1184321
BLAST score	59
E value	3.0e-24
Match length	82
% identity	94
NCBI Description	Cloning vector pCRSCRIPT SK[+], complete sequence

Seq. No.	393095
Contig ID	36604_1.R1084
5'-most EST	uC-osflM202031a02a1

Seq. No.	393096
Contig ID	36630_1.R1084
5'-most EST	uC-osflcyp140c06a1
Method	BLASTX
NCBI GI	g3252807
BLAST score	485
E value	1.0e-48
Match length	213
% identity	51
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393097
Contig ID	36633_1.R1084
5'-most EST	uC-osroM202013e02b1
Method	BLASTX
NCBI GI	g3335378
BLAST score	278
E value	4.0e-24
Match length	74
% identity	74
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	393098
Contig ID	36640_1.R1084
5'-most EST	uC-osflcyp140e11a1

Seq. No.	393099
Contig ID	36641_1.R1084
5'-most EST	uC-osroM202020e01a1

Seq. No.	393100
Contig ID	36648_1.R1084
5'-most EST	g2798840
Method	BLASTN
NCBI GI	g58067
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP

Seq. No.	393101
Contig ID	36650_1.R1084
5'-most EST	uC-osflcyp140g09a1

Seq. No.	393102
Contig ID	36654_1.R1084
5'-most EST	g2317568
Method	BLASTX
NCBI GI	g3687240
BLAST score	143
E value	1.0e-08
Match length	84
% identity	25
NCBI Description	(AC005169) extensin-like protein [Arabidopsis thaliana]

Seq. No.	393103
Contig ID	36661_1.R1084
5'-most EST	g3762777
Method	BLASTX
NCBI GI	g3335359
BLAST score	246
E value	9.0e-21
Match length	63
% identity	76
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	393104
Contig ID	36691_1.R1084
5'-most EST	uC-osflcyp131e06a1

Seq. No.	393105
Contig ID	36695_1.R1084
5'-most EST	g3767948

Seq. No.	393106
Contig ID	36697_1.R1084
5'-most EST	uC-osflcyp141g10a1
Method	BLASTX
NCBI GI	g128592
BLAST score	372
E value	2.0e-35
Match length	95
% identity	68
NCBI Description	POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR >gi_82190_pir__S22495 pollen-specific protein precursor - common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen specific protein [Nicotiana tabacum]

Seq. No.	393107
Contig ID	36698_1.R1084
5'-most EST	uC-osflM2020114b11a1

Seq. No.	393108
Contig ID	36703_1.R1084
5'-most EST	g3761067

Seq. No.	393109
Contig ID	36713_1.R1084
5'-most EST	uC-osflcyp142c06b1
Method	BLASTX
NCBI GI	g3885492
BLAST score	785
E value	6.0e-84
Match length	172
% identity	84
NCBI Description	(AF063865) tapetum specific protein [Zea mays]

Seq. No.	393110
Contig ID	36732_1.R1084
5'-most EST	g2280904
Method	BLASTX

NCBI GI g2245061
BLAST score 329
E value 1.0e-37
Match length 127
% identity 68
NCBI Description (Z97342) Clp proteinase like protein [Arabidopsis thaliana]

Seq. No. 393111
Contig ID 36736_1.R1084
5'-most EST g3768830

Seq. No. 393112
Contig ID 36737_1.R1084
5'-most EST uC-osrocyp012h09b1
Method BLASTX
NCBI GI g4138583
BLAST score 236
E value 2.0e-22
Match length 71
% identity 83
NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No. 393113
Contig ID 36743_1.R1084
5'-most EST uC-osflcyp143f01b1
Method BLASTX
NCBI GI g6018193
BLAST score 326
E value 5.0e-30
Match length 163
% identity 44
NCBI Description (AF114170) nucleotide-binding protein long form [Mus musculus]

Seq. No. 393114
Contig ID 36751_1.R1084
5'-most EST uC-osflcyp143h01b1

Seq. No. 393115
Contig ID 36765_1.R1084
5'-most EST uC-osflM202094g03b1
Method BLASTX
NCBI GI g4539404
BLAST score 376
E value 7.0e-51
Match length 164
% identity 62
NCBI Description (AL049524) putative protein [Arabidopsis thaliana]

Seq. No. 393116
Contig ID 36765_2.R1084
5'-most EST uC-osflM202040a06b1
Method BLASTX
NCBI GI g4539404
BLAST score 126
E value 1.0e-08
Match length 93

% identity	45
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]
Seq. No.	393117
Contig ID	36771_1.R1084
5'-most EST	g3762975
Seq. No.	393118
Contig ID	36775_1.R1084
5'-most EST	g568339
Seq. No.	393119
Contig ID	36792_1.R1084
5'-most EST	g3768686
Seq. No.	393120
Contig ID	36795_1.R1084
5'-most EST	g5056018
Seq. No.	393121
Contig ID	36804_1.R1084
5'-most EST	g3761604
Method	BLASTX
NCBI GI	g5579090
BLAST score	262
E value	1.0e-22
Match length	116
% identity	46
NCBI Description	(AF099186) EH domain-containing protein EHD1 [Mus musculus]
Seq. No.	393122
Contig ID	36805_1.R1084
5'-most EST	uC-osflcyp151e01a1
Seq. No.	393123
Contig ID	36810_1.R1084
5'-most EST	g3766799
Method	BLASTX
NCBI GI	g1155255
BLAST score	195
E value	9.0e-15
Match length	60
% identity	58
NCBI Description	(U39228) beta-glucosidase [Prunus avium]
Seq. No.	393124
Contig ID	36848_1.R1084
5'-most EST	uC-osflcyp152c11a1
Method	BLASTX
NCBI GI	g2501555
BLAST score	335
E value	5.0e-31
Match length	110
% identity	63
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	393125
Contig ID	36849_1.R1084
5'-most EST	uC-osflcyp152c12a1
Method	BLASTX
NCBI GI	g5734639
BLAST score	656
E value	2.0e-68
Match length	288
% identity	81
NCBI Description	(AP000391) ESTs AU056036(S20239),C72753(E2173), AU056035(S20239) correspond to a region of the predicted gene.; Similar to putative cytochrome P-450 (AC003680) [Oryza sativa]

Seq. No.	393126
Contig ID	36852_1.R1084
5'-most EST	uC-osflcyp152d05a1

Seq. No.	393127
Contig ID	36879_1.R1084
5'-most EST	uC-osflcyp152h06a1
Method	BLASTX
NCBI GI	g4490325
BLAST score	274
E value	7.0e-24
Match length	87
% identity	56
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393128
Contig ID	36890_1.R1084
5'-most EST	uC-osflcyp153b01a1
Method	BLASTX
NCBI GI	g1169736
BLAST score	163
E value	4.0e-11
Match length	85
% identity	44
NCBI Description	FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN) >gi_1083778_pir__A54837 rapamycin/FKBP12 target 1 - rat >gi_511229 (U11681) rapamycin and FKBP12 target-1 protein [Rattus norvegicus] >gi_561858 (L37085) rapamycin target [Rattus norvegicus]

Seq. No.	393129
Contig ID	36892_1.R1084
5'-most EST	uC-osflcyp153b03a1

Seq. No.	393130
Contig ID	36895_1.R1084
5'-most EST	g4715581

Seq. No.	393131
Contig ID	36901_1.R1084
5'-most EST	g4714846
Method	BLASTX
NCBI GI	g3142291

BLAST score	256
E value	2.0e-21
Match length	126
% identity	44
NCBI Description	(AC002411) Contains similarity to adenylate cyclase gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes from this gene. [Arabidopsis thaliana]

Seq. No.	393132
Contig ID	36904_1.R1084
5'-most EST	uC-osflcyp153c11a1
Method	BLASTX
NCBI GI	g4103324
BLAST score	444
E value	2.0e-62
Match length	142
% identity	81
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No.	393133
Contig ID	36919_1.R1084
5'-most EST	uC-osflcyp153f07a1

Seq. No.	393134
Contig ID	36924_1.R1084
5'-most EST	uC-osflM202063e10a1

Seq. No.	393135
Contig ID	36935_1.R1084
5'-most EST	uC-osflcyp153h10a1
Method	BLASTX
NCBI GI	g5902359
BLAST score	255
E value	2.0e-30
Match length	98
% identity	76
NCBI Description	(AC009322) Heat-shock protein [Arabidopsis thaliana]

Seq. No.	393136
Contig ID	36943_1.R1084
5'-most EST	uC-osflM202134c05a1
Method	BLASTX
NCBI GI	g4580455
BLAST score	178
E value	9.0e-13
Match length	58
% identity	69
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	393137
Contig ID	36950_1.R1084
5'-most EST	uC-osflcyp154b03a1
Method	BLASTX
NCBI GI	g2464901
BLAST score	150
E value	2.0e-09

Match length 48
% identity 58
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 393138
Contig ID 36971_1.R1084
5'-most EST uC-osflcyp154e04a1
Method BLASTX
NCBI GI g2494165
BLAST score 220
E value 1.0e-17
Match length 54
% identity 76
NCBI Description DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP]) >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis thaliana]

Seq. No. 393139
Contig ID 36976_1.R1084
5'-most EST uC-osflcyp154f02a1

Seq. No. 393140
Contig ID 36978_1.R1084
5'-most EST uC-osflM202086c06a1

Seq. No. 393141
Contig ID 36991_1.R1084
5'-most EST uC-osflM202056a11a1

Seq. No. 393142
Contig ID 36992_1.R1084
5'-most EST uC-osflcyp154h03a1

Seq. No. 393143
Contig ID 36995_1.R1084
5'-most EST uC-osflcyp154h07a1

Seq. No. 393144
Contig ID 37007_1.R1084
5'-most EST g2798119
Method BLASTX
NCBI GI g4079811
BLAST score 230
E value 1.0e-18
Match length 214
% identity 3
NCBI Description (AF071173) Herc2 [Mus musculus]

Seq. No. 393145
Contig ID 37014_1.R1084
5'-most EST uC-osflcyp155e05b1
Method BLASTX
NCBI GI g4836948
BLAST score 361
E value 3.0e-34
Match length 104

% identity	80
NCBI Description	(AC006085) Similar to human CGI-33 protein [Arabidopsis thaliana]

Seq. No.	393146
Contig ID	37015_1.R1084
5'-most EST	uC-osflcyp155e06b1

Seq. No.	393147
Contig ID	37029_1.R1084
5'-most EST	g3768781
Method	BLASTN
NCBI GI	g5714761
BLAST score	50
E value	6.0e-19
Match length	141
% identity	61
NCBI Description	Oryza sativa subsp. indica serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete cds

Seq. No.	393148
Contig ID	37031_1.R1084
5'-most EST	g3759692

Seq. No.	393149
Contig ID	37033_1.R1084
5'-most EST	g3768769

Seq. No.	393150
Contig ID	37034_1.R1084
5'-most EST	uC-osroM202019b10a1

Seq. No.	393151
Contig ID	37045_1.R1084
5'-most EST	uC-osflcyp156c07a1
Method	BLASTX
NCBI GI	g5679844
BLAST score	473
E value	2.0e-47
Match length	88
% identity	97
NCBI Description	(AJ243961) l1332.8 [Oryza sativa]

Seq. No.	393152
Contig ID	37049_1.R1084
5'-most EST	uC-osflcyp156d03a1
Method	BLASTX
NCBI GI	g4531442
BLAST score	311
E value	3.0e-28
Match length	98
% identity	65
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393153
Contig ID	37062_1.R1084

5'-most EST g3761479
Method BLASTX
NCBI GI g729944
BLAST score 355
E value 5.0e-34
Match length 102
% identity 63
NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524 major allergen mI protein - maize >gi_293902 (L14271) Zea mI [Zea mays]

Seq. No. 393154
Contig ID 37070_1.R1084
5'-most EST uC-osflcyp156h03a1

Seq. No. 393155
Contig ID 37087_1.R1084
5'-most EST g4715014

Seq. No. 393156
Contig ID 37088_1.R1084
5'-most EST g2798715

Seq. No. 393157
Contig ID 37096_1.R1084
5'-most EST g5607410

Seq. No. 393158
Contig ID 37107_1.R1084
5'-most EST uC-osflM202069e10a1
Method BLASTX
NCBI GI g1362162
BLAST score 312
E value 2.0e-28
Match length 98
% identity 55
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 393159
Contig ID 37118_1.R1084
5'-most EST uC-osflcyp157f04a1

Seq. No. 393160
Contig ID 37122_1.R1084
5'-most EST uC-osflcyp157f09a1
Method BLASTX
NCBI GI g3915866
BLAST score 342
E value 6.0e-32
Match length 92
% identity 73
NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

Seq. No. 393161

Contig ID 37124_1.R1084
5'-most EST uC-osflcyp157f11a1

Seq. No. 393162
Contig ID 37125_1.R1084
5'-most EST g2317441
Method BLASTX
NCBI GI g3256035
BLAST score 180
E value 2.0e-21
Match length 122
% identity 45
NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No. 393163
Contig ID 37134_1.R1084
5'-most EST g3762403
Method BLASTX
NCBI GI g2501356
BLAST score 715
E value 2.0e-75
Match length 180
% identity 74
NCBI Description TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK) >gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor [Solanum tuberosum]

Seq. No. 393164
Contig ID 37140_1.R1084
5'-most EST uC-osflcyp158a11a1

Seq. No. 393165
Contig ID 37160_1.R1084
5'-most EST uC-osflcyp158e02a1

Seq. No. 393166
Contig ID 37180_1.R1084
5'-most EST g4716642

Seq. No. 393167
Contig ID 37195_1.R1084
5'-most EST g3762003

Seq. No. 393168
Contig ID 37204_1.R1084
5'-most EST g4714681
Method BLASTX
NCBI GI g5262760
BLAST score 283
E value 6.0e-25
Match length 61
% identity 90
NCBI Description (AL080283) Beta-COP-like protein [Arabidopsis thaliana]

Seq. No. 393169
Contig ID 37206_1.R1084

5'-most EST	uC-osflcyp041g03b1
Method	BLASTX
NCBI GI	g3269287
BLAST score	235
E value	2.0e-19
Match length	73
% identity	58
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	393170
Contig ID	37249_1.R1084
5'-most EST	uC-osflcyp161c01a1
Method	BLASTX
NCBI GI	g5042412
BLAST score	264
E value	1.0e-22
Match length	114
% identity	49
NCBI Description	(AC006193) Similar to glucan endo-1,3-beta-glucosidase precursor [Arabidopsis thaliana]

Seq. No.	393171
Contig ID	37264_1.R1084
5'-most EST	uC-osflcyp003f02b1

Seq. No.	393172
Contig ID	37273_1.R1084
5'-most EST	uC-osflM202085h03a1

Seq. No.	393173
Contig ID	37277_1.R1084
5'-most EST	g5003235

Seq. No.	393174
Contig ID	37281_1.R1084
5'-most EST	uC-osflcyp161h10a1
Method	BLASTX
NCBI GI	g4006890
BLAST score	204
E value	2.0e-27
Match length	95
% identity	67
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	393175
Contig ID	37294_1.R1084
5'-most EST	uC-osflcyp162b03a1

Seq. No.	393176
Contig ID	37304_1.R1084
5'-most EST	uC-osroM202039e07a1
Method	BLASTX
NCBI GI	g6017109
BLAST score	192
E value	3.0e-14
Match length	45

% identity	73
NCBI Description	(AC009895) hypothetical protein [Arabidopsis thaliana]
Seq. No.	393177
Contig ID	37336_1.R1084
5'-most EST	uC-osflcyp078e07a1
Method	BLASTX
NCBI GI	g4097569
BLAST score	123
E value	1.0e-11
Match length	91
% identity	54
NCBI Description	(U64915) GMFP4 [Glycine max]
Seq. No.	393178
Contig ID	37339_1.R1084
5'-most EST	uC-osflcyp078e11a1
Seq. No.	393179
Contig ID	37355_1.R1084
5'-most EST	uC-osflM202070e02a1
Seq. No.	393180
Contig ID	37356_1.R1084
5'-most EST	g4715873
Method	BLASTX
NCBI GI	g3929358
BLAST score	129
E value	1.0e-13
Match length	45
% identity	73
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1666177_emb_CAA70326_ (Y09109) NADH dehydrogenase [Nicotiana tabacum]
Seq. No.	393181
Contig ID	37364_1.R1084
5'-most EST	uC-osflcyp079b05a1
Seq. No.	393182
Contig ID	37382_1.R1084
5'-most EST	uC-osflcyp080b12a1
Method	BLASTX
NCBI GI	g1531758
BLAST score	510
E value	3.0e-93
Match length	222
% identity	78
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.	393183
Contig ID	37383_1.R1084
5'-most EST	uC-osroM202019c02b1
Method	BLASTX
NCBI GI	g2911042
BLAST score	441

E value	1.0e-43
Match length	100
% identity	84
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	393184
Contig ID	37425_1.R1084
5'-most EST	g5003208
Method	BLASTX
NCBI GI	g4262174
BLAST score	197
E value	5.0e-15
Match length	51
% identity	71
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	393185
Contig ID	37430_1.R1084
5'-most EST	uC-osflcyp136a12a1
Method	BLASTX
NCBI GI	g4753658
BLAST score	182
E value	3.0e-13
Match length	118
% identity	40
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	393186
Contig ID	37437_1.R1084
5'-most EST	uC-osrocyp017a08b1

Seq. No.	393187
Contig ID	37445_1.R1084
5'-most EST	g5667398
Method	BLASTX
NCBI GI	g2961345
BLAST score	416
E value	2.0e-40
Match length	94
% identity	80
NCBI Description	(AL022140) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393188
Contig ID	37453_1.R1084
5'-most EST	uC-osroM202040b07b1

Seq. No.	393189
Contig ID	37482_1.R1084
5'-most EST	g3760059

Seq. No.	393190
Contig ID	37488_1.R1084
5'-most EST	uC-osflcyp082c10a1

Seq. No.	393191
Contig ID	37493_1.R1084

5'-most EST	uC-osflcyp082d05a1
Method	BLASTX
NCBI GI	g4586117
BLAST score	190
E value	5.0e-14
Match length	87
% identity	53
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	393192
Contig ID	37499_1.R1084
5'-most EST	uC-osflM202077b01b1
Method	BLASTX
NCBI GI	g3087888
BLAST score	322
E value	2.0e-29
Match length	113
% identity	58
NCBI Description	(X94302) hexokinase [Solanum tuberosum]

Seq. No.	393193
Contig ID	37500_1.R1084
5'-most EST	uC-osflcyp082e02a1

Seq. No.	393194
Contig ID	37525_1.R1084
5'-most EST	uC-osroM202025c05a1

Seq. No.	393195
Contig ID	37542_1.R1084
5'-most EST	g3763802

Seq. No.	393196
Contig ID	37549_1.R1084
5'-most EST	g3762849

Seq. No.	393197
Contig ID	37551_1.R1084
5'-most EST	uC-osflM2020118a10a1

Seq. No.	393198
Contig ID	37556_1.R1084
5'-most EST	g5038543

Seq. No.	393199
Contig ID	37565_1.R1084
5'-most EST	uC-osflM2020114g04a1
Method	BLASTN
NCBI GI	g5852170
BLAST score	33
E value	8.0e-09
Match length	67
% identity	96
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No.	393200

Contig ID 37566_1.R1084
5'-most EST uC-osrocyp034b08a1

Seq. No. 393201
Contig ID 37574_1.R1084
5'-most EST uC-osflcyp149c01a1

Seq. No. 393202
Contig ID 37591_1.R1084
5'-most EST g4714778
Method BLASTX
NCBI GI g3298541
BLAST score 227
E value 2.0e-18
Match length 158
% identity 37
NCBI Description (AC004681) putative cellulose synthase [Arabidopsis thaliana]

Seq. No. 393203
Contig ID 37593_1.R1084
5'-most EST uC-osflcyp086b11a1

Seq. No. 393204
Contig ID 37597_1.R1084
5'-most EST g3761371
Method BLASTX
NCBI GI g1550740
BLAST score 519
E value 1.0e-52
Match length 129
% identity 75
NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]

Seq. No. 393205
Contig ID 37623_1.R1084
5'-most EST uC-osflcyp086g01a1

Seq. No. 393206
Contig ID 37628_1.R1084
5'-most EST uC-osflcyp086g06a1
Method BLASTX
NCBI GI g3738338
BLAST score 143
E value 6.0e-11
Match length 99
% identity 45
NCBI Description (AC005170) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 393207
Contig ID 37630_1.R1084
5'-most EST g3768574

Seq. No. 393208
Contig ID 37635_1.R1084
5'-most EST uC-osflM202085a07a1

Seq. No. 393209
Contig ID 37641_1.R1084
5'-most EST uC-osflcyp088a02a1

Seq. No. 393210
Contig ID 37660_1.R1084
5'-most EST uC-osflcyp088e01a1

Seq. No. 393211
Contig ID 37667_1.R1084
5'-most EST uC-osflcyp088f02a1

Seq. No. 393212
Contig ID 37677_1.R1084
5'-most EST uC-osflcyp088g04a1

Seq. No. 393213
Contig ID 37681_1.R1084
5'-most EST uC-osflcyp088g10a1

Seq. No. 393214
Contig ID 37682_1.R1084
5'-most EST uC-osflcyp088g11a1

Seq. No. 393215
Contig ID 37688_1.R1084
5'-most EST uC-osflcyp088h07a1

Seq. No. 393216
Contig ID 37695_1.R1084
5'-most EST uC-osrocyp015h05a1
Method BLASTX
NCBI GI g5042155
BLAST score 176
E value 1.0e-12
Match length 54
% identity 63
NCBI Description (AL078620) putative protein [Arabidopsis thaliana]

Seq. No. 393217
Contig ID 37699_1.R1084
5'-most EST uC-osflcyp089b02a1
Method BLASTX
NCBI GI g4218144
BLAST score 146
E value 4.0e-17
Match length 92
% identity 45
NCBI Description (AJ132398) glutathione transferase, GST 10b [Arabidopsis thaliana]

Seq. No. 393218
Contig ID 37700_1.R1084
5'-most EST g3761705

Seq. No. 393219

Contig ID 37707_1.R1084
5'-most EST uC-osflcyp087h12a1

Seq. No. 393220
Contig ID 37710_1.R1084
5'-most EST g3768430

Seq. No. 393221
Contig ID 37716_1.R1084
5'-most EST g4716108
Method BLASTX
NCBI GI g1055224
BLAST score 177
E value 3.0e-12
Match length 180
% identity 11
NCBI Description (U20977) cellular nucleic acid binding protein [Xenopus laevis]

Seq. No. 393222
Contig ID 37717_1.R1084
5'-most EST uC-osroM202020d11a1
Method BLASTX
NCBI GI g3212854
BLAST score 165
E value 6.0e-11
Match length 142
% identity 37
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 393223
Contig ID 37734_1.R1084
5'-most EST g4880006

Seq. No. 393224
Contig ID 37748_1.R1084
5'-most EST g2312101
Method BLASTX
NCBI GI g4587519
BLAST score 478
E value 1.0e-50
Match length 146
% identity 73
NCBI Description (AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No. 393225
Contig ID 37761_1.R1084
5'-most EST g2798738

Seq. No. 393226
Contig ID 37780_1.R1084
5'-most EST g3761345

Seq. No. 393227

Contig ID 37783_1.R1084
5'-most EST g3768918

Seq. No. 393228
Contig ID 37788_1.R1084
5'-most EST uC-osflcyp091f10a1
Method BLASTX
NCBI GI g4490706
BLAST score 168
E value 1.0e-14
Match length 58
% identity 59
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No. 393229
Contig ID 37789_1.R1084
5'-most EST g4715883

Seq. No. 393230
Contig ID 37798_1.R1084
5'-most EST uC-osflcyp091h01a1

Seq. No. 393231
Contig ID 37804_1.R1084
5'-most EST g5455390
Method BLASTN
NCBI GI g3172047
BLAST score 63
E value 1.0e-26
Match length 119
% identity 88
NCBI Description Oryza sativa gene for starch debranching enzyme, complete cds

Seq. No. 393232
Contig ID 37846_1.R1084
5'-most EST g5607632

Seq. No. 393233
Contig ID 37857_1.R1084
5'-most EST uC-osroM202019f10a1

Seq. No. 393234
Contig ID 37861_1.R1084
5'-most EST g5607404

Seq. No. 393235
Contig ID 37871_1.R1084
5'-most EST g701018
Method BLASTX
NCBI GI g3298540
BLAST score 225
E value 2.0e-18
Match length 58
% identity 67
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 393236
Contig ID 37874_1.R1084
5'-most EST g3762858
Method BLASTX
NCBI GI g4455232
BLAST score 388
E value 3.0e-37
Match length 172
% identity 47
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 393237
Contig ID 37884_1.R1084
5'-most EST uC-osroM202039a10a1

Seq. No. 393238
Contig ID 37922_1.R1084
5'-most EST uC-osflcyp097f01b1

Seq. No. 393239
Contig ID 37925_2.R1084
5'-most EST g571676

Seq. No. 393240
Contig ID 37925_3.R1084
5'-most EST g2309913

Seq. No. 393241
Contig ID 37939_1.R1084
5'-most EST g3763792

Seq. No. 393242
Contig ID 37940_1.R1084
5'-most EST g4714687

Seq. No. 393243
Contig ID 37950_1.R1084
5'-most EST uC-osflM202031a05a1

Seq. No. 393244
Contig ID 37961_1.R1084
5'-most EST uC-osflcyp098g01a1

Seq. No. 393245
Contig ID 37990_1.R1084
5'-most EST g5056153
Method BLASTX
NCBI GI g4586109
BLAST score 234
E value 3.0e-19
Match length 72
% identity 64
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 393246
Contig ID 37991_1.R1084
5'-most EST g3106986

Seq. No. 393247
Contig ID 37997_1.R1084
5'-most EST uC-osflcyp099e12a1

Seq. No. 393248
Contig ID 37999_1.R1084
5'-most EST uC-osflcyp099f03a1

Seq. No. 393249
Contig ID 38009_1.R1084
5'-most EST g3761866

Seq. No. 393250
Contig ID 38010_1.R1084
5'-most EST g4715640
Method BLASTX
NCBI GI g3915039
BLAST score 248
E value 3.0e-35
Match length 141
% identity 50
NCBI Description SUGAR CARRIER PROTEIN C >gi_169718 (L08196) sugar carrier protein [Ricinus communis]

Seq. No. 393251
Contig ID 38012_1.R1084
5'-most EST g3759658
Method BLASTN
NCBI GI g4097947
BLAST score 58
E value 2.0e-23
Match length 66
% identity 97
NCBI Description Oryza sativa beta-1,3-glucanase precursor (Gns9) gene, complete cds

Seq. No. 393252
Contig ID 38014_1.R1084
5'-most EST uC-osflcyp172d01a1
Method BLASTX
NCBI GI g1346109
BLAST score 533
E value 3.0e-54
Match length 150
% identity 28
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231) RWD [Oryza sativa]

Seq. No. 393253
Contig ID 38021_1.R1084
5'-most EST uC-osflcyp101a12a1

Seq. No. 393254
Contig ID 38030_1.R1084
5'-most EST g3761303

Seq. No. 393255
Contig ID 38036_1.R1084
5'-most EST uC-osflcyp101c05a1

Seq. No. 393256
Contig ID 38044_1.R1084
5'-most EST g3768792

Seq. No. 393257
Contig ID 38062_1.R1084
5'-most EST g4714963

Seq. No. 393258
Contig ID 38063_1.R1084
5'-most EST uC-osflcyp101g11a1

Seq. No. 393259
Contig ID 38070_1.R1084
5'-most EST uC-osroM202029d02b1

Seq. No. 393260
Contig ID 38075_1.R1084
5'-most EST uC-osroM202003b04a2

Seq. No. 393261
Contig ID 38077_1.R1084
5'-most EST g3762209

Seq. No. 393262
Contig ID 38085_1.R1084
5'-most EST g3762901

Seq. No. 393263
Contig ID 38098_1.R1084
5'-most EST uC-osrocyp014c11b1

Seq. No. 393264
Contig ID 38125_1.R1084
5'-most EST g5003875
Method BLASTX
NCBI GI g3402751
BLAST score 341
E value 8.0e-32
Match length 112
% identity 62
NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 393265
Contig ID 38172_1.R1084
5'-most EST uC-osflcyp109a09a1

Seq. No. 393266
Contig ID 38189_1.R1084
5'-most EST uC-osflcyp109c06a1

Seq. No. 393267

Contig ID	38202_1.R1084
5'-most EST	uC-osroM202029d12a1
Method	BLASTX
NCBI GI	g5441892
BLAST score	227
E value	1.0e-18
Match length	43
% identity	100
NCBI Description	(AP000367) ESTs C96653(C10531),C96654(C10531),C28571(C61641) correspond to a region of the predicted gene.; Similar to citrate synthetase. (AC004521) [Oryza sativa]

Seq. No.	393268
Contig ID	38208_1.R1084
5'-most EST	uC-osflcyp109e12a1

Seq. No.	393269
Contig ID	38215_1.R1084
5'-most EST	g4716899
Method	BLASTX
NCBI GI	g2497540
BLAST score	436
E value	5.0e-43
Match length	108
% identity	79
NCBI Description	PYRUVATE KINASE ISOZYME G, CHLOROPLAST

Seq. No.	393270
Contig ID	38222_1.R1084
5'-most EST	g2317593

Seq. No.	393271
Contig ID	38227_1.R1084
5'-most EST	g2800216
Method	BLASTX
NCBI GI	g1353163
BLAST score	125
E value	9.0e-09
Match length	61
% identity	54
NCBI Description	HYPOTHETICAL 19.6 KD PROTEIN C23G10.2 IN CHROMOSOME III PRECURSOR >gi_1055071 (U39851) C23G10.2 gene product [Caenorhabditis elegans]

Seq. No.	393272
Contig ID	38242_1.R1084
5'-most EST	uC-osflcyp110a07a1

Seq. No.	393273
Contig ID	38243_1.R1084
5'-most EST	uC-osflcyp110a08a1

Seq. No.	393274
Contig ID	38247_1.R1084
5'-most EST	uC-osflcyp110b07a1
Method	BLASTX

NCBI GI g2618699
BLAST score 217
E value 1.0e-20
Match length 165
% identity 34
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 393275
Contig ID 38249_1.R1084
5'-most EST g3763676

Seq. No. 393276
Contig ID 38270_1.R1084
5'-most EST g3106958

Seq. No. 393277
Contig ID 38316_1.R1084
5'-most EST uC-osflcyp172b09a1
Method BLASTX
NCBI GI g4432864
BLAST score 282
E value 6.0e-25
Match length 81
% identity 70
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393278
Contig ID 38323_1.R1084
5'-most EST uC-osflcyp111b05a1

Seq. No. 393279
Contig ID 38333_1.R1084
5'-most EST g5056008
Method BLASTX
NCBI GI g2239262
BLAST score 481
E value 4.0e-48
Match length 170
% identity 54
NCBI Description (Y13285) pectin methylesterase-like protein [Zea mays]

Seq. No. 393280
Contig ID 38368_1.R1084
5'-most EST g5038799
Method BLASTX
NCBI GI g5360996
BLAST score 439
E value 1.0e-43
Match length 115
% identity 70
NCBI Description (AF134116) APETALA2 protein homolog HAP2 [Hyacinthus orientalis]

Seq. No. 393281
Contig ID 38382_1.R1084
5'-most EST g3107651
Method BLASTX

NCBI GI g3402817
BLAST score 186
E value 2.0e-13
Match length 48
% identity 77
NCBI Description (AJ007829) lacZ' [Cloning vector pGreen]

Seq. No. 393282
Contig ID 38389_1.R1084
5'-most EST uC-osflcyp014a02b1

Seq. No. 393283
Contig ID 38397_1.R1084
5'-most EST g3061000
Method BLASTX
NCBI GI g4584429
BLAST score 261
E value 1.0e-22
Match length 103
% identity 51
NCBI Description (AJ237751) aquaglyceroporin [Nicotiana tabacum]

Seq. No. 393284
Contig ID 38431_1.R1084
5'-most EST g427781

Seq. No. 393285
Contig ID 38438_1.R1084
5'-most EST uC-osflM202049f11b1
Method BLASTX
NCBI GI g4914683
BLAST score 207
E value 5.0e-16
Match length 181
% identity 30
NCBI Description (AF067728) transactivating protein BRIDGE [Rattus norvegicus]

Seq. No. 393286
Contig ID 38467_1.R1084
5'-most EST uC-osflcyp099a04b1

Seq. No. 393287
Contig ID 38475_1.R1084
5'-most EST uC-osflcyp099c01b1
Method BLASTX
NCBI GI g4874284
BLAST score 98
E value 1.0e-07
Match length 93
% identity 31
NCBI Description (AC007212) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 393288
Contig ID 38495_1.R1084
5'-most EST uC-osrocyp027e03a1

Seq. No.	393289
Contig ID	38512_1.R1084
5'-most EST	uC-osflM202063d02a1
Method	BLASTX
NCBI GI	g2982469
BLAST score	178
E value	2.0e-12
Match length	44
% identity	77
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	393290
Contig ID	38524_1.R1084
5'-most EST	uC-osflcyp115e01a1

Seq. No.	393291
Contig ID	38533_1.R1084
5'-most EST	uC-osflcyp104a12a1
Method	BLASTX
NCBI GI	g4539324
BLAST score	147
E value	4.0e-09
Match length	53
% identity	57
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	393292
Contig ID	38542_1.R1084
5'-most EST	uC-osflcyp104b04a1

Seq. No.	393293
Contig ID	38545_1.R1084
5'-most EST	uC-osflcyp104b11a1

Seq. No.	393294
Contig ID	38552_1.R1084
5'-most EST	g3761189
Method	BLASTX
NCBI GI	g4567229
BLAST score	164
E value	5.0e-12
Match length	91
% identity	43
NCBI Description	(AC007119) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	393295
Contig ID	38578_1.R1084
5'-most EST	g2798386
Method	BLASTX
NCBI GI	g4914402
BLAST score	267
E value	3.0e-24
Match length	84
% identity	70
NCBI Description	(AL050352) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393296
Contig ID 38583_1.R1084
5'-most EST g3759680

Seq. No. 393297
Contig ID 38589_1.R1084
5'-most EST g3767761

Seq. No. 393298
Contig ID 38597_1.R1084
5'-most EST g5038614

Seq. No. 393299
Contig ID 38604_1.R1084
5'-most EST uC-osflcyp105g09a1

Seq. No. 393300
Contig ID 38635_1.R1084
5'-most EST g3760285

Seq. No. 393301
Contig ID 38653_1.R1084
5'-most EST uC-osflcyp134f03a1

Seq. No. 393302
Contig ID 38676_1.R1084
5'-most EST g3767148
Method BLASTN
NCBI GI g5853039
BLAST score 94
E value 5.0e-45
Match length 105
% identity 97
NCBI Description Cloning vector pRS4110, complete sequence

Seq. No. 393303
Contig ID 38680_1.R1084
5'-most EST uC-osroM202025f10a1

Seq. No. 393304
Contig ID 38684_1.R1084
5'-most EST g3106702

Seq. No. 393305
Contig ID 38688_1.R1084
5'-most EST uC-osroM202020f03a1

Seq. No. 393306
Contig ID 38689_1.R1084
5'-most EST uC-osflcyp135b11a1

Seq. No. 393307
Contig ID 38713_1.R1084
5'-most EST uC-osflcyp135e12a1

Seq. No. 393308

Contig ID 38715_1.R1084
5'-most EST uC-osflcyp135f02a1

Seq. No. 393309
Contig ID 38732_1.R1084
5'-most EST uC-osflcyp135h04a1
Method BLASTX
NCBI GI g6094554
BLAST score 664
E value 2.0e-69
Match length 219
% identity 66
NCBI Description (AC010676) putative protein kinase [Arabidopsis thaliana]

Seq. No. 393310
Contig ID 38739_1.R1084
5'-most EST g3760112
Method BLASTX
NCBI GI g4902879
BLAST score 259
E value 1.0e-24
Match length 204
% identity 33
NCBI Description (AJ006943) phosphoribosyl pyrophosphate synthase isozyme 4 [Spinacia oleracea]

Seq. No. 393311
Contig ID 38740_1.R1084
5'-most EST uC-osflcyp136a03a1

Seq. No. 393312
Contig ID 38757_1.R1084
5'-most EST g2317610
Method BLASTX
NCBI GI g1314712
BLAST score 190
E value 3.0e-14
Match length 41
% identity 85
NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No. 393313
Contig ID 38775_1.R1084
5'-most EST uC-osroM202020h02a1

Seq. No. 393314
Contig ID 38778_1.R1084
5'-most EST g5667611
Method BLASTX
NCBI GI g5441889
BLAST score 163
E value 6.0e-11
Match length 67
% identity 46
NCBI Description (AP000367) Similar to SEC7 protein, Saccharomyces cerevisiae, PIR2:S49764; Contains Immunoglobulins and major

histocompatibility complex proteins signature. (AL022604)
[Oryza sativa]

Seq. No.	393315
Contig ID	38782_1.R1084
5'-most EST	uC-osflcyp136f05a1
Method	BLASTN
NCBI GI	g6069643
BLAST score	374
E value	0.0e+00
Match length	469
% identity	79
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0514G12

Seq. No.	393316
Contig ID	38785_2.R1084
5'-most EST	uC-osflcyp136f10a1

Seq. No.	393317
Contig ID	38785_3.R1084
5'-most EST	g2312409

Seq. No.	393318
Contig ID	38799_1.R1084
5'-most EST	g3761546

Seq. No.	393319
Contig ID	38812_1.R1084
5'-most EST	uC-osflcyp162c10a1

Seq. No.	393320
Contig ID	38815_1.R1084
5'-most EST	uC-osflcyp162d01a1

Seq. No.	393321
Contig ID	38834_1.R1084
5'-most EST	uC-osflcyp162f03a1
Method	BLASTX
NCBI GI	g5499713
BLAST score	360
E value	4.0e-34
Match length	124
% identity	60
NCBI Description	(U78762) receptor-like kinase ARK1AS [Triticum aestivum]

Seq. No.	393322
Contig ID	38850_1.R1084
5'-most EST	uC-osflcyp162h04a1

Seq. No.	393323
Contig ID	38861_1.R1084
5'-most EST	g5003294
Method	BLASTX
NCBI GI	g2914703
BLAST score	407
E value	2.0e-39
Match length	136

% identity	57
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	393324
Contig ID	38868_1.R1084
5'-most EST	uC-osflcyp168b05a1
Method	BLASTX
NCBI GI	g3549652
BLAST score	340
E value	1.0e-31
Match length	74
% identity	91
NCBI Description	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]

Seq. No.	393325
Contig ID	38871_1.R1084
5'-most EST	uC-osflcyp168b11a1
Method	BLASTX
NCBI GI	g4850369
BLAST score	240
E value	5.0e-20
Match length	72
% identity	65
NCBI Description	(AB027151) threonine synthase [Arabidopsis thaliana] >gi_4914408_emb_CAB43659.1_ (AL050352) threonine synthase [Arabidopsis thaliana]

Seq. No.	393326
Contig ID	38872_1.R1084
5'-most EST	uC-osflcyp168b12a1
Method	BLASTX
NCBI GI	g2924509
BLAST score	276
E value	5.0e-24
Match length	181
% identity	39
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	393327
Contig ID	38900_1.R1084
5'-most EST	g4714149
Method	BLASTX
NCBI GI	g2341033
BLAST score	268
E value	2.0e-23
Match length	78
% identity	64
NCBI Description	(AC000104) Similar to Babesia aldo-keto reductase (gb_M93122). [Arabidopsis thaliana]

Seq. No.	393328
Contig ID	38905_1.R1084
5'-most EST	uC-osflcyp172h10a1
Method	BLASTX
NCBI GI	g4895232

BLAST score	245
E value	8.0e-21
Match length	60
% identity	72
NCBI Description	(AC007660) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393329
Contig ID	38915_1.R1084
5'-most EST	uC-osflcyp168h11a1

Seq. No.	393330
Contig ID	38949_1.R1084
5'-most EST	g3767494
Method	BLASTX
NCBI GI	g1362103
BLAST score	478
E value	9.0e-48
Match length	161
% identity	58
NCBI Description	ubiquitin conjugating enzyme - tomato >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating enzyme [Lycopersicon esculentum]

Seq. No.	393331
Contig ID	38965_1.R1084
5'-most EST	uC-osflcyp169g04b1
Method	BLASTX
NCBI GI	g2459411
BLAST score	136
E value	7.0e-13
Match length	174
% identity	33
NCBI Description	(AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393332
Contig ID	38967_1.R1084
5'-most EST	g3767721

Seq. No.	393333
Contig ID	38974_1.R1084
5'-most EST	uC-osroM202038h11b1
Method	BLASTX
NCBI GI	g5734741
BLAST score	178
E value	1.0e-12
Match length	70
% identity	54
NCBI Description	(AC007651) Similar to Ubiquitin Conjugating Enzyme [Arabidopsis thaliana]

Seq. No.	393334
Contig ID	38988_1.R1084
5'-most EST	uC-osflcyp170c04a1

Seq. No.	393335
Contig ID	38989_1.R1084
5'-most EST	uC-osflcyp170c05a1

Seq. No.	393336
Contig ID	39000_1.R1084
5'-most EST	uC-osflcyp009c07b1
Method	BLASTX
NCBI GI	g4688621
BLAST score	760
E value	1.0e-80
Match length	215
% identity	77
NCBI Description	(AJ237848) hypothetical protein [Brassica napus]

Seq. No.	393337
Contig ID	39022_1.R1084
5'-most EST	g5003239

Seq. No.	393338
Contig ID	39041_1.R1084
5'-most EST	uC-osflcyp171a05a1
Method	BLASTX
NCBI GI	g4335735
BLAST score	299
E value	9.0e-27
Match length	144
% identity	44
NCBI Description	(AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393339
Contig ID	39042_1.R1084
5'-most EST	uC-osflcyp171a12a1

Seq. No.	393340
Contig ID	39056_1.R1084
5'-most EST	uC-osflcyp171c06a1

Seq. No.	393341
Contig ID	39067_1.R1084
5'-most EST	g4715041
Method	BLASTX
NCBI GI	g2801536
BLAST score	251
E value	3.0e-21
Match length	75
% identity	67
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	393342
Contig ID	39068_1.R1084
5'-most EST	uC-osflcyp171e01a1
Method	BLASTX
NCBI GI	g2435522
BLAST score	207
E value	3.0e-16
Match length	66
% identity	64
NCBI Description	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No.	393343
Contig ID	39084_1.R1084
5'-most EST	uC-osrocyp015a04a1
Method	BLASTX
NCBI GI	g4191782
BLAST score	324
E value	8.0e-30
Match length	93
% identity	62
NCBI Description	(AC005917) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	393344
Contig ID	39086_1.R1084
5'-most EST	uC-osflcyp173a05a1

Seq. No.	393345
Contig ID	39091_1.R1084
5'-most EST	uC-osflcyp171g09a1
Method	BLASTX
NCBI GI	g5830789
BLAST score	262
E value	2.0e-22
Match length	83
% identity	64
NCBI Description	(AL117188) putative protein [Arabidopsis thaliana]

Seq. No.	393346
Contig ID	39095_1.R1084
5'-most EST	uC-osrocyp029h11a1

Seq. No.	393347
Contig ID	39116_1.R1084
5'-most EST	uC-osflcyp172c07a1
Method	BLASTX
NCBI GI	g2191197
BLAST score	347
E value	1.0e-32
Match length	98
% identity	77
NCBI Description	(AF007271) contains similarity to Synechococcus PCC7942 chromosomal region used as basis of neutral siteII recombinational cloning vector (PID:g1174192) [Arabidopsis thaliana]

Seq. No.	393348
Contig ID	39123_1.R1084
5'-most EST	uC-osflM2020118c04a1
Method	BLASTX
NCBI GI	g3378493
BLAST score	252
E value	2.0e-21
Match length	118
% identity	45
NCBI Description	(AJ007579) cysteine proteinase [Ribes nigrum]

Seq. No.	393349

Contig ID 39125_1.R1084
5'-most EST g3462536
Method BLASTX
NCBI GI g4584110
BLAST score 394
E value 7.0e-38
Match length 139
% identity 51
NCBI Description (AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No. 393350
Contig ID 39135_1.R1084
5'-most EST g4716228

Seq. No. 393351
Contig ID 39145_1.R1084
5'-most EST g2799983

Seq. No. 393352
Contig ID 39147_1.R1084
5'-most EST uC-osflcyp172g06a1
Method BLASTX
NCBI GI g2911148
BLAST score 158
E value 1.0e-10
Match length 34
% identity 85
NCBI Description (AB005808) NADP-malic enzyme [Aloe arborescens]

Seq. No. 393353
Contig ID 39152_1.R1084
5'-most EST uC-osrocyp002b11a1

Seq. No. 393354
Contig ID 39157_1.R1084
5'-most EST uC-osflcyp178e06a1
Method BLASTX
NCBI GI g6041808
BLAST score 304
E value 2.0e-27
Match length 88
% identity 61
NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]

Seq. No. 393355
Contig ID 39159_1.R1084
5'-most EST g2796827

Seq. No. 393356
Contig ID 39172_1.R1084
5'-most EST uC-osflcyp173b03a1

Seq. No. 393357
Contig ID 39191_1.R1084
5'-most EST uC-osflcyp173e12a1

Seq. No. 393358

Contig ID 39193_1.R1084
5'-most EST uC-osflcyp178f10a1

Seq. No. 393359
Contig ID 39206_1.R1084
5'-most EST uC-osroM202032b02a1

Seq. No. 393360
Contig ID 39214_1.R1084
5'-most EST uC-osflcyp173f11a1

Seq. No. 393361
Contig ID 39216_1.R1084
5'-most EST uC-osflcyp173g01a1

Seq. No. 393362
Contig ID 39232_1.R1084
5'-most EST uC-osflcyp173h09a1
Method BLASTX
NCBI GI g3738302
BLAST score 332
E value 5.0e-31
Match length 106
% identity 59
NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No. 393363
Contig ID 39248_1.R1084
5'-most EST g2442904
Method BLASTX
NCBI GI g4512325
BLAST score 174
E value 2.0e-20
Match length 85
% identity 57
NCBI Description (AB023619) methyltransferase related protein [Mus musculus]

Seq. No. 393364
Contig ID 39251_1.R1084
5'-most EST g2799034
Method BLASTX
NCBI GI g4678297
BLAST score 252
E value 3.0e-21
Match length 95
% identity 54
NCBI Description (AL049655) protein disulfide-isomerase-like protein [Arabidopsis thaliana]

Seq. No. 393365
Contig ID 39267_1.R1084
5'-most EST uC-osflM2020114g01a1

Seq. No. 393366
Contig ID 39272_1.R1084

5'-most EST	uC-osflcyp174d11a1
Method	BLASTX
NCBI GI	g4874285
BLAST score	290
E value	9.0e-42
Match length	119
% identity	69
NCBI Description	(AC007212) putative phosphatidylinositol/phophatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No.	393367
Contig ID	39279_1.R1084
5'-most EST	g3761182

Seq. No.	393368
Contig ID	39284_1.R1084
5'-most EST	uC-osflcyp174f01a1

Seq. No.	393369
Contig ID	39293_1.R1084
5'-most EST	uC-osflcyp174g04a1

Seq. No.	393370
Contig ID	39307_1.R1084
5'-most EST	g3106853
Method	BLASTX
NCBI GI	g3875708
BLAST score	148
E value	2.0e-09
Match length	143
% identity	5
NCBI Description	(Z35598) Asparagine, Serine and Glycine rich predicted protein [Caenorhabditis elegans] >gi_3880108_emb_CAA86461.1_ (Z46343) Asparagine, Serine and Glycine rich predicted protein [Caenorhabditis elegans]

Seq. No.	393371
Contig ID	39319_1.R1084
5'-most EST	g1631706
Method	BLASTX
NCBI GI	g5915821
BLAST score	600
E value	4.0e-62
Match length	178
% identity	60
NCBI Description	CYTOCHROME P450 77A3 >gi_2739010_gb_AAB94593_ (AF022464) CYP77A3p [Glycine max]

Seq. No.	393372
Contig ID	39325_1.R1084
5'-most EST	g569698
Method	BLASTX
NCBI GI	g4504909
BLAST score	493
E value	2.0e-49
Match length	244
% identity	44

NCBI Description	karyopherin (importin) beta 3 >gi_2102696 (U72761) karyopherin beta 3 [Homo sapiens]

Seq. No.	393373
Contig ID	39344_1.R1084
5'-most EST	uC-osflcyp176g01b1
Method	BLASTX
NCBI GI	g5921647
BLAST score	387
E value	3.0e-37
Match length	120
% identity	62
NCBI Description	(AF155332) flavonoid 3'-hydroxylase [Petunia x hybrida]

Seq. No.	393374
Contig ID	39353_1.R1084
5'-most EST	uC-osflcyp177a01a1

Seq. No.	393375
Contig ID	39361_1.R1084
5'-most EST	uC-osflcyp177b01a1

Seq. No.	393376
Contig ID	39387_1.R1084
5'-most EST	uC-osflcyp179b12a1

Seq. No.	393377
Contig ID	39388_1.R1084
5'-most EST	uC-osroM202030a02a1
Method	BLASTX
NCBI GI	g2440029
BLAST score	254
E value	7.0e-45
Match length	133
% identity	72
NCBI Description	(Y14851) DAL1 protein [Arabidopsis thaliana] >gi_2440031_emb_CAA75115_ (Y14850) DAL1 protein [Arabidopsis thaliana]

Seq. No.	393378
Contig ID	39389_1.R1084
5'-most EST	g3763761

Seq. No.	393379
Contig ID	39441_1.R1084
5'-most EST	uC-osflM202081b03b1
Method	BLASTX
NCBI GI	g1363488
BLAST score	167
E value	2.0e-11
Match length	42
% identity	64
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	393380
Contig ID	39463_1.R1084
5'-most EST	uC-osflcyp178f03a1
Seq. No.	393381
Contig ID	39471_1.R1084
5'-most EST	uC-osflcyp178g04a1
Seq. No.	393382
Contig ID	39477_1.R1084
5'-most EST	uC-osflcyp178g12a1
Seq. No.	393383
Contig ID	39479_1.R1084
5'-most EST	g3763546
Method	BLASTX
NCBI GI	g629688
BLAST score	274
E value	1.0e-23
Match length	111
% identity	56
NCBI Description	dehydroquinase shikimate dehydrogenase - Common tobacco >gi_535771 (L32794) dehydroquinate dehydratase/shikimate dehydrogenase [Nicotiana tabacum]
Seq. No.	393384
Contig ID	39480_1.R1084
5'-most EST	uC-osflcyp178h04a1
Seq. No.	393385
Contig ID	39508_1.R1084
5'-most EST	uC-osflcyp179c03a1
Seq. No.	393386
Contig ID	39569_1.R1084
5'-most EST	uC-osflcyp122f04b1
Seq. No.	393387
Contig ID	39571_1.R1084
5'-most EST	uC-osflM202048f02b1
Method	BLASTX
NCBI GI	g4803931
BLAST score	332
E value	8.0e-31
Match length	125
% identity	57
NCBI Description	(AC006264) unknown protein [Arabidopsis thaliana]
Seq. No.	393388
Contig ID	39583_1.R1084
5'-most EST	g4262660
Seq. No.	393389
Contig ID	39592_1.R1084
5'-most EST	uC-osflM2020116d02a1
Seq. No.	393390

Contig ID 39599_1.R1084
5'-most EST g3107731

Seq. No. 393391
Contig ID 39607_1.R1084
5'-most EST uC-osflcyp129a01a1

Seq. No. 393392
Contig ID 39615_1.R1084
5'-most EST g3762957
Method BLASTX
NCBI GI g2586127
BLAST score 340
E value 1.0e-31
Match length 89
% identity 69
NCBI Description (U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No. 393393
Contig ID 39616_1.R1084
5'-most EST uC-osflcyp130a05a1
Method BLASTX
NCBI GI g3894187
BLAST score 160
E value 2.0e-10
Match length 63
% identity 54
NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393394
Contig ID 39632_1.R1084
5'-most EST uC-osflcyp131g09a1

Seq. No. 393395
Contig ID 39639_1.R1084
5'-most EST uC-osflcyp132e07a1

Seq. No. 393396
Contig ID 39646_1.R1084
5'-most EST uC-osflcyp134d12a1

Seq. No. 393397
Contig ID 39649_1.R1084
5'-most EST uC-osflM202074h06a1
Method BLASTX
NCBI GI g4759280
BLAST score 235
E value 3.0e-19
Match length 56
% identity 79
NCBI Description U5 snRNP-specific protein, 116 kD >gi_434759_dbj_BAA04699_ (D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]

Seq. No. 393398
Contig ID 39678_1.R1084
5'-most EST g3761250

Seq. No. 393399
Contig ID 39689_1.R1084
5'-most EST g5004730

Seq. No. 393400
Contig ID 39700_1.R1084
5'-most EST g3759627
Method BLASTX
NCBI GI g3608495
BLAST score 198
E value 4.0e-15
Match length 74
% identity 59
NCBI Description (AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid division protein FtsZ [Arabidopsis thaliana]

Seq. No. 393401
Contig ID 39713_1.R1084
5'-most EST g3761963
Method BLASTX
NCBI GI g3550483
BLAST score 479
E value 7.0e-63
Match length 181
% identity 54
NCBI Description (AJ224324) cp31BHv [Hordeum vulgare]

Seq. No. 393402
Contig ID 39716_1.R1084
5'-most EST g700664

Seq. No. 393403
Contig ID 39732_1.R1084
5'-most EST uC-osflcyp159g04a1

Seq. No. 393404
Contig ID 39759_1.R1084
5'-most EST uC-osflM202089c08b1

Seq. No. 393405
Contig ID 39774_1.R1084
5'-most EST g3766795

Seq. No. 393406
Contig ID 39776_1.R1084
5'-most EST uC-osflcyp155f06b1

Seq. No. 393407
Contig ID 39781_1.R1084
5'-most EST g4715094

Seq. No. 393408
Contig ID 39795_1.R1084
5'-most EST uC-osflcyp157e02a1

Seq. No.	393409
Contig ID	39796_1.R1084
5'-most EST	g4879157
Method	BLASTX
NCBI GI	g4454032
BLAST score	355
E value	1.0e-35
Match length	148
% identity	52
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	393410
Contig ID	39808_1.R1084
5'-most EST	uC-osflcyp158f08a1

Seq. No.	393411
Contig ID	39825_1.R1084
5'-most EST	uC-osflcyp160d02a1

Seq. No.	393412
Contig ID	39828_1.R1084
5'-most EST	g3762049
Method	BLASTX
NCBI GI	g2598575
BLAST score	304
E value	2.0e-27
Match length	121
% identity	49
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	393413
Contig ID	39840_1.R1084
5'-most EST	uC-osflcyp161g06b1
Method	BLASTX
NCBI GI	g3132478
BLAST score	380
E value	4.0e-36
Match length	289
% identity	33
NCBI Description	(AC003096) bZIP-like protein [Arabidopsis thaliana]

Seq. No.	393414
Contig ID	39841_1.R1084
5'-most EST	g3768168

Seq. No.	393415
Contig ID	39848_1.R1084
5'-most EST	g3763214

Seq. No.	393416
Contig ID	39852_1.R1084
5'-most EST	g5038718

Seq. No.	393417
Contig ID	39874_1.R1084
5'-most EST	uC-osflcyp067g05a1

Seq. No.	393418
Contig ID	39898_1.R1084
5'-most EST	uC-osflcyp171f04a1

Seq. No.	393419
Contig ID	39908_1.R1084
5'-most EST	g3761156
Method	BLASTX
NCBI GI	g4337196
BLAST score	238
E value	1.0e-19
Match length	122
% identity	39
NCBI Description	(AC006403) putative serine/threonine receptor kinase [Arabidopsis thaliana]

Seq. No.	393420
Contig ID	39911_1.R1084
5'-most EST	uC-osflcyp172f06b1
Method	BLASTN
NCBI GI	g5852170
BLAST score	401
E value	0.0e+00
Match length	438
% identity	98
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No.	393421
Contig ID	39914_1.R1084
5'-most EST	uC-osroM202039a02b1
Method	BLASTX
NCBI GI	g2384671
BLAST score	253
E value	2.0e-21
Match length	68
% identity	74
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No.	393422
Contig ID	39915_1.R1084
5'-most EST	uC-osflcyp172h06a1
Method	BLASTX
NCBI GI	g2583117
BLAST score	147
E value	6.0e-09
Match length	43
% identity	74
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393423
Contig ID	39925_1.R1084
5'-most EST	uC-osflcyp173e08b1

Seq. No.	393424
Contig ID	39933_1.R1084

5'-most EST	g5056127
Method	BLASTX
NCBI GI	g5882729
BLAST score	167
E value	3.0e-11
Match length	70
% identity	44
NCBI Description	(AC008263) ESTs gb_T04387, gb_R84022 and gb_T42239 come from this gene. [Arabidopsis thaliana]

Seq. No.	393425
Contig ID	39942_1.R1084
5'-most EST	uC-osflcyp175a02b1
Method	BLASTX
NCBI GI	g4803944
BLAST score	694
E value	4.0e-73
Match length	210
% identity	50
NCBI Description	(AC006264) putative C2-domain protein (prosite: PDOC00380) [Arabidopsis thaliana]

Seq. No.	393426
Contig ID	39946_1.R1084
5'-most EST	uC-osflcyp175g04b1
Method	BLASTX
NCBI GI	g4337210
BLAST score	636
E value	5.0e-66
Match length	239
% identity	52
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393427
Contig ID	39951_1.R1084
5'-most EST	g5607572
Method	BLASTX
NCBI GI	g4835226
BLAST score	255
E value	9.0e-22
Match length	91
% identity	52
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	393428
Contig ID	39951_2.R1084
5'-most EST	uC-osflcyp176f08b1
Method	BLASTX
NCBI GI	g2832617
BLAST score	237
E value	6.0e-26
Match length	103
% identity	63
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	393429
Contig ID	39967_1.R1084

5'-most EST	g5900756
Method	BLASTX
NCBI GI	g4759288
BLAST score	236
E value	2.0e-19
Match length	73
% identity	62
NCBI Description	homolog of yeast (S. cerevisiae) ufd2 >gi_2495703_sp_Q14139_Y126_HUMAN HYPOTHETICAL PROTEIN KIAA0126 >gi_1469175_dbj_BAA09475_ (D50916) The KIAA0126 gene is partially related to a yeast gene. [Homo sapiens]

Seq. No.	393430
Contig ID	39985_1.R1084
5'-most EST	uC-osflcyp179d04b1
Method	BLASTX
NCBI GI	g5081779
BLAST score	1203
E value	1.0e-132
Match length	266
% identity	87
NCBI Description	(AF150630) cellulose synthase [Gossypium hirsutum]

Seq. No.	393431
Contig ID	40003_1.R1084
5'-most EST	uC-osflcyp005e05b2

Seq. No.	393432
Contig ID	40004_1.R1084
5'-most EST	g2799137
Method	BLASTX
NCBI GI	g4336436
BLAST score	261
E value	2.0e-22
Match length	112
% identity	51
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	393433
Contig ID	40004_2.R1084
5'-most EST	g3761281
Method	BLASTX
NCBI GI	g4336436
BLAST score	390
E value	1.0e-37
Match length	106
% identity	71
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	393434
Contig ID	40005_1.R1084
5'-most EST	uC-osflcyp005g05b2

Seq. No.	393435
Contig ID	40009_1.R1084
5'-most EST	uC-osflcyp006b09b2

Seq. No.	393436
Contig ID	40012_1.R1084
5'-most EST	g5003818
Method	BLASTX
NCBI GI	g1749546
BLAST score	252
E value	5.0e-21
Match length	93
% identity	58
NCBI Description	(D89169) similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]

Seq. No.	393437
Contig ID	40013_1.R1084
5'-most EST	g2275943

Seq. No.	393438
Contig ID	40017_1.R1084
5'-most EST	g701247

Seq. No.	393439
Contig ID	40051_1.R1084
5'-most EST	uC-osflcyp011a09b1
Method	BLASTX
NCBI GI	g4680697
BLAST score	131
E value	6.0e-15
Match length	87
% identity	54
NCBI Description	(AF132963) CGI-29 protein [Homo sapiens]

Seq. No.	393440
Contig ID	40064_1.R1084
5'-most EST	uC-osflcyp012a01b2
Method	BLASTX
NCBI GI	g5430753
BLAST score	169
E value	1.0e-11
Match length	127
% identity	34
NCBI Description	(AC007504) Unknown Protein [Arabidopsis thaliana]

Seq. No.	393441
Contig ID	40071_1.R1084
5'-most EST	uC-osflcyp012e09b2

Seq. No.	393442
Contig ID	40077_1.R1084
5'-most EST	g700034

Seq. No.	393443
Contig ID	40079_1.R1084
5'-most EST	g4715260

Seq. No.	393444
Contig ID	40099_1.R1084

5'-most EST	uC-osroM202003e02a2
Seq. No.	393445
Contig ID	40100_1.R1084
5'-most EST	g2312506
Method	BLASTX
NCBI GI	g1174850
BLAST score	466
E value	2.0e-46
Match length	121
% identity	79
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)
Seq. No.	393446
Contig ID	40115_1.R1084
5'-most EST	g3761523
Method	BLASTX
NCBI GI	g2239262
BLAST score	524
E value	7.0e-60
Match length	147
% identity	80
NCBI Description	(Y13285) pectin methylesterase-like protein [Zea mays]
Seq. No.	393447
Contig ID	40118_1.R1084
5'-most EST	uC-osrocyp026e11a1
Method	BLASTX
NCBI GI	g4038034
BLAST score	245
E value	1.0e-20
Match length	62
% identity	76
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]
Seq. No.	393448
Contig ID	40128_1.R1084
5'-most EST	uC-osflcyp018b10b2
Seq. No.	393449
Contig ID	40140_1.R1084
5'-most EST	uC-osflcyp019c12b2
Seq. No.	393450
Contig ID	40156_1.R1084
5'-most EST	g3767993
Method	BLASTX
NCBI GI	g3935181
BLAST score	472
E value	4.0e-47
Match length	101
% identity	86
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]
Seq. No.	393451
Contig ID	40158_1.R1084

5'-most EST	uC-osflcyp021d08b2
Method	BLASTX
NCBI GI	g2582800
BLAST score	466
E value	2.0e-46
Match length	190
% identity	53
NCBI Description	(Y11607) protein phosphatase 2C [Medicago sativa]

Seq. No.	393452
Contig ID	40164_1.R1084
5'-most EST	g5038742
Method	BLASTX
NCBI GI	g4731374
BLAST score	377
E value	4.0e-40
Match length	154
% identity	58
NCBI Description	(AF133839) papain-like cysteine protease [Sandersonia aurantiaca]

Seq. No.	393453
Contig ID	40171_1.R1084
5'-most EST	uC-osflcyp022c11b1
Method	BLASTX
NCBI GI	g4678322
BLAST score	231
E value	5.0e-19
Match length	83
% identity	60
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	393454
Contig ID	40192_1.R1084
5'-most EST	uC-osflcyp023f10b2
Method	BLASTX
NCBI GI	g3142292
BLAST score	534
E value	3.0e-54
Match length	138
% identity	68
NCBI Description	(AC002411) Contains similarity to tetratricopeptide repeat protein gb_U46571 from home sapiens. EST gb_Z47802 and gb_Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No.	393455
Contig ID	40195_1.R1084
5'-most EST	uC-osflcyp023h02b2

Seq. No.	393456
Contig ID	40196_1.R1084
5'-most EST	g4714074

Seq. No.	393457
Contig ID	40202_1.R1084
5'-most EST	g3759054

Seq. No.	393458
Contig ID	40239_1.R1084
5'-most EST	uC-osflcyp027g11a1
Method	BLASTX
NCBI GI	g2960364
BLAST score	280
E value	1.0e-24
Match length	90
% identity	59
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	393459
Contig ID	40242_1.R1084
5'-most EST	g3763029
Method	BLASTX
NCBI GI	g1345978
BLAST score	433
E value	2.0e-42
Match length	101
% identity	81
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_457631 (L29214) omega-6 desaturase [Brassica napus]

Seq. No.	393460
Contig ID	40244_1.R1084
5'-most EST	uC-osflcyp028a11a1

Seq. No.	393461
Contig ID	40259_1.R1084
5'-most EST	g1036885
Method	BLASTX
NCBI GI	g2146741
BLAST score	481
E value	3.0e-48
Match length	98
% identity	89
NCBI Description	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) - Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Arabidopsis thaliana]

Seq. No.	393462
Contig ID	40260_1.R1084
5'-most EST	uC-osflcyp029c11a1
Method	BLASTX
NCBI GI	g6016720
BLAST score	289
E value	1.0e-25
Match length	69
% identity	74
NCBI Description	(AC009325) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393463
Contig ID	40261_1.R1084
5'-most EST	uC-osflcyp029d07a1

Seq. No.	393464
Contig ID	40267_1.R1084
5'-most EST	uC-osflcyp029g11a1

Seq. No.	393465
Contig ID	40286_1.R1084
5'-most EST	g2799764
Method	BLASTN
NCBI GI	g488161
BLAST score	453
E value	0.0e+00
Match length	469
% identity	100
NCBI Description	Rice ribosomal external intergenic spacer DNA

Seq. No.	393466
Contig ID	40290_1.R1084
5'-most EST	uC-osflcyp031c10b1
Method	BLASTX
NCBI GI	g3219815
BLAST score	143
E value	1.0e-08
Match length	59
% identity	51
NCBI Description	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM22 HOMOLOG >gi_2104453_emb_CAB08780_ (Z95397) unknown [Schizosaccharomyces pombe]

Seq. No.	393467
Contig ID	40306_1.R1084
5'-most EST	uC-osflcyp032g09b1

Seq. No.	393468
Contig ID	40321_1.R1084
5'-most EST	g3760327
Method	BLASTX
NCBI GI	g4580521
BLAST score	211
E value	7.0e-17
Match length	63
% identity	65
NCBI Description	(AF036304) scarecrow-like 7 [Arabidopsis thaliana]

Seq. No.	393469
Contig ID	40340_1.R1084
5'-most EST	uC-osflM202065b02a1

Seq. No.	393470
Contig ID	40347_1.R1084
5'-most EST	uC-osrocyp017f03a1
Method	BLASTX
NCBI GI	g2224915
BLAST score	311
E value	2.0e-28
Match length	113
% identity	61
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No. 393471
Contig ID 40352_1.R1084
5'-most EST uC-osroM202004d06a2

Seq. No. 393472
Contig ID 40361_1.R1084
5'-most EST g2801201

Seq. No. 393473
Contig ID 40372_1.R1084
5'-most EST uC-osflM202064b01a1

Seq. No. 393474
Contig ID 40395_1.R1084
5'-most EST uC-osflcyp045b09b1
Method BLASTX
NCBI GI g2921830
BLAST score 284
E value 5.0e-25
Match length 144
% identity 34
NCBI Description (AF047031) IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq. No. 393475
Contig ID 40396_1.R1084
5'-most EST uC-osflcyp045c05b1
Method BLASTX
NCBI GI g3819697
BLAST score 225
E value 3.0e-18
Match length 105
% identity 49
NCBI Description (AJ009608) BnMAP4K alpha1 [Brassica napus]

Seq. No. 393476
Contig ID 40406_1.R1084
5'-most EST uC-osflM202016g06b1

Seq. No. 393477
Contig ID 40416_1.R1084
5'-most EST g5002923
Method BLASTX
NCBI GI g2494115
BLAST score 298
E value 1.0e-26
Match length 121
% identity 68
NCBI Description (AC002376) Strong similarity to Arabidopsis ATHSAR1 (gb_M90418). ESTs gb_T44122,gb_N65276,gb_AA041135 come from this gene. [Arabidopsis thaliana]

Seq. No. 393478
Contig ID 40420_1.R1084
5'-most EST g3761278

Seq. No. 393479

Contig ID	40428_1.R1084
5'-most EST	g4715251
Method	BLASTX
NCBI GI	g3860264
BLAST score	638
E value	1.0e-66
Match length	170
% identity	74
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	393480
Contig ID	40442_1.R1084
5'-most EST	uC-osflcyp052e11a1

Seq. No.	393481
Contig ID	40458_1.R1084
5'-most EST	uC-osflcyp053g03a1

Seq. No.	393482
Contig ID	40461_1.R1084
5'-most EST	g3760150

Seq. No.	393483
Contig ID	40485_1.R1084
5'-most EST	g3762737
Method	BLASTX
NCBI GI	g3128209
BLAST score	167
E value	2.0e-11
Match length	63
% identity	51
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]

Seq. No.	393484
Contig ID	40498_1.R1084
5'-most EST	uC-osflcyp058e07a1
Method	BLASTX
NCBI GI	g2764574
BLAST score	202
E value	1.0e-15
Match length	74
% identity	50
NCBI Description	(AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

Seq. No.	393485
Contig ID	40504_1.R1084
5'-most EST	uC-osflcyp061a07a1

Seq. No.	393486
Contig ID	40534_1.R1084
5'-most EST	g2800901
Method	BLASTN
NCBI GI	g2280517
BLAST score	42
E value	3.0e-14
Match length	66
% identity	91

NCBI Description	Nicotiana tabacum mRNA for BYJ15, partial cds
Seq. No.	393487
Contig ID	40538_1.R1084
5'-most EST	uC-osflcyp065g12b1
Seq. No.	393488
Contig ID	40544_1.R1084
5'-most EST	uC-osflcyp066c03a1
Seq. No.	393489
Contig ID	40553_1.R1084
5'-most EST	uC-osflcyp067f05a1
Seq. No.	393490
Contig ID	40568_1.R1084
5'-most EST	uC-osroM202038h12b1
Seq. No.	393491
Contig ID	40570_1.R1084
5'-most EST	uC-osflcyp071g01a1
Seq. No.	393492
Contig ID	40571_1.R1084
5'-most EST	uC-osflcyp071g09a1
Method	BLASTN
NCBI GI	g1177581
BLAST score	35
E value	9.0e-10
Match length	59
% identity	92
NCBI Description	O.sativa pRRD8 gene promoter region
Seq. No.	393493
Contig ID	40596_1.R1084
5'-most EST	uC-osflcyp075f07b1
Method	BLASTN
NCBI GI	g11957
BLAST score	192
E value	1.0e-104
Match length	244
% identity	95
NCBI Description	Rice complete chloroplast genome
Seq. No.	393494
Contig ID	40613_1.R1084
5'-most EST	g2799059
Method	BLASTN
NCBI GI	g1698774
BLAST score	54
E value	4.0e-21
Match length	54
% identity	100
NCBI Description	Filamentous phage display expression cloning vector pZGT5 with murine Ig kappa light chain fragment insert, complete sequence

Seq. No.	393495
Contig ID	40617_1.R1084
5'-most EST	g4715676
Seq. No.	393496
Contig ID	40624_1.R1084
5'-most EST	uC-osflm202109b08b1
Method	BLASTX
NCBI GI	g4455180
BLAST score	253
E value	1.0e-21
Match length	110
% identity	48
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]
Seq. No.	393497
Contig ID	40641_1.R1084
5'-most EST	uC-osflcyp082b02a1
Method	BLASTX
NCBI GI	g3360289
BLAST score	246
E value	3.0e-42
Match length	167
% identity	29
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]
Seq. No.	393498
Contig ID	40660_1.R1084
5'-most EST	uC-osrocyp033e02a1
Seq. No.	393499
Contig ID	40661_1.R1084
5'-most EST	uC-osroM202016e04a1
Method	BLASTX
NCBI GI	g4587519
BLAST score	477
E value	3.0e-52
Match length	125
% identity	83
NCBI Description	(AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g
Seq. No.	393500
Contig ID	40661_2.R1084
5'-most EST	g3766932
Method	BLASTX
NCBI GI	g3402817
BLAST score	277
E value	3.0e-24
Match length	56
% identity	95
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]
Seq. No.	393501

Contig ID	40668_1.R1084
5'-most EST	g2428945
Seq. No.	393502
Contig ID	40684_1.R1084
5'-most EST	uC-osflcyp086e12b1
Method	BLASTX
NCBI GI	g2827711
BLAST score	523
E value	4.0e-53
Match length	181
% identity	65
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]
Seq. No.	393503
Contig ID	40685_1.R1084
5'-most EST	uC-osflcyp086f04a1
Method	BLASTX
NCBI GI	g4432861
BLAST score	237
E value	1.0e-19
Match length	71
% identity	58
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]
Seq. No.	393504
Contig ID	40693_1.R1084
5'-most EST	uC-osflM202088b10a1
Seq. No.	393505
Contig ID	40702_1.R1084
5'-most EST	g4714374
Seq. No.	393506
Contig ID	40715_1.R1084
5'-most EST	g5771043
Seq. No.	393507
Contig ID	40717_1.R1084
5'-most EST	g2800569
Method	BLASTX
NCBI GI	g729304
BLAST score	272
E value	1.0e-23
Match length	84
% identity	68
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi_479730_pir__S35258 pyruvate decarboxylase (EC 4.1.1.1) 2 - maize (fragment) >gi_22763_emb_CAA79818_ (Z21721) pyruvate decarboxylase [Zea mays] >gi_217970_dbj_BAA03353_ (D14456) Pyruvate Decarboxylase [Zea mays]
Seq. No.	393508
Contig ID	40727_1.R1084
5'-most EST	g3763320
Method	BLASTX

NCBI GI g6016731
BLAST score 186
E value 2.0e-25
Match length 80
% identity 75
NCBI Description (AC009325) unknown protein [Arabidopsis thaliana] >gi_6091718_gb_AAF03430.1_AC010797_6 (AC010797) unknown protein [Arabidopsis thaliana]

Seq. No. 393509
Contig ID 40775_1.R1084
5'-most EST uC-osflcyp003d06b1
Method BLASTX
NCBI GI g3193320
BLAST score 136
E value 8.0e-10
Match length 89
% identity 51
NCBI Description (AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]

Seq. No. 393510
Contig ID 40790_1.R1084
5'-most EST g702201
Method BLASTX
NCBI GI g3128217
BLAST score 108
E value 7.0e-12
Match length 77
% identity 56
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana] >gi_3337374 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393511
Contig ID 40851_1.R1084
5'-most EST g5004989
Method BLASTX
NCBI GI g4895215
BLAST score 201
E value 1.0e-15
Match length 69
% identity 58
NCBI Description (AC007660) putative 1-phosphatidylinositol-4,5-biphosphate phosphodiesterase [Arabidopsis thaliana]

Seq. No. 393512
Contig ID 40861_1.R1084
5'-most EST g3761238

Seq. No. 393513
Contig ID 40897_1.R1084
5'-most EST uC-osflcyp116h01a1

Seq. No. 393514

Contig ID	40923_1.R1084
5'-most EST	g2428858

Seq. No.	393515
Contig ID	40924_1.R1084
5'-most EST	g5667317
Method	BLASTX
NCBI GI	g4263509
BLAST score	361
E value	2.0e-37
Match length	131
% identity	67
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393516
Contig ID	40926_1.R1084
5'-most EST	uC-osf1M202014h05b1
Method	BLASTX
NCBI GI	g2832660
BLAST score	395
E value	1.0e-51
Match length	205
% identity	51
NCBI Description	(AL021710) lipase-like protein [Arabidopsis thaliana]

Seq. No.	393517
Contig ID	40929_1.R1084
5'-most EST	uC-osf1cyp121g06b1
Method	BLASTX
NCBI GI	g419760
BLAST score	476
E value	3.0e-49
Match length	166
% identity	34
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana] >gi_4883607_gb_AAD31576.1_AC006922_8 (AC006922) putative P-glycoprotein pgp1 [Arabidopsis thaliana]

Seq. No.	393518
Contig ID	40932_1.R1084
5'-most EST	uC-osf1cyp003a05b1
Method	BLASTX
NCBI GI	g5002212
BLAST score	115
E value	4.0e-10
Match length	84
% identity	48
NCBI Description	(AF144078) alpha-xylosidase precursor [Arabidopsis thaliana] >gi_5734722_gb_AAD49987.1_AC008075_20 (AC008075) Identical to gb_AF144078 alpha-xylosidase precursor from Arabidopsis thaliana. ESTs gb_W43892, gb_N96165, gb_T46694, gb_N37141, gb_R64965, gb_R90271, gb_AA651443, gb_AA712305, gb_T04189 and gb_AA597852 c

Seq. No.	393519

Contig ID	40938_1.R1084
5'-most EST	uC-osflcyp003b09b1
Method	BLASTN
NCBI GI	g5821066
BLAST score	432
E value	0.0e+00
Match length	456
% identity	99
NCBI Description	Oryza sativa gene for WHO4, complete cds

Seq. No.	393520
Contig ID	40962_1.R1084
5'-most EST	g3760678
Method	BLASTX
NCBI GI	g1669655
BLAST score	146
E value	8.0e-09
Match length	103
% identity	35
NCBI Description	(X95962) CER3 [Arabidopsis thaliana]

Seq. No.	393521
Contig ID	40964_1.R1084
5'-most EST	uC-osflcyp003g01b1
Method	BLASTX
NCBI GI	g5734768
BLAST score	753
E value	5.0e-80
Match length	181
% identity	71
NCBI Description	(AC007651) Hypothetical Protein [Arabidopsis thaliana]

Seq. No.	393522
Contig ID	40965_1.R1084
5'-most EST	uC-osrocyp011h03a1
Method	BLASTX
NCBI GI	g1546696
BLAST score	368
E value	4.0e-35
Match length	99
% identity	68
NCBI Description	(X98807) peroxidase ATP21a [Arabidopsis thaliana]

Seq. No.	393523
Contig ID	40982_1.R1084
5'-most EST	uC-osflcyp005b01b1
Method	BLASTX
NCBI GI	g6056196
BLAST score	300
E value	5.0e-27
Match length	131
% identity	50
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	393524
Contig ID	40993_1.R1084
5'-most EST	g2443103

Method	BLASTX
NCBI GI	g129960
BLAST score	326
E value	3.0e-30
Match length	150
% identity	49
NCBI Description	4-NITROPHENYLPHOSPHATASE (PNPPASE) >gi_5924022_emb_CAB56540.1_ (X51611) p-nitrophenylphosphatase [Saccharomyces cerevisiae]

Seq. No.	393525
Contig ID	41004_1.R1084
5'-most EST	g4880243
Method	BLASTX
NCBI GI	g3024505
BLAST score	497
E value	3.0e-88
Match length	204
% identity	80
NCBI Description	RAS-RELATED PROTEIN RAB11D >gi_623580 (L29270) putative [Nicotiana tabacum]

Seq. No.	393526
Contig ID	41032_1.R1084
5'-most EST	uC-osflM202088c10a1

Seq. No.	393527
Contig ID	41053_1.R1084
5'-most EST	g3760392

Seq. No.	393528
Contig ID	41062_1.R1084
5'-most EST	uC-osflcyp085d03b1
Method	BLASTX
NCBI GI	g3413706
BLAST score	313
E value	2.0e-28
Match length	95
% identity	60
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393529
Contig ID	41080_1.R1084
5'-most EST	uC-osflcyp085h12b1
Method	BLASTX
NCBI GI	g5051781
BLAST score	355
E value	2.0e-36
Match length	145
% identity	54
NCBI Description	(AL078637) transport inhibitor response-like protein [Arabidopsis thaliana]

Seq. No.	393530
Contig ID	41091_2.R1084
5'-most EST	g571876
Method	BLASTX

NCBI GI	g1621268
BLAST score	737
E value	1.0e-86
Match length	203
% identity	76
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	393531
Contig ID	41092_1.R1084
5'-most EST	uC-osflcyp086c09b1

Seq. No.	393532
Contig ID	41093_1.R1084
5'-most EST	g4715765
Method	BLASTX
NCBI GI	g2980770
BLAST score	577
E value	2.0e-59
Match length	146
% identity	75
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	393533
Contig ID	41109_1.R1084
5'-most EST	uC-osflcyp086h07b1
Method	BLASTX
NCBI GI	g132712
BLAST score	464
E value	4.0e-56
Match length	135
% identity	75
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 >gi_71250_pir__R5RZ16 ribosomal protein L16 - rice chloroplast >gi_669084_emb_CAA33933_ (X15901) ribosomal protein L16 [Oryza sativa] >gi_226645_prf__1603356BV ribosomal protein L16 [Oryza sativa]

Seq. No.	393534
Contig ID	41116_1.R1084
5'-most EST	uC-osflcyp106b11b1

Seq. No.	393535
Contig ID	41121_1.R1084
5'-most EST	uC-osflcyp106c12b1
Method	BLASTX
NCBI GI	g1351834
BLAST score	213
E value	6.0e-17
Match length	65
% identity	66
NCBI Description	PROBABLE ATP-DEPENDENT TRANSPORTER YCF16 >gi_1016162 (U30821) ABC transporter subunit [Cyanophora paradoxa]

Seq. No.	393536
Contig ID	41141_1.R1084
5'-most EST	g3763298
Method	BLASTX

NCBI GI	g5734707
BLAST score	154
E value	1.0e-09
Match length	52
% identity	58
NCBI Description	(AC008075) F24J5.3 [Arabidopsis thaliana]

Seq. No.	393537
Contig ID	41151_1.R1084
5'-most EST	uC-osflcyp131b09a1

Seq. No.	393538
Contig ID	41156_1.R1084
5'-most EST	g3768562

Seq. No.	393539
Contig ID	41159_1.R1084
5'-most EST	uC-osroM202019h08a1
Method	BLASTN
NCBI GI	g2864607
BLAST score	36
E value	2.0e-10
Match length	104
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	393540
Contig ID	41165_1.R1084
5'-most EST	uC-osroM202010d09a1
Method	BLASTX
NCBI GI	g4115377
BLAST score	220
E value	8.0e-18
Match length	51
% identity	82
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	393541
Contig ID	41176_1.R1084
5'-most EST	g5005142

Seq. No.	393542
Contig ID	41179_1.R1084
5'-most EST	g4715768

Seq. No.	393543
Contig ID	41182_1.R1084
5'-most EST	g3107520

Seq. No.	393544
Contig ID	41183_1.R1084
5'-most EST	uC-osroM202029c04a1
Method	BLASTN
NCBI GI	g168641
BLAST score	57
E value	6.0e-23

Match length	153
% identity	89
NCBI Description	Maize Mu transposable element MRS-A

Seq. No.	393545
Contig ID	41195_1.R1084
5'-most EST	uC-osflcyp131h12a1

Seq. No.	393546
Contig ID	41202_1.R1084
5'-most EST	g2798168

Seq. No.	393547
Contig ID	41230_1.R1084
5'-most EST	g4715940

Seq. No.	393548
Contig ID	41244_1.R1084
5'-most EST	g4714067

Seq. No.	393549
Contig ID	41250_1.R1084
5'-most EST	g2442694
Method	BLASTN
NCBI GI	g5679837
BLAST score	407
E value	0.0e+00
Match length	603
% identity	99
NCBI Description	Oryza sativa chromosome 4 BAC l1332 genomic sequences

Seq. No.	393550
Contig ID	41287_1.R1084
5'-most EST	g3767916
Method	BLASTX
NCBI GI	g4322304
BLAST score	246
E value	4.0e-24
Match length	108
% identity	56
NCBI Description	(AF078035) translation initiation factor IF2 [Homo sapiens]

Seq. No.	393551
Contig ID	41292_1.R1084
5'-most EST	g2799261
Method	BLASTX
NCBI GI	g5016095
BLAST score	289
E value	6.0e-26
Match length	70
% identity	84
NCBI Description	(AF003551) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Zea mays]

Seq. No.	393552
Contig ID	41297_1.R1084
5'-most EST	g3760980

Method	BLASTX
NCBI GI	g595768
BLAST score	185
E value	1.0e-16
Match length	50
% identity	94
NCBI Description	(U13866) non-functional lacZ alpha peptide [Cloning vector]

Seq. No.	393553
Contig ID	41302_1.R1084
5'-most EST	g3769052

Seq. No.	393554
Contig ID	41307_1.R1084
5'-most EST	g3760457
Method	BLASTX
NCBI GI	g3329475
BLAST score	186
E value	4.0e-20
Match length	166
% identity	39
NCBI Description	(AF069781) Bem46-like protein [Drosophila melanogaster]

Seq. No.	393555
Contig ID	41318_1.R1084
5'-most EST	g3768491

Seq. No.	393556
Contig ID	41324_1.R1084
5'-most EST	g2428083
Method	BLASTX
NCBI GI	g4049346
BLAST score	248
E value	5.0e-21
Match length	106
% identity	51
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	393557
Contig ID	41328_1.R1084
5'-most EST	uC-osflcyp141g11b1
Method	BLASTX
NCBI GI	g6006848
BLAST score	742
E value	1.0e-138
Match length	292
% identity	64
NCBI Description	(AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	393558
Contig ID	41330_1.R1084
5'-most EST	uC-osflcyp141h01b1
Method	BLASTX
NCBI GI	g1845195
BLAST score	255
E value	8.0e-22

Match length	113
% identity	41
NCBI Description	(Y08297) HMGc1 [Zea mays] >gi_5441504_emb_CAB46753.1_ (AJ131374) HMGc1 protein [Zea mays]

Seq. No.	393559
Contig ID	41339_1.R1084
5'-most EST	uC-osflcyp168b11b1
Method	BLASTX
NCBI GI	g4850369
BLAST score	530
E value	6.0e-54
Match length	146
% identity	72
NCBI Description	(AB027151) threonine synthase [Arabidopsis thaliana] >gi_4914408_emb_CAB43659.1_ (AL050352) threonine synthase [Arabidopsis thaliana]

Seq. No.	393560
Contig ID	41344_1.R1084
5'-most EST	uC-osflM202088b08a1
Method	BLASTX
NCBI GI	g1314711
BLAST score	463
E value	7.0e-51
Match length	184
% identity	61
NCBI Description	(U54615) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_3068712 (AF049236) calcium dependent protein kinase [Arabidopsis thaliana]

Seq. No.	393561
Contig ID	41356_1.R1084
5'-most EST	uC-osflcyp168f11b1
Method	BLASTX
NCBI GI	g4895232
BLAST score	183
E value	2.0e-16
Match length	110
% identity	45
NCBI Description	(AC007660) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393562
Contig ID	41395_1.R1084
5'-most EST	g5607475

Seq. No.	393563
Contig ID	41411_1.R1084
5'-most EST	uC-osroM202016g12b1

Seq. No.	393564
Contig ID	41420_1.R1084
5'-most EST	uC-osflcyp172h07b1
Method	BLASTX
NCBI GI	g4803836
BLAST score	163
E value	3.0e-15

Match length 141
% identity 39
NCBI Description (AB026987) a dynamin-like protein ADL3 [Arabidopsis thaliana]

Seq. No. 393565
Contig ID 41422_1.R1084
5'-most EST uC-osflcyp173a01b1
Method BLASTX
NCBI GI g5002520
BLAST score 943
E value 1.0e-106
Match length 253
% identity 72
NCBI Description (AL078606) putative phospholipase D-gamma [Arabidopsis thaliana]

Seq. No. 393566
Contig ID 41430_1.R1084
5'-most EST uC-osflcyp173e10b1
Method BLASTX
NCBI GI g4886280
BLAST score 144
E value 6.0e-09
Match length 93
% identity 37
NCBI Description (AL050300) putative protein [Arabidopsis thaliana]

Seq. No. 393567
Contig ID 41439_1.R1084
5'-most EST uC-osflcyp173h09b1
Method BLASTX
NCBI GI g4309738
BLAST score 289
E value 1.0e-25
Match length 80
% identity 71
NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No. 393568
Contig ID 41448_1.R1084
5'-most EST g2800565
Method BLASTX
NCBI GI g5281036
BLAST score 307
E value 1.0e-39
Match length 161
% identity 60
NCBI Description (AL080318) nucleotide sugar epimerase-like protein [Arabidopsis thaliana]

Seq. No. 393569
Contig ID 41448_2.R1084
5'-most EST uC-osflcyp017c03b1
Method BLASTX
NCBI GI g3193316
BLAST score 413

E value	3.0e-40
Match length	191
% identity	61
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	393570
Contig ID	41464_1.R1084
5'-most EST	g569815
Method	BLASTX
NCBI GI	g2129636
BLAST score	192
E value	3.0e-30
Match length	158
% identity	49
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	393571
Contig ID	41487_1.R1084
5'-most EST	uC-osroM202035c09b1
Method	BLASTX
NCBI GI	g322525
BLAST score	642
E value	7.0e-67
Match length	152
% identity	78
NCBI Description	omnipotent suppressor protein SUP1 homolog (clone A18) - Arabidopsis thaliana (fragment) >gi_16512_emb_CAA49171_ (X69374) similar to yeast omnipotent suppressor protein SUP1 (SUP45); ORF [Arabidopsis thaliana]

Seq. No.	393572
Contig ID	41501_1.R1084
5'-most EST	uC-osflM202050a08b1
Method	BLASTX
NCBI GI	g2654868
BLAST score	691
E value	8.0e-73
Match length	212
% identity	59
NCBI Description	(AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No.	393573
Contig ID	41504_1.R1084
5'-most EST	g572225
Method	BLASTX
NCBI GI	g3023751
BLAST score	300
E value	9.0e-27
Match length	153
% identity	19
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	393574
Contig ID	41505_1.R1084
5'-most EST	uC-osflcyp026a11b1
Method	BLASTN
NCBI GI	g6002775
BLAST score	249
E value	1.0e-137
Match length	484
% identity	99
NCBI Description	Oryza sativa hypothetical protein, fertilin alpha subunit, membrane protein homolog, and Myb-related protein genes, complete cds; and unknown gene

Seq. No.	393575
Contig ID	41520_1.R1084
5'-most EST	uC-osflcyp026f07b1
Method	BLASTX
NCBI GI	g3913202
BLAST score	739
E value	2.0e-78
Match length	200
% identity	71
NCBI Description	CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi_2239214_emb_CAB10431.1_ (Z97210) centromere/microtubule binding protein cbf5 [Schizosaccharomyces pombe]

Seq. No.	393576
Contig ID	41522_1.R1084
5'-most EST	uC-osflcyp026f11b1
Method	BLASTX
NCBI GI	g2826786
BLAST score	350
E value	1.0e-32
Match length	113
% identity	64
NCBI Description	(Y10905) RAPB protein [Oryza sativa]

Seq. No.	393577
Contig ID	41536_1.R1084
5'-most EST	uC-osrocyp016c07b1

Seq. No.	393578
Contig ID	41541_1.R1084
5'-most EST	g3107699

Seq. No.	393579
Contig ID	41559_1.R1084
5'-most EST	uC-osflcyp028e06b1

Seq. No.	393580
Contig ID	41565_1.R1084
5'-most EST	g1632534
Method	BLASTX
NCBI GI	g4263521
BLAST score	197

E value	1.0e-21
Match length	108
% identity	22
NCBI Description	(AC004044) putative WD-repeat protein [Arabidopsis thaliana]

Seq. No.	393581
Contig ID	41587_1.R1084
5'-most EST	uC-osflcyp055f02b1

Seq. No.	393582
Contig ID	41601_1.R1084
5'-most EST	uC-osflcyp065b10b1

Seq. No.	393583
Contig ID	41611_1.R1084
5'-most EST	uC-osflcyp065f12b1
Method	BLASTX
NCBI GI	g4585976
BLAST score	251
E value	3.0e-21
Match length	97
% identity	53
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	393584
Contig ID	41633_1.R1084
5'-most EST	g3761464

Seq. No.	393585
Contig ID	41640_1.R1084
5'-most EST	uC-osflcyp066c07a1
Method	BLASTX
NCBI GI	g2267597
BLAST score	246
E value	3.0e-27
Match length	78
% identity	84
NCBI Description	(AF009413) 10 kDa chaperonin [Oryza sativa]

Seq. No.	393586
Contig ID	41648_1.R1084
5'-most EST	g5803409

Seq. No.	393587
Contig ID	41648_2.R1084
5'-most EST	g4715126

Seq. No.	393588
Contig ID	41649_1.R1084
5'-most EST	uC-osroM202032h05a1

Seq. No.	393589
Contig ID	41674_1.R1084
5'-most EST	uC-osflcyp066h01a1
Method	BLASTX
NCBI GI	g2980795

BLAST score	201
E value	1.0e-29
Match length	76
% identity	70
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	393590
Contig ID	41678_1.R1084
5'-most EST	g3760756
Method	BLASTX
NCBI GI	g1931631
BLAST score	672
E value	2.0e-70
Match length	140
% identity	92
NCBI Description	(U93561) glutamate dehydrogenase [Zea mays]

Seq. No.	393591
Contig ID	41684_1.R1084
5'-most EST	g3769007

Seq. No.	393592
Contig ID	41687_1.R1084
5'-most EST	g2317287

Seq. No.	393593
Contig ID	41688_1.R1084
5'-most EST	uC-osflcyp067a08a1
Method	BLASTN
NCBI GI	g2854048
BLAST score	33
E value	9.0e-09
Match length	45
% identity	96
NCBI Description	Oryza sativa receptor serine/threonine kinase mRNA, partial cds

Seq. No.	393594
Contig ID	41691_1.R1084
5'-most EST	uC-osflcyp067b01a1

Seq. No.	393595
Contig ID	41699_1.R1084
5'-most EST	uC-osflcyp067c12a1
Method	BLASTX
NCBI GI	g4567229
BLAST score	163
E value	7.0e-11
Match length	75
% identity	41
NCBI Description	(AC007119) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	393596
Contig ID	41705_1.R1084
5'-most EST	uC-osflcyp067d01a1

Seq. No.	393597
Contig ID	41714_1.R1084
5'-most EST	g2428964
Method	BLASTX
NCBI GI	g480109
BLAST score	166
E value	3.0e-11
Match length	79
% identity	1
NCBI Description	EPPT protein - hydromedusa (Podocoryne carnea) (fragment) >gi_396743_emb_CAA52402_ (X74358) Pod-EPPT [Podocoryne carnea]

Seq. No.	393598
Contig ID	41718_1.R1084
5'-most EST	uC-osflcyp067e10a1
Method	BLASTX
NCBI GI	g4539009
BLAST score	203
E value	1.0e-15
Match length	68
% identity	56
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	393599
Contig ID	41736_1.R1084
5'-most EST	uC-osflcyp067g11a1

Seq. No.	393600
Contig ID	41741_1.R1084
5'-most EST	uC-osflcyp067h06a1

Seq. No.	393601
Contig ID	41752_1.R1084
5'-most EST	uC-osflcyp071c01b1
Method	BLASTX
NCBI GI	g6056388
BLAST score	696
E value	2.0e-73
Match length	150
% identity	89
NCBI Description	(AC009324) 26S proteasome ATPase subunit [Arabidopsis thaliana]

Seq. No.	393602
Contig ID	41755_1.R1084
5'-most EST	g4714927

Seq. No.	393603
Contig ID	41761_1.R1084
5'-most EST	g2866115
Method	BLASTX
NCBI GI	g3128173
BLAST score	345
E value	3.0e-32
Match length	91
% identity	76

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393604
Contig ID 41762_1.R1084
5'-most EST uC-osflM202040g12b1
Method BLASTX
NCBI GI g5731737
BLAST score 495
E value 2.0e-50
Match length 159
% identity 69
NCBI Description (AB021878) similar to yeast sodium/proton exchanger [Oryza sativa]

Seq. No. 393605
Contig ID 41770_1.R1084
5'-most EST uC-osrocyp008a01b1
Method BLASTX
NCBI GI g2842493
BLAST score 384
E value 6.0e-37
Match length 101
% identity 70
NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No. 393606
Contig ID 41783_1.R1084
5'-most EST uC-osroM202032h03a1

Seq. No. 393607
Contig ID 41795_1.R1084
5'-most EST g3761195
Method BLASTX
NCBI GI g4580389
BLAST score 181
E value 8.0e-18
Match length 79
% identity 54
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 393608
Contig ID 41800_1.R1084
5'-most EST uC-osflcyp079e12a1

Seq. No. 393609
Contig ID 41819_1.R1084
5'-most EST g3762754

Seq. No. 393610
Contig ID 41829_1.R1084
5'-most EST g4968961

Seq. No. 393611
Contig ID 41849_1.R1084
5'-most EST uC-osrocyp017g07b1

Seq. No. 393612

Contig ID 41892_1.R1084
5'-most EST uC-osflcyp116c04a1

Seq. No. 393613
Contig ID 41901_1.R1084
5'-most EST uC-osflcyp116d10a1

Seq. No. 393614
Contig ID 41913_1.R1084
5'-most EST uC-osflcyp116e10a1

Seq. No. 393615
Contig ID 41926_1.R1084
5'-most EST uC-osflcyp116g04a1

Seq. No. 393616
Contig ID 41928_1.R1084
5'-most EST uC-osflM202085g07a1
Method BLASTX
NCBI GI g3413481
BLAST score 258
E value 5.0e-22
Match length 136
% identity 43
NCBI Description (AJ006786) serine protease [Lycopersicon esculentum]

Seq. No. 393617
Contig ID 41930_1.R1084
5'-most EST uC-osflcyp116g11a1

Seq. No. 393618
Contig ID 41947_1.R1084
5'-most EST g5002729
Method BLASTX
NCBI GI g4097579
BLAST score 189
E value 4.0e-14
Match length 42
% identity 88
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 393619
Contig ID 41948_1.R1084
5'-most EST uC-osflcyp117c03a1

Seq. No. 393620
Contig ID 41954_1.R1084
5'-most EST uC-osflcyp117d02a1
Method BLASTX
NCBI GI g4455278
BLAST score 166
E value 2.0e-11
Match length 78
% identity 45
NCBI Description (AL035527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393621

Contig ID	41960_1.R1084
5'-most EST	uC-osrocyp008b08a1
Method	BLASTX
NCBI GI	g5103846
BLAST score	391
E value	2.0e-37
Match length	143
% identity	29
NCBI Description	(AC007591) F9L1.43 [Arabidopsis thaliana]

Seq. No.	393622
Contig ID	41961_1.R1084
5'-most EST	uC-osflcyp117d12a1

Seq. No.	393623
Contig ID	41978_1.R1084
5'-most EST	g5056021
Method	BLASTX
NCBI GI	g6017123
BLAST score	332
E value	1.0e-51
Match length	149
% identity	74
NCBI Description	(AC009895) unknown protein [Arabidopsis thaliana]

Seq. No.	393624
Contig ID	41987_1.R1084
5'-most EST	g5003132

Seq. No.	393625
Contig ID	41989_1.R1084
5'-most EST	uC-osflcyp117h08a1

Seq. No.	393626
Contig ID	42003_1.R1084
5'-most EST	uC-osflcyp118b07a1
Method	BLASTX
NCBI GI	g4006886
BLAST score	599
E value	7.0e-62
Match length	191
% identity	49
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	393627
Contig ID	42051_1.R1084
5'-most EST	g3769057
Method	BLASTX
NCBI GI	g4522009
BLAST score	192
E value	3.0e-14
Match length	70
% identity	61
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	393628
Contig ID	42054_1.R1084

5'-most EST	uC-osroM202023e04b1
Seq. No.	393629
Contig ID	42057_1.R1084
5'-most EST	uC-osflcyp128g09a1
Seq. No.	393630
Contig ID	42060_1.R1084
5'-most EST	uC-osflcyp152a02b1
Seq. No.	393631
Contig ID	42061_1.R1084
5'-most EST	uC-osflcyp152a04b1
Seq. No.	393632
Contig ID	42089_1.R1084
5'-most EST	uC-osflcyp153b09b1
Method	BLASTX
NCBI GI	g4490292
BLAST score	266
E value	5.0e-31
Match length	162
% identity	55
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]
Seq. No.	393633
Contig ID	42100_1.R1084
5'-most EST	uC-osroM202041e05b1
Seq. No.	393634
Contig ID	42105_1.R1084
5'-most EST	uC-osflcyp153f07b1
Seq. No.	393635
Contig ID	42110_1.R1084
5'-most EST	uC-osrocyp031f01b1
Method	BLASTX
NCBI GI	g3258575
BLAST score	689
E value	2.0e-72
Match length	205
% identity	64
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	393636
Contig ID	42115_1.R1084
5'-most EST	uC-osflcyp154e04b1
Method	BLASTX
NCBI GI	g2494165
BLAST score	735
E value	5.0e-78
Match length	181
% identity	75
NCBI Description	DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP]) >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis thaliana]

Seq. No.	393637
Contig ID	42173_1.R1084
5'-most EST	g5004690

Seq. No.	393638
Contig ID	42174_1.R1084
5'-most EST	g3766566
Method	BLASTX
NCBI GI	g4455208
BLAST score	181
E value	6.0e-13
Match length	142
% identity	34
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	393639
Contig ID	42190_1.R1084
5'-most EST	g3761979

Seq. No.	393640
Contig ID	42193_1.R1084
5'-most EST	uC-osflcyp087d06a1

Seq. No.	393641
Contig ID	42215_1.R1084
5'-most EST	uC-osflcyp087g11a1
Method	BLASTX
NCBI GI	g3641837
BLAST score	532
E value	4.0e-54
Match length	137
% identity	72
NCBI Description	(AL023094) Nonclathrin coat protein gamma-like protein [Arabidopsis thaliana]

Seq. No.	393642
Contig ID	42233_1.R1084
5'-most EST	g428840
Method	BLASTX
NCBI GI	g4049401
BLAST score	312
E value	2.0e-28
Match length	82
% identity	72
NCBI Description	(AJ131580) glutathione transferase AtGST 10 [Arabidopsis thaliana]

Seq. No.	393643
Contig ID	42235_1.R1084
5'-most EST	uC-osflcyp089b12b1
Method	BLASTX
NCBI GI	g4468985
BLAST score	158
E value	2.0e-10
Match length	73
% identity	45

NCBI Description	(AL035605) hypothetical protein [Arabidopsis thaliana]
Seq. No.	393644
Contig ID	42246_1.R1084
5'-most EST	uC-osflM202090h01b1
Method	BLASTX
NCBI GI	g5734466
BLAST score	288
E value	9.0e-33
Match length	208
% identity	44
NCBI Description	(AL109832) putative gtpase activating protein [Schizosaccharomyces pombe]
Seq. No.	393645
Contig ID	42272_1.R1084
5'-most EST	uC-osrocyp003b10a1
Method	BLASTX
NCBI GI	g4926866
BLAST score	441
E value	2.0e-43
Match length	130
% identity	62
NCBI Description	(AC007509) putative amp-binding protein [Arabidopsis thaliana]
Seq. No.	393646
Contig ID	42286_1.R1084
5'-most EST	uC-osroM202027e10a1
Seq. No.	393647
Contig ID	42300_1.R1084
5'-most EST	uC-osflM202048e10b1
Method	BLASTX
NCBI GI	g3608138
BLAST score	454
E value	6.0e-45
Match length	153
% identity	58
NCBI Description	(AC005314) hypothetical protein [Arabidopsis thaliana]
Seq. No.	393648
Contig ID	42323_1.R1084
5'-most EST	uC-osflcyp103a06a1
Seq. No.	393649
Contig ID	42356_1.R1084
5'-most EST	uC-osflM202014c03b1
Seq. No.	393650
Contig ID	42362_1.R1084
5'-most EST	g4715843
Method	BLASTX
NCBI GI	g2642158
BLAST score	320
E value	5.0e-29
Match length	140

% identity	49
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393651
Contig ID	42364_1.R1084
5'-most EST	g2310683
Method	BLASTX
NCBI GI	g3451474
BLAST score	383
E value	4.0e-47
Match length	227
% identity	43
NCBI Description	(AL031349) conserved hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	393652
Contig ID	42368_1.R1084
5'-most EST	uC-osf1M202014e04b1

Seq. No.	393653
Contig ID	42373_1.R1084
5'-most EST	g2431431
Method	BLASTX
NCBI GI	g6091734
BLAST score	208
E value	3.0e-16
Match length	64
% identity	59
NCBI Description	(AC010797) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393654
Contig ID	42382_1.R1084
5'-most EST	uC-osf1M202014f09b1
Method	BLASTX
NCBI GI	g3928088
BLAST score	267
E value	3.0e-23
Match length	87
% identity	57
NCBI Description	(AC005770) putative peroxidase [Arabidopsis thaliana]

Seq. No.	393655
Contig ID	42383_1.R1084
5'-most EST	uC-osf1M202014f10b1
Method	BLASTX
NCBI GI	g3776057
BLAST score	153
E value	1.0e-09
Match length	73
% identity	22
NCBI Description	(AL008725) dJ148E22.2 (similar to PAB1) [Homo sapiens]

Seq. No.	393656
Contig ID	42384_1.R1084
5'-most EST	uC-osf1M202014f06b1
Method	BLASTX
NCBI GI	g2191136

BLAST score	231
E value	2.0e-20
Match length	124
% identity	44
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	393657
Contig ID	42393_1.R1084
5'-most EST	uC-osf1M202014h08b1
Method	BLASTX
NCBI GI	g4585903
BLAST score	182
E value	9.0e-21
Match length	69
% identity	72
NCBI Description	(AC007133) putative guanylate binding protein [Arabidopsis thaliana]

Seq. No.	393658
Contig ID	42396_1.R1084
5'-most EST	g3763586
Method	BLASTX
NCBI GI	g3377822
BLAST score	162
E value	4.0e-11
Match length	45
% identity	64
NCBI Description	(AF076275) contains similarity to Caenorhabditis elegans MEL-26 (GB:U67737) [Arabidopsis thaliana]

Seq. No.	393659
Contig ID	42401_1.R1084
5'-most EST	uC-osf1M202016a02b1
Method	BLASTX
NCBI GI	g3978474
BLAST score	163
E value	5.0e-11
Match length	100
% identity	44
NCBI Description	(AF092918) MetZ homolog [Pseudomonas alcaligenes]

Seq. No.	393660
Contig ID	42403_1.R1084
5'-most EST	uC-osf1M202016a06b1
Method	BLASTX
NCBI GI	g1125754
BLAST score	263
E value	9.0e-23
Match length	100
% identity	45
NCBI Description	(U42833) coded for by C. elegans cDNA cm16f6; coded for by C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1 protein (SP:P33750) [Caenorhabditis elegans]

Seq. No.	393661
Contig ID	42418_1.R1084
5'-most EST	g5667614
Seq. No.	393662
Contig ID	42427_1.R1084
5'-most EST	uC-osflM202016d10b1
Method	BLASTX
NCBI GI	g6056374
BLAST score	263
E value	9.0e-23
Match length	108
% identity	46
NCBI Description	(AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]
Seq. No.	393663
Contig ID	42429_1.R1084
5'-most EST	uC-osflM202016e01b1
Seq. No.	393664
Contig ID	42434_1.R1084
5'-most EST	uC-osflM202016e09b1
Method	BLASTX
NCBI GI	g2213615
BLAST score	151
E value	1.0e-09
Match length	96
% identity	32
NCBI Description	(AC000103) F21J9.9 [Arabidopsis thaliana]
Seq. No.	393665
Contig ID	42435_1.R1084
5'-most EST	uC-osflM202016e10b1
Seq. No.	393666
Contig ID	42439_1.R1084
5'-most EST	uC-osflm202109b07b1
Method	BLASTX
NCBI GI	g4539453
BLAST score	449
E value	2.0e-44
Match length	131
% identity	66
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]
Seq. No.	393667
Contig ID	42443_1.R1084
5'-most EST	uC-osflM202016f11b1
Seq. No.	393668
Contig ID	42444_1.R1084
5'-most EST	uC-osflM202016g01b1
Method	BLASTX
NCBI GI	g1244566
BLAST score	351
E value	4.0e-67

Match length	151
% identity	91
NCBI Description	(U39321) acetyl-CoA carboxylase [Triticum aestivum] >gi_1588584_prf__2208491A Ac-CoA carboxylase [Triticum aestivum]

Seq. No.	393669
Contig ID	42449_1.R1084
5'-most EST	uC-osflM202016g11b1
Method	BLASTX
NCBI GI	g4006829
BLAST score	498
E value	4.0e-50
Match length	159
% identity	64
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	393670
Contig ID	42451_1.R1084
5'-most EST	uC-osflM202016h02b1
Method	BLASTX
NCBI GI	g5302775
BLAST score	408
E value	9.0e-40
Match length	141
% identity	60
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393671
Contig ID	42455_1.R1084
5'-most EST	uC-osrocyp015d05b1
Method	BLASTX
NCBI GI	g1076316
BLAST score	174
E value	3.0e-12
Match length	69
% identity	42
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	393672
Contig ID	42458_1.R1084
5'-most EST	uC-osflM202016h12b1

Seq. No.	393673
Contig ID	42462_1.R1084
5'-most EST	uC-osflM202020a08b1

Seq. No.	393674
Contig ID	42476_1.R1084
5'-most EST	uC-osflM202020d01b1

Seq. No.	393675
Contig ID	42478_1.R1084
5'-most EST	g2428418
Method	BLASTX

NCBI GI g3080524
BLAST score 345
E value 7.0e-39
Match length 182
% identity 45
NCBI Description (AL022599) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 393676
Contig ID 42482_1.R1084
5'-most EST uC-osrocyp033g03b1

Seq. No. 393677
Contig ID 42486_1.R1084
5'-most EST uC-osflM202020e03b1
Method BLASTX
NCBI GI g2146739
BLAST score 554
E value 8.0e-57
Match length 150
% identity 71
NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana] >gi_4972059_emb_CAB43927.1_ (AL078470) hexokinase [Arabidopsis thaliana]

Seq. No. 393678
Contig ID 42496_1.R1084
5'-most EST uC-osroM202039f12b1
Method BLASTX
NCBI GI g4586107
BLAST score 363
E value 6.0e-62
Match length 307
% identity 16
NCBI Description (AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No. 393679
Contig ID 42504_1.R1084
5'-most EST g427305

Seq. No. 393680
Contig ID 42513_1.R1084
5'-most EST g2428285

Seq. No. 393681
Contig ID 42517_1.R1084
5'-most EST g2442740

Seq. No. 393682
Contig ID 42519_1.R1084
5'-most EST uC-osflM202035a10b1
Method BLASTX
NCBI GI g4803952
BLAST score 113
E value 2.0e-11
Match length 116

% identity	39
NCBI Description	(AC006202) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393683
Contig ID	42528_1.R1084
5'-most EST	uC-osrocyp008c09b1

Seq. No.	393684
Contig ID	42536_1.R1084
5'-most EST	g4880164
Method	BLASTX
NCBI GI	g4589981
BLAST score	187
E value	7.0e-14
Match length	75
% identity	48
NCBI Description	(AC007195) amidophosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	393685
Contig ID	42559_1.R1084
5'-most EST	uC-osf1M202035f08b1

Seq. No.	393686
Contig ID	42560_1.R1084
5'-most EST	g2427640
Method	BLASTN
NCBI GI	g4874281
BLAST score	36
E value	3.0e-10
Match length	44
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F8D23 genomic sequence, complete sequence

Seq. No.	393687
Contig ID	42562_1.R1084
5'-most EST	uC-osf1M202035g04b1
Method	BLASTX
NCBI GI	g2252863
BLAST score	160
E value	1.0e-10
Match length	43
% identity	70
NCBI Description	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]

Seq. No.	393688
Contig ID	42568_1.R1084
5'-most EST	g2428337
Method	BLASTX
NCBI GI	g5091611
BLAST score	523
E value	4.0e-53
Match length	177
% identity	65
NCBI Description	(AC007858) Similar to gb_U43629 integral membrane protein

from Beta vulgaris and is a member of the sugar transporter family PF_00083. ES [Oryza sativa]

Seq. No.	393689
Contig ID	42609_1.R1084
5'-most EST	uC-osf1M202037d10b1

Seq. No.	393690
Contig ID	42616_1.R1084
5'-most EST	uC-osf1M202037e09b1
Method	BLASTX
NCBI GI	g3396079
BLAST score	233
E value	3.0e-19
Match length	106
% identity	45
NCBI Description	(AF080173) inositol 1,3,4-trisphosphate 5/6-kinase [Arabidopsis thaliana]

Seq. No.	393691
Contig ID	42621_1.R1084
5'-most EST	uC-osrocyp010g05b1
Method	BLASTX
NCBI GI	g3047077
BLAST score	388
E value	2.0e-37
Match length	177
% identity	51
NCBI Description	(AF058914) contains similarity to the conserved C-terminal domain of helicases (Pfam: helicase_C.hmm, score: 90.11), similar to DEAD-box helicases [Arabidopsis thaliana]

Seq. No.	393692
Contig ID	42626_1.R1084
5'-most EST	g572208

Seq. No.	393693
Contig ID	42631_1.R1084
5'-most EST	uC-osf1M202037g05b1

Seq. No.	393694
Contig ID	42638_1.R1084
5'-most EST	g3767435

Seq. No.	393695
Contig ID	42645_1.R1084
5'-most EST	uC-osf1M202039a04b1

Seq. No.	393696
Contig ID	42666_1.R1084
5'-most EST	g2428413
Method	BLASTX
NCBI GI	g3540194
BLAST score	475
E value	2.0e-47
Match length	140
% identity	66

NCBI Description	(AC004260) AtVPS45p [Arabidopsis thaliana]
Seq. No.	393697
Contig ID	42687_1.R1084
5'-most EST	g5003351
Method	BLASTN
NCBI GI	g871985
BLAST score	118
E value	2.0e-59
Match length	271
% identity	91
NCBI Description	A.sativa Aspk11 mRNA
Seq. No.	393698
Contig ID	42689_1.R1084
5'-most EST	g4716446
Method	BLASTX
NCBI GI	g2146739
BLAST score	272
E value	4.0e-25
Match length	170
% identity	40
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana] >gi_4972059_emb_CAB43927.1_ (AL078470) hexokinase [Arabidopsis thaliana]
Seq. No.	393699
Contig ID	42705_1.R1084
5'-most EST	uC-osflM202040d12b1
Seq. No.	393700
Contig ID	42709_1.R1084
5'-most EST	uC-osflM202040e04b1
Method	BLASTX
NCBI GI	g4455335
BLAST score	443
E value	9.0e-44
Match length	202
% identity	25
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]
Seq. No.	393701
Contig ID	42731_1.R1084
5'-most EST	uC-osflM202043a02b1
Seq. No.	393702
Contig ID	42732_1.R1084
5'-most EST	uC-osflm202107c07b1
Method	BLASTX
NCBI GI	g114657
BLAST score	720
E value	3.0e-76
Match length	140
% identity	97
NCBI Description	ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV) >gi_67926_pir__LWRZ6 H+-transporting ATP synthase (EC

3.6.1.34) chain a - rice chloroplast
>gi_11975_emb_CAA33990_ (X15901) ATPase a subunit [Oryza sativa] >gi_226693_prf__1603356U ATPase a [Oryza sativa]

Seq. No.	393703
Contig ID	42736_1.R1084
5'-most EST	uC-osf1M202050f06b1
Method	BLASTX
NCBI GI	g4102839
BLAST score	412
E value	3.0e-40
Match length	93
% identity	78
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	393704
Contig ID	42739_1.R1084
5'-most EST	uC-osf1M202052g03b1
Method	BLASTX
NCBI GI	g2145356
BLAST score	629
E value	2.0e-65
Match length	197
% identity	65
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	393705
Contig ID	42740_1.R1084
5'-most EST	g701779
Method	BLASTX
NCBI GI	g5430764
BLAST score	443
E value	1.0e-64
Match length	174
% identity	76
NCBI Description	(AC007504) Putative Phosphatidylinositol 4-kinase PI4K [Arabidopsis thaliana]

Seq. No.	393706
Contig ID	42744_1.R1084
5'-most EST	uC-osf1M202043c04b1

Seq. No.	393707
Contig ID	42766_1.R1084
5'-most EST	uC-osf1M202043e12b1

Seq. No.	393708
Contig ID	42779_1.R1084
5'-most EST	uC-osf1M202043g10b1
Method	BLASTX
NCBI GI	g584862
BLAST score	110
E value	1.0e-08
Match length	71
% identity	51
NCBI Description	CYTOCHROME P450 71A3 (CYPLXXIA3) (P-450EG3)

>gi_480397_pir__S36807 cytochrome P450 71A3 - eggplant (fragment) >gi_408142_emb_CAA50313_ (X70982) P450 hydroxylase [Solanum melongena]

Seq. No.	393709
Contig ID	42784_1.R1084
5'-most EST	uC-osf1M202047a07b1
Method	BLASTX
NCBI GI	g2495719
BLAST score	192
E value	2.0e-14
Match length	109
% identity	35
NCBI Description	HYPOTHETICAL PROTEIN KIAA0196 >gi_1228043_dbj_BAA12109_ (D83780) the KIAA0196 gene is expressed ubiquitously. [Homo sapiens]

Seq. No.	393710
Contig ID	42788_1.R1084
5'-most EST	g700572
Method	BLASTX
NCBI GI	g5734634
BLAST score	446
E value	3.0e-44
Match length	128
% identity	62
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No.	393711
Contig ID	42790_1.R1084
5'-most EST	uC-osf1M202043h10b1

Seq. No.	393712
Contig ID	42802_1.R1084
5'-most EST	g3107764
Method	BLASTX
NCBI GI	g551428
BLAST score	606
E value	1.0e-109
Match length	284
% identity	71
NCBI Description	(X78996) tetrafunctional protein [Cucumis sativus]

Seq. No.	393713
Contig ID	42813_1.R1084
5'-most EST	g4878788
Method	BLASTX
NCBI GI	g3319355
BLAST score	735
E value	8.0e-78
Match length	167
% identity	84
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No. 393714

Contig ID	42817_1.R1084
5'-most EST	g5004791
Method	BLASTX
NCBI GI	g1669341
BLAST score	145
E value	7.0e-19
Match length	75
% identity	65
NCBI Description	(D45066) AOBP (ascorbate oxidase promoter-binding protein) [Cucurbita maxima]

Seq. No.	393715
Contig ID	42828_1.R1084
5'-most EST	g2312757
Method	BLASTX
NCBI GI	g4006877
BLAST score	231
E value	6.0e-19
Match length	80
% identity	31
NCBI Description	(Z99707) RNA-binding like protein [Arabidopsis thaliana]

Seq. No.	393716
Contig ID	42832_1.R1084
5'-most EST	uC-osflM202046f08b1
Method	BLASTX
NCBI GI	g836954
BLAST score	227
E value	5.0e-25
Match length	112
% identity	56
NCBI Description	(U20948) receptor protein kinase [Ipomoea trifida]

Seq. No.	393717
Contig ID	42834_1.R1084
5'-most EST	uC-osflM202046f10b1
Method	BLASTN
NCBI GI	g5821066
BLAST score	35
E value	7.0e-10
Match length	51
% identity	92
NCBI Description	Oryza sativa gene for WHO4, complete cds

Seq. No.	393718
Contig ID	42836_1.R1084
5'-most EST	uC-osflM202096d01b1

Seq. No.	393719
Contig ID	42837_1.R1084
5'-most EST	g701661

Seq. No.	393720
Contig ID	42838_1.R1084
5'-most EST	uC-osflM202046g05b1
Method	BLASTX
NCBI GI	g3461820

BLAST score 286
E value 3.0e-25
Match length 64
% identity 73
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 393721
Contig ID 42847_1.R1084
5'-most EST g702637

Seq. No. 393722
Contig ID 42852_1.R1084
5'-most EST uC-osflM202061h11b1

Seq. No. 393723
Contig ID 42859_1.R1084
5'-most EST uC-osroM202016e10b1

Seq. No. 393724
Contig ID 42860_1.R1084
5'-most EST uC-osflM202047b07b1
Method BLASTN
NCBI GI g5803242
BLAST score 77
E value 5.0e-35
Match length 158
% identity 86
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No. 393725
Contig ID 42904_1.R1084
5'-most EST uC-osflM202048a05b1
Method BLASTX
NCBI GI g4406780
BLAST score 457
E value 2.0e-45
Match length 113
% identity 74
NCBI Description (AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No. 393726
Contig ID 42909_1.R1084
5'-most EST g3759067
Method BLASTX
NCBI GI g5923675
BLAST score 161
E value 1.0e-15
Match length 103
% identity 50
NCBI Description (AC009326) putative mRNA capping enzyme, RNA guanylyltransferase [Arabidopsis thaliana]

Seq. No. 393727
Contig ID 42911_1.R1084
5'-most EST uC-osflm202101f12b1
Method BLASTX

NCBI GI g4585977
BLAST score 308
E value 5.0e-28
Match length 85
% identity 62
NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No. 393728
Contig ID 42912_1.R1084
5'-most EST uC-osflM202048b05b1
Method BLASTX
NCBI GI g5668645
BLAST score 598
E value 7.0e-62
Match length 194
% identity 66
NCBI Description (AL109619) putative protein [Arabidopsis thaliana]

Seq. No. 393729
Contig ID 42918_1.R1084
5'-most EST g5607418
Method BLASTX
NCBI GI g1771160
BLAST score 375
E value 7.0e-36
Match length 142
% identity 49
NCBI Description (X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999.1_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No. 393730
Contig ID 42922_1.R1084
5'-most EST uC-osflM202048c09b1
Method BLASTX
NCBI GI g4538967
BLAST score 629
E value 1.0e-65
Match length 175
% identity 74
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis thaliana]

Seq. No. 393731
Contig ID 42925_1.R1084
5'-most EST g4715387
Method BLASTX
NCBI GI g3327196
BLAST score 215
E value 2.0e-54
Match length 228
% identity 51
NCBI Description (AB014591) KIAA0691 protein [Homo sapiens]

Seq. No. 393732
Contig ID 42926_1.R1084
5'-most EST g3759022

Seq. No. 393733
Contig ID 42931_1.R1084
5'-most EST g2427417
Method BLASTX
NCBI GI g4587585
BLAST score 470
E value 5.0e-47
Match length 107
% identity 79
NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393734
Contig ID 42934_1.R1084
5'-most EST g2312158

Seq. No. 393735
Contig ID 42941_1.R1084
5'-most EST g2431446
Method BLASTX
NCBI GI g2980778
BLAST score 151
E value 1.0e-09
Match length 77
% identity 40
NCBI Description (AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393736
Contig ID 42945_1.R1084
5'-most EST uC-osf1M202068f01b1

Seq. No. 393737
Contig ID 42948_1.R1084
5'-most EST g286734

Seq. No. 393738
Contig ID 42957_1.R1084
5'-most EST g2442663
Method BLASTX
NCBI GI g6017111
BLAST score 228
E value 3.0e-37
Match length 129
% identity 63
NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]

Seq. No. 393739
Contig ID 42965_1.R1084
5'-most EST g570124

Seq. No. 393740
Contig ID 42972_1.R1084
5'-most EST uC-osf1M202049b08b1

Seq. No. 393741
Contig ID 42981_1.R1084
5'-most EST g569863

Seq. No. 393742
Contig ID 42984_1.R1084
5'-most EST g428323
Method BLASTX
NCBI GI g5734786
BLAST score 298
E value 2.0e-33
Match length 113
% identity 59
NCBI Description (AC007980) Similar to oligopeptidases [Arabidopsis thaliana]

Seq. No. 393743
Contig ID 42993_1.R1084
5'-most EST uC-osf1M202049f04b1

Seq. No. 393744
Contig ID 42995_1.R1084
5'-most EST uC-osf1M202049f06b1

Seq. No. 393745
Contig ID 43005_1.R1084
5'-most EST uC-osrocyp013e08b1

Seq. No. 393746
Contig ID 43012_1.R1084
5'-most EST uC-osf1M202049h06b1
Method BLASTX
NCBI GI g4455192
BLAST score 344
E value 3.0e-32
Match length 158
% identity 27
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 393747
Contig ID 43018_1.R1084
5'-most EST uC-osf1M202050a06b1
Method BLASTX
NCBI GI g5902445
BLAST score 170
E value 1.0e-12
Match length 67
% identity 55
NCBI Description (AB030283) GAG-POL precursor [Oryza sativa]

Seq. No. 393748
Contig ID 43023_1.R1084
5'-most EST g4881059

Seq. No. 393749
Contig ID 43026_1.R1084
5'-most EST g1632086
Method BLASTX
NCBI GI g4218120
BLAST score 407

E value	6.0e-65
Match length	190
% identity	66
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	393750
Contig ID	43028_1.R1084
5'-most EST	uC-osflM202050d06b1
Method	BLASTX
NCBI GI	g3063693
BLAST score	306
E value	1.0e-27
Match length	149
% identity	34
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	393751
Contig ID	43031_1.R1084
5'-most EST	g5456487
Method	BLASTX
NCBI GI	g2909521
BLAST score	143
E value	1.0e-08
Match length	184
% identity	27
NCBI Description	(AL021932) hypothetical protein Rv0446c [Mycobacterium tuberculosis]

Seq. No.	393752
Contig ID	43039_1.R1084
5'-most EST	g2431475
Method	BLASTX
NCBI GI	g4371293
BLAST score	160
E value	1.0e-10
Match length	100
% identity	42
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393753
Contig ID	43045_1.R1084
5'-most EST	uC-osflm202106h07b1

Seq. No.	393754
Contig ID	43056_1.R1084
5'-most EST	uC-osroM202037g05b1
Method	BLASTN
NCBI GI	g5410347
BLAST score	51
E value	2.0e-19
Match length	115
% identity	86
NCBI Description	Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No.	393755
Contig ID	43081_1.R1084

5'-most EST	uC-osf1M202051d03b1
Seq. No.	393756
Contig ID	43098_1.R1084
5'-most EST	uC-osf1M202051g10b1
Seq. No.	393757
Contig ID	43110_1.R1084
5'-most EST	uC-osf1m202104h02b1
Seq. No.	393758
Contig ID	43115_1.R1084
5'-most EST	g5004802
Method	BLASTX
NCBI GI	g2062167
BLAST score	439
E value	3.0e-43
Match length	154
% identity	61
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]
Seq. No.	393759
Contig ID	43117_2.R1084
5'-most EST	g2800973
Method	BLASTN
NCBI GI	g5670155
BLAST score	59
E value	3.0e-24
Match length	360
% identity	52
NCBI Description	Oryza sativa subsp. japonica BAC clone 34K24, complete sequence
Seq. No.	393760
Contig ID	43126_1.R1084
5'-most EST	uC-osf1M202040b01b1
Seq. No.	393761
Contig ID	43131_1.R1084
5'-most EST	uC-osf1m202002d11b1
Method	BLASTX
NCBI GI	g3327868
BLAST score	353
E value	5.0e-33
Match length	129
% identity	57
NCBI Description	(AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana] >gi_4972068_emb_CAB43875.1_ (AL078467) COP1-interacting protein 7 (CIP7) [Arabidopsis thaliana]
Seq. No.	393762
Contig ID	43153_1.R1084
5'-most EST	uC-osf1M202053a05b1
Method	BLASTX
NCBI GI	g3132825
BLAST score	546

E value 6.0e-56
Match length 174
% identity 60
NCBI Description (AF063403) putative cytosine-5 DNA methyltransferase [Zea mays]

Seq. No. 393763
Contig ID 43164_1.R1084
5'-most EST uC-osf1M202053c01b1
Method BLASTX
NCBI GI g4803944
BLAST score 267
E value 5.0e-35
Match length 154
% identity 51
NCBI Description (AC006264) putative C2-domain protein (prosite: PD0C00380) [Arabidopsis thaliana]

Seq. No. 393764
Contig ID 43210_1.R1084
5'-most EST g5038934
Method BLASTX
NCBI GI g4099914
BLAST score 212
E value 8.0e-17
Match length 58
% identity 67
NCBI Description (U91857) ethylene-responsive element binding protein homolog [Stylosanthes hamata]

Seq. No. 393765
Contig ID 43215_1.R1084
5'-most EST g5851110
Method BLASTX
NCBI GI g2827651
BLAST score 315
E value 1.0e-33
Match length 151
% identity 25
NCBI Description (AL021637) putative protein [Arabidopsis thaliana]

Seq. No. 393766
Contig ID 43221_1.R1084
5'-most EST uC-osf1M202054c01b1

Seq. No. 393767
Contig ID 43229_1.R1084
5'-most EST uC-osf1M202054d06b1
Method BLASTX
NCBI GI g4006914
BLAST score 465
E value 1.0e-61
Match length 158
% identity 73
NCBI Description (Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]

Seq. No.	393768
Contig ID	43234_1.R1084
5'-most EST	uC-osflM202054d12b1
Method	BLASTX
NCBI GI	g3292830
BLAST score	158
E value	2.0e-10
Match length	122
% identity	37
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	393769
Contig ID	43240_1.R1084
5'-most EST	uC-osflM202092d12b1

Seq. No.	393770
Contig ID	43242_1.R1084
5'-most EST	uC-osflM202051b09b1

Seq. No.	393771
Contig ID	43246_1.R1084
5'-most EST	g2428331

Seq. No.	393772
Contig ID	43252_1.R1084
5'-most EST	uC-osrocyp012d06b1

Seq. No.	393773
Contig ID	43255_1.R1084
5'-most EST	uC-osflM202054g06b1

Seq. No.	393774
Contig ID	43266_1.R1084
5'-most EST	g3759773

Seq. No.	393775
Contig ID	43268_1.R1084
5'-most EST	g2427324
Method	BLASTX
NCBI GI	g1351117
BLAST score	144
E value	1.0e-08
Match length	136
% identity	8
NCBI Description	SEX-DETERMINING REGION Y PROTEIN (TESTIS-DETERMINING FACTOR) >gi_479881_pir__S35565 sex-determining protein - mouse >gi_1085549_pir__S43344 sex-determining protein - mouse >gi_2623375 (U70655) sex determining protein [Mus musculus] >gi_2623377 (U70656) sex determining protein [Mus musculus] >gi_6006571_emb_CAB56798.1_ (X67204) sex determining region of Y protein [Mus musculus]

Seq. No.	393776
Contig ID	43270_1.R1084
5'-most EST	g569390

Seq. No.	393777

Contig ID	43286_1.R1084
5'-most EST	g2312198
Method	BLASTX
NCBI GI	g2493646
BLAST score	240
E value	4.0e-20
Match length	95
% identity	65
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi_309559 (L21008) chaperonin 60 [Zea mays] >gi_309561 (L21006) mitochondrial chaperonin 60 [Zea mays]

Seq. No.	393778
Contig ID	43289_1.R1084
5'-most EST	g1631748
Method	BLASTX
NCBI GI	g544250
BLAST score	278
E value	9.0e-27
Match length	109
% identity	61
NCBI Description	ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) >gi_541860_pir__A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana

Seq. No.	393779
Contig ID	43297_1.R1084
5'-most EST	g2312592
Method	BLASTX
NCBI GI	g3426039
BLAST score	409
E value	1.0e-39
Match length	133
% identity	59
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	393780
Contig ID	43303_1.R1084
5'-most EST	uC-osf1M202061d03b1

Seq. No.	393781
Contig ID	43309_1.R1084
5'-most EST	g286739

Seq. No.	393782
Contig ID	43338_1.R1084
5'-most EST	uC-osf1M202062b03b1
Method	BLASTX
NCBI GI	g283004
BLAST score	431
E value	3.0e-42
Match length	125
% identity	38
NCBI Description	DNA-binding protein Gt-2 - rice >gi_20249_emb_CAA48328_ (X68261) gt-2 [Oryza sativa]

Seq. No.	393783

Contig ID	43355_1.R1084
5'-most EST	g572394
Method	BLASTX
NCBI GI	g2062167
BLAST score	594
E value	2.0e-61
Match length	155
% identity	72
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	393784
Contig ID	43363_1.R1084
5'-most EST	uC-osflm202120f03b1

Seq. No.	393785
Contig ID	43374_1.R1084
5'-most EST	g286811

Seq. No.	393786
Contig ID	43379_1.R1084
5'-most EST	uC-osrocyp007h11b1

Seq. No.	393787
Contig ID	43382_1.R1084
5'-most EST	uC-osflM202066b03b1

Seq. No.	393788
Contig ID	43388_1.R1084
5'-most EST	uC-osflM202066b11b1
Method	BLASTX
NCBI GI	g3395429
BLAST score	268
E value	3.0e-23
Match length	131
% identity	41
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393789
Contig ID	43390_1.R1084
5'-most EST	uC-osflm202101f06b1
Method	BLASTX
NCBI GI	g4680201
BLAST score	272
E value	8.0e-24
Match length	99
% identity	61
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	393790
Contig ID	43392_1.R1084
5'-most EST	g700986
Method	BLASTX
NCBI GI	g5668772
BLAST score	198
E value	9.0e-28
Match length	147

% identity	50
NCBI Description	(AC005916) Similar to gb_Z84571 anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus. [Arabidopsis thaliana]

Seq. No.	393791
Contig ID	43394_1.R1084
5'-most EST	uC-osflM202066c09b1
Method	BLASTX
NCBI GI	g4539333
BLAST score	194
E value	1.0e-14
Match length	83
% identity	55
NCBI Description	(AL035539) putative amino acid transport protein [Arabidopsis thaliana]

Seq. No.	393792
Contig ID	43397_1.R1084
5'-most EST	g5005053
Method	BLASTX
NCBI GI	g5103827
BLAST score	277
E value	2.0e-25
Match length	99
% identity	56
NCBI Description	(AC007591) ESTs gb_F20110 and gb_F20109 come from this gene. [Arabidopsis thaliana]

Seq. No.	393793
Contig ID	43399_1.R1084
5'-most EST	uC-osflM202066d02b1
Method	BLASTX
NCBI GI	g4587584
BLAST score	423
E value	7.0e-64
Match length	172
% identity	48
NCBI Description	(AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	393794
Contig ID	43413_1.R1084
5'-most EST	g5002803
Method	BLASTX
NCBI GI	g5917666
BLAST score	197
E value	8.0e-18
Match length	105
% identity	53
NCBI Description	(AF159297) extensin-like protein [Zea mays]

Seq. No.	393795
Contig ID	43425_1.R1084
5'-most EST	uC-osflM202066f09b1
Method	BLASTX
NCBI GI	g1362162
BLAST score	507

E value	3.0e-51
Match length	151
% identity	63
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	393796
Contig ID	43426_1.R1084
5'-most EST	uC-osflM202066f10b1
Method	BLASTX
NCBI GI	g2459424
BLAST score	485
E value	1.0e-48
Match length	180
% identity	50
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	393797
Contig ID	43431_1.R1084
5'-most EST	g5803407

Seq. No.	393798
Contig ID	43448_1.R1084
5'-most EST	g4715603
Method	BLASTX
NCBI GI	g2760832
BLAST score	173
E value	3.0e-12
Match length	100
% identity	45
NCBI Description	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]

Seq. No.	393799
Contig ID	43453_1.R1084
5'-most EST	uC-osflM202068b10b1

Seq. No.	393800
Contig ID	43454_1.R1084
5'-most EST	uC-osflM202068b12b1

Seq. No.	393801
Contig ID	43459_1.R1084
5'-most EST	g570061
Method	BLASTX
NCBI GI	g4091117
BLAST score	419
E value	5.0e-41
Match length	109
% identity	72
NCBI Description	(AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No.	393802
Contig ID	43473_1.R1084
5'-most EST	g3061025

Seq. No.	393803

Contig ID	43488_1.R1084
5'-most EST	uC-osrocyp015c08b1
Method	BLASTX
NCBI GI	g1399277
BLAST score	183
E value	3.0e-13
Match length	119
% identity	37
NCBI Description	(U31836) calmodulin-domain protein kinase CDPK isoform 7 [Arabidopsis thaliana]

Seq. No.	393804
Contig ID	43502_1.R1084
5'-most EST	g4880958
Method	BLASTX
NCBI GI	g5668813
BLAST score	144
E value	2.0e-21
Match length	111
% identity	51
NCBI Description	(AC007519) Similar to gb_X77136 HSR203J protein from Nicotiana tabacum and is a member of the PF_00135 Carboxylesterase family. ESTs gb_Z25688 and gb_F14025 come from this gene. [Arabidopsis thaliana]

Seq. No.	393805
Contig ID	43507_1.R1084
5'-most EST	g2427475
Method	BLASTX
NCBI GI	g3914005
BLAST score	1024
E value	1.0e-143
Match length	292
% identity	92
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays]

Seq. No.	393806
Contig ID	43528_1.R1084
5'-most EST	uC-osf1M202075a02b1

Seq. No.	393807
Contig ID	43544_1.R1084
5'-most EST	g702369
Method	BLASTX
NCBI GI	g2465925
BLAST score	174
E value	2.0e-12
Match length	62
% identity	53
NCBI Description	(AF024649) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	393808
Contig ID	43545_1.R1084
5'-most EST	uC-osf1M202075h10b1
Method	BLASTX

NCBI GI g2388585
BLAST score 400
E value 1.0e-38
Match length 139
% identity 55
NCBI Description (AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb_U88169). [Arabidopsis thaliana]

Seq. No. 393809
Contig ID 43545_2.R1084
5'-most EST g5002992
Method BLASTX
NCBI GI g2388585
BLAST score 664
E value 1.0e-69
Match length 176
% identity 78
NCBI Description (AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb_U88169). [Arabidopsis thaliana]

Seq. No. 393810
Contig ID 43546_1.R1084
5'-most EST uC-osflM202076a09b1

Seq. No. 393811
Contig ID 43548_1.R1084
5'-most EST uC-osflM202076b07b1

Seq. No. 393812
Contig ID 43575_1.R1084
5'-most EST g3061191

Seq. No. 393813
Contig ID 43582_1.R1084
5'-most EST uC-osflM202080d10b1
Method BLASTX
NCBI GI g5042409
BLAST score 154
E value 1.0e-09
Match length 66
% identity 44
NCBI Description (AC006193) Putative membrane related protein [Arabidopsis thaliana]

Seq. No. 393814
Contig ID 43584_1.R1084
5'-most EST uC-osflM202080e02b1
Method BLASTX
NCBI GI g4971998
BLAST score 527
E value 1.0e-53
Match length 157
% identity 68
NCBI Description (Y14685) polynucleotide phosphorylase [Arabidopsis thaliana] >gi_4972000_emb_CAB43865.1_ (Y14686) polynucleotide phosphorylase [Arabidopsis thaliana]

Seq. No. 393815
Contig ID 43613_1.R1084
5'-most EST g426431

Seq. No. 393816
Contig ID 43614_1.R1084
5'-most EST g5055957

Seq. No. 393817
Contig ID 43617_1.R1084
5'-most EST uC-osflM202081d01b1
Method BLASTX
NCBI GI g4220476
BLAST score 551
E value 3.0e-56
Match length 222
% identity 51
NCBI Description (AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No. 393818
Contig ID 43625_1.R1084
5'-most EST g2309915
Method BLASTX
NCBI GI g542058
BLAST score 252
E value 1.0e-21
Match length 96
% identity 51
NCBI Description HSR203J protein - common tobacco >gi_444002_emb_CAA54393_ (X77136) HSR203J [Nicotiana tabacum]

Seq. No. 393819
Contig ID 43631_1.R1084
5'-most EST uC-osflM202081f07b1

Seq. No. 393820
Contig ID 43632_1.R1084
5'-most EST g2312637

Seq. No. 393821
Contig ID 43635_1.R1084
5'-most EST uC-osflM202089h03b1

Seq. No. 393822
Contig ID 43640_1.R1084
5'-most EST g569087
Method BLASTX
NCBI GI g1174718
BLAST score 396
E value 3.0e-38
Match length 191
% identity 29
NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	393823
Contig ID	43649_2.R1084
5'-most EST	uC-osflM202082b08b1
Seq. No.	393824
Contig ID	43661_1.R1084
5'-most EST	uC-osflM202082e04b1
Method	BLASTX
NCBI GI	g4455287
BLAST score	311
E value	2.0e-28
Match length	97
% identity	64
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]
Seq. No.	393825
Contig ID	43664_1.R1084
5'-most EST	uC-osflm202002h07b1
Method	BLASTX
NCBI GI	g1848212
BLAST score	716
E value	9.0e-76
Match length	148
% identity	44
NCBI Description	(Y11209) protein disulfide-isomerase precursor [Nicotiana tabacum]
Seq. No.	393826
Contig ID	43668_1.R1084
5'-most EST	g4879060
Method	BLASTX
NCBI GI	g3292830
BLAST score	223
E value	4.0e-18
Match length	121
% identity	45
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	393827
Contig ID	43672_1.R1084
5'-most EST	g2309702
Method	BLASTX
NCBI GI	g1854378
BLAST score	1458
E value	1.0e-162
Match length	324
% identity	85
NCBI Description	(AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]
Seq. No.	393828
Contig ID	43680_1.R1084
5'-most EST	uC-osflM202082h08b1
Method	BLASTX
NCBI GI	g1272347
BLAST score	204
E value	6.0e-16

Match length	79
% identity	52
NCBI Description	(U51739) secreted glycoprotein 2 [Ipomoea trifida]

Seq. No.	393829
Contig ID	43702_1.R1084
5'-most EST	uC-osf1m202106e05b1
Method	BLASTX
NCBI GI	g3395432
BLAST score	718
E value	8.0e-76
Match length	190
% identity	72
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana] >gi_5731261_gb_AAD48838.1_AF166352_1 (AF166352) alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis thaliana]

Seq. No.	393830
Contig ID	43707_1.R1084
5'-most EST	uC-osf1m202100b02b1

Seq. No.	393831
Contig ID	43708_1.R1084
5'-most EST	g1854160
Method	BLASTX
NCBI GI	g3080420
BLAST score	555
E value	7.0e-57
Match length	134
% identity	81
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	393832
Contig ID	43717_1.R1084
5'-most EST	uC-osf1M202083g01b1
Method	BLASTX
NCBI GI	g4982479
BLAST score	234
E value	2.0e-19
Match length	159
% identity	33
NCBI Description	(AF069441) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	393833
Contig ID	43727_1.R1084
5'-most EST	uC-osf1M202089a02b1

Seq. No.	393834
Contig ID	43734_1.R1084
5'-most EST	uC-osf1M202089c04b1

Seq. No.	393835
Contig ID	43739_1.R1084
5'-most EST	uC-osf1M202089b07b1

Method	BLASTN
NCBI GI	g169819
BLAST score	403
E value	0.0e+00
Match length	526
% identity	95
NCBI Description	Rice gene encoding three ribosomal RNA's: the 17S, 3' end; 5.8S, complete; 25S, 5' end

Seq. No.	393836
Contig ID	43775_1.R1084
5'-most EST	g1631404
Method	BLASTX
NCBI GI	g266463
BLAST score	554
E value	9.0e-57
Match length	118
% identity	88
NCBI Description	3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_82259_pir__S25670 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor - potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi_445064_prf__1908380A beta isopropylmalate dehydrogenase [Solanum tuberosum]

Seq. No.	393837
Contig ID	43800_1.R1084
5'-most EST	uC-osf1M202090b12b1

Seq. No.	393838
Contig ID	43801_1.R1084
5'-most EST	uC-osf1M202090c07b1
Method	BLASTX
NCBI GI	g4056477
BLAST score	208
E value	1.0e-16
Match length	51
% identity	37
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	393839
Contig ID	43819_1.R1084
5'-most EST	g4878574

Seq. No.	393840
Contig ID	43821_1.R1084
5'-most EST	uC-osf1M202090f03b1
Method	BLASTX
NCBI GI	g2911058
BLAST score	344
E value	1.0e-40
Match length	173
% identity	57
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 393841

Contig ID	43825_1.R1084
5'-most EST	g3106493
Method	BLASTX
NCBI GI	g4104060
BLAST score	501
E value	1.0e-54
Match length	133
% identity	80
NCBI Description	(AF031231) S222 [Triticum aestivum]

Seq. No.	393842
Contig ID	43841_1.R1084
5'-most EST	uC-osf1M202091a09b1

Seq. No.	393843
Contig ID	43842_1.R1084
5'-most EST	uC-osf1M202094h03b1
Method	BLASTX
NCBI GI	g5360953
BLAST score	360
E value	2.0e-38
Match length	106
% identity	83
NCBI Description	(AJ225059) v-ATPase subunit D [Arabidopsis thaliana]

Seq. No.	393844
Contig ID	43850_1.R1084
5'-most EST	uC-osf1M202091d02b1
Method	BLASTX
NCBI GI	g4063743
BLAST score	147
E value	3.0e-09
Match length	64
% identity	48
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393845
Contig ID	43856_1.R1084
5'-most EST	g3766658
Method	BLASTX
NCBI GI	g1706082
BLAST score	610
E value	3.0e-68
Match length	151
% identity	85
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478.1_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	393846
Contig ID	43867_1.R1084
5'-most EST	uC-osf1M202092a09b1
Method	BLASTX

NCBI GI	g2781347
BLAST score	396
E value	4.0e-40
Match length	142
% identity	59
NCBI Description	(AC003113) F24O1.3 [Arabidopsis thaliana]

Seq. No.	393847
Contig ID	43870_1.R1084
5'-most EST	uC-osflm202104f12b1
Method	BLASTX
NCBI GI	g5738367
BLAST score	285
E value	4.0e-25
Match length	186
% identity	45
NCBI Description	(AL078620) putative protein [Arabidopsis thaliana]

Seq. No.	393848
Contig ID	43874_1.R1084
5'-most EST	g3761381
Method	BLASTX
NCBI GI	g1203832
BLAST score	279
E value	9.0e-42
Match length	133
% identity	67
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No.	393849
Contig ID	43888_1.R1084
5'-most EST	g5038552

Seq. No.	393850
Contig ID	43898_1.R1084
5'-most EST	uC-osflM202092e09b1
Method	BLASTX
NCBI GI	g1001478
BLAST score	223
E value	4.0e-21
Match length	156
% identity	36
NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]

Seq. No.	393851
Contig ID	43909_1.R1084
5'-most EST	uC-osflM202092f12b1

Seq. No.	393852
Contig ID	43925_1.R1084
5'-most EST	g3762374
Method	BLASTX
NCBI GI	g2980641
BLAST score	434
E value	1.0e-77

Match length 201
% identity 80
NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No. 393853
Contig ID 43929_1.R1084
5'-most EST g1631616
Method BLASTX
NCBI GI g6006867
BLAST score 175
E value 2.0e-12
Match length 79
% identity 50
NCBI Description (AC009540) unknown protein [Arabidopsis thaliana]

Seq. No. 393854
Contig ID 43933_1.R1084
5'-most EST uC-osflm202002a05b1
Method BLASTX
NCBI GI g3128186
BLAST score 214
E value 6.0e-17
Match length 60
% identity 65
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393855
Contig ID 43943_1.R1084
5'-most EST uC-osflM202094c07b1

Seq. No. 393856
Contig ID 43945_1.R1084
5'-most EST g2310120
Method BLASTX
NCBI GI g4689108
BLAST score 193
E value 1.0e-14
Match length 94
% identity 41
NCBI Description (AF077030) hypothetical 43.2 kDa protein [Homo sapiens] >gi_4929577_gb_AAD34049.1_AF151812_1 (AF151812) CGI-54 protein [Homo sapiens]

Seq. No. 393857
Contig ID 43947_1.R1084
5'-most EST uC-osflM202094d03b1
Method BLASTX
NCBI GI g2499709
BLAST score 538
E value 6.0e-65
Match length 152
% identity 88
NCBI Description PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1) >gi_1020415_dbj_BAA11136_ (D73411) phospholipase D [Oryza sativa] >gi_1902903_dbj_BAA19467_ (AB001920) phospholipase D [Oryza sativa]

Seq. No. 393858
Contig ID 43949_1.R1084
5'-most EST g2800227
Method BLASTX
NCBI GI g4467126
BLAST score 183
E value 2.0e-13
Match length 132
% identity 30
NCBI Description (AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No. 393859
Contig ID 43965_1.R1084
5'-most EST g700358

Seq. No. 393860
Contig ID 43967_1.R1084
5'-most EST uC-osroM202022e03b1
Method BLASTX
NCBI GI g2827552
BLAST score 282
E value 5.0e-25
Match length 97
% identity 56
NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 393861
Contig ID 43975_1.R1084
5'-most EST g5004163
Method BLASTN
NCBI GI g600766
BLAST score 40
E value 6.0e-13
Match length 88
% identity 88
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds

Seq. No. 393862
Contig ID 43980_1.R1084
5'-most EST g571738
Method BLASTX
NCBI GI g6006379
BLAST score 520
E value 1.0e-52
Match length 251
% identity 44
NCBI Description (AP000559) ESTs AU078277(S1084),AU078273(S13585), D47857(S13585) correspond to a region of the predicted gene.; Similar to Caenorhabditis elegans cosmid C15H9; hypothetical protein (U56965) [Oryza sativa]

Seq. No. 393863
Contig ID 43982_1.R1084
5'-most EST g4879589
Method BLASTX

NCBI GI g3915039
BLAST score 287
E value 1.0e-25
Match length 98
% identity 60
NCBI Description SUGAR CARRIER PROTEIN C >gi_169718 (L08196) sugar carrier protein [Ricinus communis]

Seq. No. 393864
Contig ID 43983_1.R1084
5'-most EST uC-osflM202095a12b1
Method BLASTX
NCBI GI g2827665
BLAST score 262
E value 2.0e-22
Match length 77
% identity 64
NCBI Description (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No. 393865
Contig ID 43985_1.R1084
5'-most EST g4969340

Seq. No. 393866
Contig ID 43990_1.R1084
5'-most EST uC-osflM202095a09b1
Method BLASTX
NCBI GI g4582467
BLAST score 444
E value 1.0e-43
Match length 166
% identity 54
NCBI Description (AC007071) putative calcium dependent protein kinase; contains protein kinase domain [Arabidopsis thaliana] >gi_4589951_gb_AAD26469.1_AC007169_1 (AC007169) putative calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No. 393867
Contig ID 44036_1.R1084
5'-most EST uC-osflM202095h12b1

Seq. No. 393868
Contig ID 44045_1.R1084
5'-most EST uC-osflM202096b05b1
Method BLASTN
NCBI GI g5734616
BLAST score 173
E value 1.0e-92
Match length 173
% identity 100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No. 393869
Contig ID 44048_1.R1084
5'-most EST g2800589
Method BLASTX

NCBI GI	g4835797
BLAST score	392
E value	8.0e-38
Match length	158
% identity	55
NCBI Description	(AC007296) Strong similarity to gb_U61231 cytochrome P450 from Arabidopsis thaliana and is a member of the PF_00067 Cytochrome P450 family. ESTs gb_Z30775 and gb_Z30776 come from this gene

Seq. No.	393870
Contig ID	44056_1.R1084
5'-most EST	uC-osflM202096e05b1

Seq. No.	393871
Contig ID	44064_1.R1084
5'-most EST	g2428173
Method	BLASTX
NCBI GI	g2921830
BLAST score	218
E value	3.0e-32
Match length	116
% identity	59
NCBI Description	(AF047031) IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq. No.	393872
Contig ID	44071_1.R1084
5'-most EST	g426322

Seq. No.	393873
Contig ID	44095_1.R1084
5'-most EST	uC-osflM202047f01b1
Method	BLASTX
NCBI GI	g5932551
BLAST score	308
E value	5.0e-28
Match length	124
% identity	51
NCBI Description	(AC009465) unknown protein [Arabidopsis thaliana]

Seq. No.	393874
Contig ID	44096_1.R1084
5'-most EST	uC-osflM202097e07b1
Method	BLASTX
NCBI GI	g4887010
BLAST score	351
E value	1.0e-54
Match length	165
% identity	68
NCBI Description	(AF123503) Nt-gh3 deduced protein [Nicotiana tabacum]

Seq. No.	393875
Contig ID	44113_1.R1084
5'-most EST	g2428879

Seq. No.	393876
Contig ID	44147_1.R1084

5'-most EST	g3106653
Seq. No.	393877
Contig ID	44157_1.R1084
5'-most EST	uC-osflM202115a04b1
Method	BLASTX
NCBI GI	g6041792
BLAST score	229
E value	4.0e-19
Match length	65
% identity	74
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.	393878
Contig ID	44168_1.R1084
5'-most EST	g701079
Seq. No.	393879
Contig ID	44168_2.R1084
5'-most EST	uC-osflM202115e01b1
Seq. No.	393880
Contig ID	44175_1.R1084
5'-most EST	g569987
Seq. No.	393881
Contig ID	44176_1.R1084
5'-most EST	uC-osflM202115h03b1
Seq. No.	393882
Contig ID	44208_1.R1084
5'-most EST	g700782
Method	BLASTX
NCBI GI	g1076288
BLAST score	409
E value	7.0e-40
Match length	105
% identity	71
NCBI Description	amino acid permease AAP3 - Arabidopsis thaliana
Seq. No.	393883
Contig ID	44238_1.R1084
5'-most EST	g2310640
Method	BLASTX
NCBI GI	g4490292
BLAST score	210
E value	9.0e-17
Match length	72
% identity	60
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]
Seq. No.	393884
Contig ID	44247_1.R1084
5'-most EST	uC-osflm202002a12b1
Method	BLASTX
NCBI GI	g5042423
BLAST score	243

E value	2.0e-20
Match length	108
% identity	48
NCBI Description	(AC006193) Hypothetical Protein [Arabidopsis thaliana]

Seq. No.	393885
Contig ID	44248_1.R1084
5'-most EST	g701528
Method	BLASTX
NCBI GI	g4836919
BLAST score	143
E value	2.0e-16
Match length	69
% identity	70
NCBI Description	(AC007153) 99202 [Arabidopsis thaliana]

Seq. No.	393886
Contig ID	44255_1.R1084
5'-most EST	uC-osflm202002c08b1
Method	BLASTX
NCBI GI	g2894288
BLAST score	205
E value	5.0e-16
Match length	87
% identity	48
NCBI Description	(AL021837) putative proteome subunit [Schizosaccharomyces pombe]

Seq. No.	393887
Contig ID	44258_1.R1084
5'-most EST	uC-osflm202002c06b1
Method	BLASTX
NCBI GI	g5080792
BLAST score	266
E value	5.0e-23
Match length	119
% identity	46
NCBI Description	(AC007576) Unknown protein [Arabidopsis thaliana]

Seq. No.	393888
Contig ID	44273_1.R1084
5'-most EST	g3762069
Method	BLASTX
NCBI GI	g1907270
BLAST score	188
E value	5.0e-14
Match length	44
% identity	73
NCBI Description	(X96761) sulphate transporter protein [Sporobolus stapfianus]

Seq. No.	393889
Contig ID	44289_1.R1084
5'-most EST	uC-osroM202022g09b1

Seq. No.	393890
Contig ID	44292_1.R1084

5'-most EST	uC-osflm202002g10b1
Method	BLASTX
NCBI GI	g4887543
BLAST score	503
E value	9.0e-51
Match length	116
% identity	83
NCBI Description	(AJ012278) ATP-dependent Clp protease subunit ClpP [Arabidopsis thaliana] >gi_5360579_dbj_BAA82065.1_ (AB022326) nClpP1 [Arabidopsis thaliana]

Seq. No.	393891
Contig ID	44303_1.R1084
5'-most EST	uC-osflm202099a06b1

Seq. No.	393892
Contig ID	44306_1.R1084
5'-most EST	uC-osflm202099a11b1
Method	BLASTX
NCBI GI	g115577
BLAST score	663
E value	1.0e-69
Match length	143
% identity	87
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME (PEPCASE) >gi_348536_pir__S28614 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sugarcane hybrid H32-8560 >gi_169844 (M86661) phosphoenolpyruvate carboxylase [Saccharum sp.]

Seq. No.	393893
Contig ID	44322_1.R1084
5'-most EST	uC-osrocyp033e02b1

Seq. No.	393894
Contig ID	44341_1.R1084
5'-most EST	uC-osflm202099f10b1
Method	BLASTX
NCBI GI	g4220477
BLAST score	154
E value	5.0e-10
Match length	117
% identity	40
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	393895
Contig ID	44351_1.R1084
5'-most EST	uC-osflm202099h04b1

Seq. No.	393896
Contig ID	44355_1.R1084
5'-most EST	g2312667
Method	BLASTX
NCBI GI	g3236259
BLAST score	224
E value	3.0e-31
Match length	116

% identity	67
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana] >gi_4895207_gb_AAD32794.1_AC007661_31 (AC007661) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	393897
Contig ID	44357_1.R1084
5'-most EST	g2312125
Method	BLASTX
NCBI GI	g4508077
BLAST score	320
E value	2.0e-29
Match length	74
% identity	80
NCBI Description	(AC005882) 62114 [Arabidopsis thaliana]

Seq. No.	393898
Contig ID	44362_1.R1084
5'-most EST	g427868
Method	BLASTX
NCBI GI	g1314711
BLAST score	314
E value	1.0e-28
Match length	135
% identity	51
NCBI Description	(U54615) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_3068712 (AF049236) calcium dependent protein kinase [Arabidopsis thaliana]

Seq. No.	393899
Contig ID	44379_1.R1084
5'-most EST	g2309917

Seq. No.	393900
Contig ID	44382_1.R1084
5'-most EST	uC-osflm202100c08b1

Seq. No.	393901
Contig ID	44402_1.R1084
5'-most EST	uC-osflm202100e09b1

Seq. No.	393902
Contig ID	44406_1.R1084
5'-most EST	uC-osflm202100f03b1
Method	BLASTN
NCBI GI	g3819495
BLAST score	78
E value	1.0e-35
Match length	168
% identity	87
NCBI Description	Hordeum vulgare genomic DNA fragment; clone MWG2025.rev

Seq. No.	393903
Contig ID	44408_1.R1084
5'-most EST	g3762386
Method	BLASTX
NCBI GI	g2506139

BLAST score 454
E value 3.0e-79
Match length 205
% identity 75
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No. 393904
Contig ID 44408_2.R1084
5'-most EST g3768184
Method BLASTN
NCBI GI g1314048
BLAST score 41
E value 1.0e-13
Match length 89
% identity 87
NCBI Description O.sativa mRNA for archain/delta-COP

Seq. No. 393905
Contig ID 44409_1.R1084
5'-most EST uC-osflm202100f07b1

Seq. No. 393906
Contig ID 44425_1.R1084
5'-most EST g3107169

Seq. No. 393907
Contig ID 44454_1.R1084
5'-most EST uC-osflm202101c01b1
Method BLASTX
NCBI GI g3046815
BLAST score 180
E value 5.0e-13
Match length 41
% identity 78
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 393908
Contig ID 44460_1.R1084
5'-most EST uC-osflm202108e07b1
Method BLASTX
NCBI GI g3850108
BLAST score 300
E value 6.0e-46
Match length 247
% identity 46
NCBI Description (AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe]

Seq. No. 393909
Contig ID 44502_1.R1084
5'-most EST uC-osroM202016e04b1
Method BLASTX
NCBI GI g3738319
BLAST score 216
E value 5.0e-29

Match length 99
% identity 65
NCBI Description (AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393910
Contig ID 44522_1.R1084
5'-most EST uC-osflm202102d11b1

Seq. No. 393911
Contig ID 44523_1.R1084
5'-most EST uC-osflm202102b10b1

Seq. No. 393912
Contig ID 44529_1.R1084
5'-most EST g2312084

Seq. No. 393913
Contig ID 44531_1.R1084
5'-most EST uC-osflm202102e09b1

Seq. No. 393914
Contig ID 44539_1.R1084
5'-most EST g4879698
Method BLASTX
NCBI GI g5478530
BLAST score 550
E value 2.0e-56
Match length 149
% identity 17
NCBI Description (AF130441) UVB-resistance protein UVR8 [Arabidopsis thaliana]

Seq. No. 393915
Contig ID 44543_1.R1084
5'-most EST g2442825
Method BLASTN
NCBI GI g5441876
BLAST score 43
E value 1.0e-14
Match length 102
% identity 93
NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No. 393916
Contig ID 44546_1.R1084
5'-most EST g2310983

Seq. No. 393917
Contig ID 44572_1.R1084
5'-most EST uC-osrocyp014b08b1
Method BLASTX
NCBI GI g3063694
BLAST score 123
E value 6.0e-15
Match length 69
% identity 64

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 393918
Contig ID 44575_1.R1084
5'-most EST g5003854

Seq. No. 393919
Contig ID 44606_1.R1084
5'-most EST uC-osflm202104e06b1
Method BLASTX
NCBI GI g3093294
BLAST score 1037
E value 1.0e-113
Match length 307
% identity 38
NCBI Description (Y12782) putative villin [Arabidopsis thaliana] >gi_5730126_emb_CAB52460.1_ (AL109796) putative villin [Arabidopsis thaliana]

Seq. No. 393920
Contig ID 44616_1.R1084
5'-most EST g4715345

Seq. No. 393921
Contig ID 44617_1.R1084
5'-most EST uC-osflm202104f11b1

Seq. No. 393922
Contig ID 44629_1.R1084
5'-most EST uC-osflm202104h06b1
Method BLASTX
NCBI GI g4502897
BLAST score 513
E value 5.0e-69
Match length 277
% identity 49
NCBI Description cleft lip and palate associated transmembrane protein 1 >gi_4039014 (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi_4063033 (AF037339) cleft lip and palate transmembrane protein 1 [Homo sapiens]

Seq. No. 393923
Contig ID 44634_1.R1084
5'-most EST uC-osflm202106a04b1
Method BLASTX
NCBI GI g1698670
BLAST score 284
E value 3.0e-25
Match length 95
% identity 53
NCBI Description (U66241) S-like RNase [Zea mays]

Seq. No. 393924
Contig ID 44639_1.R1084
5'-most EST uC-osflm202106b02b1
Method BLASTX
NCBI GI g1173194

BLAST score	240
E value	2.0e-40
Match length	148
% identity	59
NCBI Description	30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi_2119093_pir__S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013_ (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana] >gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413_ (X86734) plastid ribosomal protein S13 [Arabidopsis thaliana]

Seq. No.	393925
Contig ID	44647_1.R1084
5'-most EST	g3767947
Method	BLASTX
NCBI GI	g3193292
BLAST score	325
E value	4.0e-30
Match length	91
% identity	68
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	393926
Contig ID	44649_1.R1084
5'-most EST	uC-osflm202106c05b1

Seq. No.	393927
Contig ID	44656_1.R1084
5'-most EST	uC-osflm202106d08b1
Method	BLASTX
NCBI GI	g3335347
BLAST score	1036
E value	1.0e-149
Match length	390
% identity	64
NCBI Description	(AC004512) Contains similarity to ARI, RING finger protein gb_X98309 from Drosophila melanogaster. ESTs gb_T44383, gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and gb_AA042359 come from this gene. [Arabidopsis thaliana]

Seq. No.	393928
Contig ID	44663_1.R1084
5'-most EST	uC-osflm202106f01b1
Method	BLASTX
NCBI GI	g4995051
BLAST score	212
E value	9.0e-17
Match length	79
% identity	46
NCBI Description	(Y12695) Isovaleryl-CoA Dehydrogenase [Arabidopsis thaliana]

Seq. No.	393929
Contig ID	44674_1.R1084
5'-most EST	uC-osflm202106g02b1
Method	BLASTX
NCBI GI	g3540207
BLAST score	328
E value	2.0e-30
Match length	145
% identity	49
NCBI Description	(AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	393930
Contig ID	44692_1.R1084
5'-most EST	g4715557
Method	BLASTN
NCBI GI	g297126
BLAST score	38
E value	2.0e-11
Match length	74
% identity	88
NCBI Description	A.thaliana target DNA

Seq. No.	393931
Contig ID	44695_1.R1084
5'-most EST	g2310880
Method	BLASTX
NCBI GI	g4490737
BLAST score	338
E value	2.0e-31
Match length	154
% identity	53
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	393932
Contig ID	44707_1.R1084
5'-most EST	uC-osflm202107c03b1
Method	BLASTX
NCBI GI	g3128169
BLAST score	194
E value	1.0e-14
Match length	48
% identity	73
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393933
Contig ID	44713_1.R1084
5'-most EST	uC-osflm202107c10b1
Method	BLASTX
NCBI GI	g1245182
BLAST score	353
E value	2.0e-61
Match length	136
% identity	85
NCBI Description	(U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No.	393934

Contig ID 44718_1.R1084
5'-most EST uC-osflm202107d06b1
Method BLASTX
NCBI GI g1174470
BLAST score 180
E value 2.0e-23
Match length 87
% identity 61
NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No. 393935
Contig ID 44725_1.R1084
5'-most EST uC-osflm202107e02b1
Method BLASTX
NCBI GI g4128197
BLAST score 196
E value 5.0e-15
Match length 119
% identity 40
NCBI Description (U75273) acyl-CoA binding protein [Arabidopsis thaliana]

Seq. No. 393936
Contig ID 44731_1.R1084
5'-most EST uC-osflm202107e12b1
Method BLASTX
NCBI GI g1644291
BLAST score 162
E value 7.0e-11
Match length 134
% identity 35
NCBI Description (Z73295) receptor-like protein kinase [Catharanthus roseus]

Seq. No. 393937
Contig ID 44745_1.R1084
5'-most EST g2442728
Method BLASTX
NCBI GI g6006864
BLAST score 188
E value 6.0e-14
Match length 71
% identity 54
NCBI Description (AC009540) hypothetical protein [Arabidopsis thaliana]

Seq. No. 393938
Contig ID 44750_1.R1084
5'-most EST uC-osflM202016d07b1
Method BLASTX
NCBI GI g1657619
BLAST score 224
E value 4.0e-18
Match length 124
% identity 40
NCBI Description (U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No.	393939
Contig ID	44753_1.R1084
5'-most EST	g5056065
Method	BLASTX
NCBI GI	g2739044
BLAST score	504
E value	7.0e-51
Match length	129
% identity	72
NCBI Description	(AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max]

Seq. No.	393940
Contig ID	44778_1.R1084
5'-most EST	uC-osflm202108c09b1
Method	BLASTX
NCBI GI	g2894612
BLAST score	370
E value	3.0e-35
Match length	121
% identity	57
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	393941
Contig ID	44781_1.R1084
5'-most EST	g569170
Method	BLASTX
NCBI GI	g4115926
BLAST score	242
E value	2.0e-24
Match length	155
% identity	39
NCBI Description	(AF118222) similar to the subtilase family of serine proteases (Pfam: PF00082, Score=50.7, E=4.7e-13, n=3) [Arabidopsis thaliana] >gi_4539413_emb_CAB40046.1_ (AL049524) putative subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	393942
Contig ID	44797_1.R1084
5'-most EST	uC-osroM202037c03b1
Method	BLASTX
NCBI GI	g1170851
BLAST score	145
E value	7.0e-09
Match length	92
% identity	42
NCBI Description	MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (MAN(9)-ALPHA-MANNOSIDASE) (ALPHA-MANNOSIDASE 1A) >gi_1083410_pir__A54408 mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) - mouse >gi_474280 (U04299) mannosyl-oligosaccharide alpha-1,2-mannosidase [Mus musculus]

Seq. No.	393943
Contig ID	44803_1.R1084

5'-most EST	uC-osflm202108g02b1
Method	BLASTX
NCBI GI	g5903104
BLAST score	198
E value	4.0e-15
Match length	135
% identity	41
NCBI Description	(AC008017) Highly similar to non intermediate filament IFA binding protein [Arabidopsis thaliana]

Seq. No.	393944
Contig ID	44807_1.R1084
5'-most EST	uC-osflm202108g09b1

Seq. No.	393945
Contig ID	44809_1.R1084
5'-most EST	g570112

Seq. No.	393946
Contig ID	44809_2.R1084
5'-most EST	uC-osroM202004d08b1
Method	BLASTX
NCBI GI	g4406756
BLAST score	584
E value	2.0e-60
Match length	143
% identity	78
NCBI Description	(AC006836) putative integral membrane protein A3 [Arabidopsis thaliana]

Seq. No.	393947
Contig ID	44809_3.R1084
5'-most EST	g569944
Method	BLASTX
NCBI GI	g4406756
BLAST score	169
E value	5.0e-12
Match length	40
% identity	78
NCBI Description	(AC006836) putative integral membrane protein A3 [Arabidopsis thaliana]

Seq. No.	393948
Contig ID	44811_1.R1084
5'-most EST	g286943
Method	BLASTX
NCBI GI	g2342724
BLAST score	210
E value	8.0e-17
Match length	80
% identity	53
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	393949
Contig ID	44816_1.R1084
5'-most EST	g5701703

Seq. No.	393950
Contig ID	44826_1.R1084
5'-most EST	g2311126
Method	BLASTX
NCBI GI	g2117355
BLAST score	262
E value	7.0e-31
Match length	113
% identity	67
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) alpha-II chain precursor - potato >gi_587562_emb_CAA56520_ (X80236) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	393951
Contig ID	44852_1.R1084
5'-most EST	uC-osflm202109e10b1
Method	BLASTX
NCBI GI	g1621463
BLAST score	470
E value	6.0e-47
Match length	113
% identity	72
NCBI Description	(U73104) laccase [Liriodendron tulipifera]

Seq. No.	393952
Contig ID	44856_1.R1084
5'-most EST	g5002926
Method	BLASTX
NCBI GI	g5734634
BLAST score	308
E value	2.0e-28
Match length	116
% identity	62
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No.	393953
Contig ID	44856_2.R1084
5'-most EST	g5002862
Method	BLASTX
NCBI GI	g5734634
BLAST score	198
E value	9.0e-19
Match length	93
% identity	55
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No.	393954
Contig ID	44866_1.R1084
5'-most EST	g5003771
Method	BLASTX
NCBI GI	g2497543
BLAST score	514
E value	4.0e-54
Match length	147
% identity	78

NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No.	393955
Contig ID	44884_1.R1084
5'-most EST	uC-osrocyp036g07b1
Method	BLASTX
NCBI GI	g2245378
BLAST score	797
E value	4.0e-85
Match length	228
% identity	65
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana] >gi_5080809_gb_AAD39318.1_AC007258_7 (AC007258) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	393956
Contig ID	44886_1.R1084
5'-most EST	uC-osflm202110b12b1
Method	BLASTX
NCBI GI	g1706551
BLAST score	468
E value	8.0e-47
Match length	118
% identity	80
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_924953 (U30323) beta 1,3-glucanase [Triticum aestivum]

Seq. No.	393957
Contig ID	44893_1.R1084
5'-most EST	uC-osflM2020118h09a1

Seq. No.	393958
Contig ID	44912_1.R1084
5'-most EST	g701882
Method	BLASTX
NCBI GI	g2191136
BLAST score	184
E value	2.0e-13
Match length	102
% identity	44
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	393959
Contig ID	44923_1.R1084
5'-most EST	uC-osflm202110h06b1

Seq. No.	393960
Contig ID	44927_1.R1084
5'-most EST	g3761744

Seq. No.	393961
Contig ID	44935_1.R1084
5'-most EST	uC-osflm202111b02b1
Method	BLASTX
NCBI GI	g5091552
BLAST score	309
E value	4.0e-28
Match length	152
% identity	43
NCBI Description	(AC007067) T10O24.21 [Arabidopsis thaliana]

Seq. No.	393962
Contig ID	44941_1.R1084
5'-most EST	uC-osflm202111b09b1

Seq. No.	393963
Contig ID	44948_2.R1084
5'-most EST	uC-osflm202111d05b1
Method	BLASTX
NCBI GI	g4335715
BLAST score	379
E value	4.0e-36
Match length	142
% identity	52
NCBI Description	(AC006248) putative immediate-early salicylate-induced glucosyltransferase [Arabidopsis thaliana]

Seq. No.	393964
Contig ID	44962_1.R1084
5'-most EST	uC-osflm202111f06b1
Method	BLASTX
NCBI GI	g5915822
BLAST score	580
E value	1.0e-59
Match length	201
% identity	55
NCBI Description	CYTOCHROME P450 79A1 (CYTOCHROME P450TYR) >gi_2130096_pir__S68203 cytochrome P450tyr - sorghum >gi_984543 (U32624) cytochrome P-450 [Sorghum bicolor]

Seq. No.	393965
Contig ID	44971_1.R1084
5'-most EST	uC-osflM202083e05b1

Seq. No.	393966
Contig ID	44983_1.R1084
5'-most EST	g3768773

Seq. No.	393967
Contig ID	44989_1.R1084
5'-most EST	g427390
Method	BLASTX
NCBI GI	g4490705
BLAST score	360
E value	4.0e-34
Match length	86
% identity	80

NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	393968
Contig ID	45009_1.R1084
5'-most EST	g3767115
Method	BLASTX
NCBI GI	g417360
BLAST score	294
E value	3.0e-26
Match length	104
% identity	49
NCBI Description	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2 >gi_2131280_pir__S67767 high mobility group-like protein NHP2 - yeast (Saccharomyces cerevisiae) >gi_666101_emb_CAA40885_ (X57714) high mobility group-like nuclear protein 2 [Saccharomyces cerevisiae] >gi_1429348_emb_CAA67483_ (X99000) high-mobility-group-like protein [Saccharomyces cerevisiae] >gi_1431346_emb_CAA98786_ (Z74256) ORF YDL208w [Saccharomyces cerevisiae]

Seq. No.	393969
Contig ID	45018_1.R1084
5'-most EST	g5004414
Method	BLASTX
NCBI GI	g3319355
BLAST score	480
E value	3.0e-48
Match length	105
% identity	90
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No.	393970
Contig ID	45021_1.R1084
5'-most EST	g5003205

Seq. No.	393971
Contig ID	45023_1.R1084
5'-most EST	g426211

Seq. No.	393972
Contig ID	45025_1.R1084
5'-most EST	uC-osroM202003b01a2
Method	BLASTX
NCBI GI	g2462828
BLAST score	222
E value	7.0e-18
Match length	74
% identity	54
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	393973
Contig ID	45048_1.R1084
5'-most EST	uC-osflm202113b03b1
Method	BLASTN

NCBI GI	g5679837
BLAST score	413
E value	0.0e+00
Match length	515
% identity	98
NCBI Description	Oryza sativa chromosome 4 BAC l1332 genomic sequences

Seq. No.	393974
Contig ID	45055_1.R1084
5'-most EST	uC-osflM202097g12b1

Seq. No.	393975
Contig ID	45084_1.R1084
5'-most EST	g4879673
Method	BLASTX
NCBI GI	g2842493
BLAST score	221
E value	7.0e-18
Match length	144
% identity	29
NCBI Description	(AL021749) predicted protein [Arabidopsis thaliana]

Seq. No.	393976
Contig ID	45103_1.R1084
5'-most EST	g2798783
Method	BLASTX
NCBI GI	g1922938
BLAST score	733
E value	1.0e-77
Match length	227
% identity	60
NCBI Description	(AC000106) Similar to Caenorhabditis hypothetical protein CO7A9.11 (gb_Z29094). [Arabidopsis thaliana]

Seq. No.	393977
Contig ID	45110_1.R1084
5'-most EST	uC-osflm202120b09b1

Seq. No.	393978
Contig ID	45125_1.R1084
5'-most EST	uC-osflm202120d07b1

Seq. No.	393979
Contig ID	45127_1.R1084
5'-most EST	uC-osflm202120d09b1

Seq. No.	393980
Contig ID	45132_1.R1084
5'-most EST	uC-osflm202120e07b1

Seq. No.	393981
Contig ID	45148_1.R1084
5'-most EST	g700539
Method	BLASTX
NCBI GI	g115583
BLAST score	546
E value	1.0e-62

Match length	157
% identity	78
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE) (CP28) >gi_100758_pir__S18240 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sorghum >gi_22593_emb_CAA42549_ (X59925) phosphoenolpyruvate carboxylase [Sorghum bicolor]

Seq. No.	393982
Contig ID	45157_1.R1084
5'-most EST	g4716212
Method	BLASTX
NCBI GI	g3080436
BLAST score	248
E value	5.0e-21
Match length	67
% identity	67
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	393983
Contig ID	45173_1.R1084
5'-most EST	uC-osroM202012e11a1

Seq. No.	393984
Contig ID	45175_1.R1084
5'-most EST	g3766913

Seq. No.	393985
Contig ID	45185_1.R1084
5'-most EST	uC-osflM2020114c03a1
Method	BLASTX
NCBI GI	g3360291
BLAST score	427
E value	6.0e-42
Match length	115
% identity	73
NCBI Description	(AF023165) leucine-rich repeat transmembrane protein kinase 2 [Zea mays]

Seq. No.	393986
Contig ID	45205_1.R1084
5'-most EST	g2428581
Method	BLASTX
NCBI GI	g4337196
BLAST score	872
E value	5.0e-94
Match length	197
% identity	82
NCBI Description	(AC006403) putative serine/threonine receptor kinase [Arabidopsis thaliana]

Seq. No.	393987
Contig ID	45206_1.R1084
5'-most EST	g3768368

Seq. No.	393988
Contig ID	45209_1.R1084
5'-most EST	g3762435

Method	BLASTX
NCBI GI	g3482914
BLAST score	232
E value	6.0e-19
Match length	87
% identity	48
NCBI Description	(AC003970) Similar to nodulins and lipase [Arabidopsis thaliana]

Seq. No.	393989
Contig ID	45221_1.R1084
5'-most EST	g5003303
Method	BLASTX
NCBI GI	g2842689
BLAST score	180
E value	1.0e-19
Match length	153
% identity	39
NCBI Description	HYPOTHETICAL 50.4 KD PROTEIN C1F8.04C IN CHROMOSOME I >gi_1638851_emb_CAB03598_ (Z81312) unknown [Schizosaccharomyces pombe]

Seq. No.	393990
Contig ID	45238_1.R1084
5'-most EST	g5607561

Seq. No.	393991
Contig ID	45239_1.R1084
5'-most EST	uC-osflM2020116b11a1
Method	BLASTX
NCBI GI	g3660471
BLAST score	356
E value	2.0e-33
Match length	96
% identity	69
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No.	393992
Contig ID	45256_1.R1084
5'-most EST	uC-osflM2020117b05a1
Method	BLASTX
NCBI GI	g3540199
BLAST score	520
E value	6.0e-53
Match length	151
% identity	66
NCBI Description	(AC004260) Putative monosaccharide transport protein [Arabidopsis thaliana]

Seq. No.	393993
Contig ID	45262_1.R1084
5'-most EST	uC-osflM2020117b11a1

Seq. No.	393994
Contig ID	45268_1.R1084
5'-most EST	uC-osflM2020117c05a1

Seq. No.	393995
Contig ID	45273_1.R1084
5'-most EST	g5607534
Method	BLASTX
NCBI GI	g1022811
BLAST score	249
E value	4.0e-21
Match length	70
% identity	73
NCBI Description	(U37703) ORF 62 [Hordeum vulgare]

Seq. No.	393996
Contig ID	45286_1.R1084
5'-most EST	uC-osflM2020117e03a1
Method	BLASTN
NCBI GI	g3819386
BLAST score	74
E value	5.0e-33
Match length	126
% identity	90
NCBI Description	Hordeum vulgare genomic DNA fragment; clone MWG0872.rev

Seq. No.	393997
Contig ID	45288_1.R1084
5'-most EST	g2275891
Method	BLASTX
NCBI GI	g4678385
BLAST score	203
E value	3.0e-26
Match length	91
% identity	81
NCBI Description	(AL049656) putative protein [Arabidopsis thaliana]

Seq. No.	393998
Contig ID	45310_1.R1084
5'-most EST	g3768793

Seq. No.	393999
Contig ID	45326_1.R1084
5'-most EST	uC-osflM2020117h07a1

Seq. No.	394000
Contig ID	45332_1.R1084
5'-most EST	uC-osroM202039f12a1

Seq. No.	394001
Contig ID	45344_1.R1084
5'-most EST	uC-osflM202065d02a1

Seq. No.	394002
Contig ID	45346_1.R1084
5'-most EST	uC-osflM2020118b07a1

Seq. No.	394003
Contig ID	45348_1.R1084
5'-most EST	g5003664

Seq. No.	394004
Contig ID	45359_1.R1084
5'-most EST	g3760293
Seq. No.	394005
Contig ID	45373_1.R1084
5'-most EST	g2798698
Seq. No.	394006
Contig ID	45403_1.R1084
5'-most EST	g4714126
Seq. No.	394007
Contig ID	45408_1.R1084
5'-most EST	g4714050
Method	BLASTX
NCBI GI	g4678262
BLAST score	183
E value	5.0e-22
Match length	74
% identity	71
NCBI Description	(AL049657) argininosuccinate synthase-like protein [Arabidopsis thaliana]
Seq. No.	394008
Contig ID	45411_1.R1084
5'-most EST	uC-osflM202037a11b1
Method	BLASTX
NCBI GI	g1572819
BLAST score	275
E value	5.0e-24
Match length	136
% identity	43
NCBI Description	(U70855) similar to the RAS gene family [Caenorhabditis elegans]
Seq. No.	394009
Contig ID	45413_1.R1084
5'-most EST	uC-osflM202037b12b1
Method	BLASTX
NCBI GI	g3482918
BLAST score	446
E value	2.0e-48
Match length	123
% identity	85
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]
Seq. No.	394010
Contig ID	45430_1.R1084
5'-most EST	uC-osflM202037g10b1
Method	BLASTX
NCBI GI	g6006371
BLAST score	97
E value	2.0e-14
Match length	93

% identity	51
NCBI Description	(AP000559) Similar to hypothetical protein - potato (S31196) [Oryza sativa]

Seq. No.	394011
Contig ID	45434_1.R1084
5'-most EST	g3767342
Method	BLASTX
NCBI GI	g2618698
BLAST score	232
E value	6.0e-19
Match length	66
% identity	64
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	394012
Contig ID	45438_1.R1084
5'-most EST	uC-osflM202050a09b1

Seq. No.	394013
Contig ID	45441_1.R1084
5'-most EST	g702497

Seq. No.	394014
Contig ID	45448_1.R1084
5'-most EST	uC-osflM202050d12b1

Seq. No.	394015
Contig ID	45478_1.R1084
5'-most EST	g702583

Seq. No.	394016
Contig ID	45482_1.R1084
5'-most EST	uC-osflM202081a07b1
Method	BLASTX
NCBI GI	g1652971
BLAST score	152
E value	1.0e-09
Match length	69
% identity	42
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	394017
Contig ID	45492_1.R1084
5'-most EST	uC-osflM202081e04b1

Seq. No.	394018
Contig ID	45493_1.R1084
5'-most EST	g571917

Seq. No.	394019
Contig ID	45496_1.R1084
5'-most EST	g4878353
Method	BLASTX
NCBI GI	g3738284
BLAST score	234
E value	2.0e-19

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Match length	65
% identity	60
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	394020
Contig ID	45517_1.R1084
5'-most EST	uC-osroM202023d08b1
Method	BLASTX
NCBI GI	g4938503
BLAST score	354
E value	2.0e-33
Match length	90
% identity	40
NCBI Description	(AL078465) hnRNP-like protein [Arabidopsis thaliana]

Seq. No.	394021
Contig ID	45537_1.R1084
5'-most EST	g700178
Method	BLASTX
NCBI GI	g4581856
BLAST score	450
E value	1.0e-44
Match length	145
% identity	66
NCBI Description	(AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase [Mentha x piperita]

Seq. No.	394022
Contig ID	45556_2.R1084
5'-most EST	uC-osflM202084b04a1

Seq. No.	394023
Contig ID	45587_1.R1084
5'-most EST	g3761382
Method	BLASTX
NCBI GI	g1203832
BLAST score	170
E value	3.0e-30
Match length	126
% identity	64
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No.	394024
Contig ID	45590_1.R1084
5'-most EST	uC-osflM202084e09a1
Method	BLASTX
NCBI GI	g2494116
BLAST score	325
E value	5.0e-30
Match length	82
% identity	73
NCBI Description	(AC002376) Similar to Synechocystis hypothetical protein (gb_D90915). [Arabidopsis thaliana]

Seq. No.	394025

Contig ID	45595_1.R1084
5'-most EST	g5455506
Seq. No.	394026
Contig ID	45606_1.R1084
5'-most EST	uC-osroM202020h01a1
Method	BLASTX
NCBI GI	g729944
BLAST score	188
E value	4.0e-14
Match length	51
% identity	61
NCBI Description	POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524 major allergen mI protein - maize >gi_293902 (L14271) Zea mI [Zea mays]
Seq. No.	394027
Contig ID	45619_1.R1084
5'-most EST	g3106525
Seq. No.	394028
Contig ID	45623_1.R1084
5'-most EST	uC-osflM202084h10a1
Seq. No.	394029
Contig ID	45628_1.R1084
5'-most EST	uC-osflM202088a04a1
Seq. No.	394030
Contig ID	45631_1.R1084
5'-most EST	uC-osflM202088a08a1
Method	BLASTX
NCBI GI	g4678345
BLAST score	281
E value	5.0e-34
Match length	119
% identity	51
NCBI Description	(AL049659) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	394031
Contig ID	45637_1.R1084
5'-most EST	uC-osflM202088c12a1
Method	BLASTX
NCBI GI	g1706958
BLAST score	498
E value	1.0e-50
Match length	93
% identity	95
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]
Seq. No.	394032
Contig ID	45644_1.R1084
5'-most EST	g4715638
Seq. No.	394033
Contig ID	45653_1.R1084

5'-most EST	uC-osflM202088e10a1
Seq. No.	394034
Contig ID	45654_1.R1084
5'-most EST	uC-osflM202088d10a1
Seq. No.	394035
Contig ID	45655_1.R1084
5'-most EST	uC-osroM202012d06a1
Seq. No.	394036
Contig ID	45660_1.R1084
5'-most EST	uC-osroM202024b03b1
Method	BLASTX
NCBI GI	g3132310
BLAST score	747
E value	3.0e-79
Match length	168
% identity	91
NCBI Description	(AB012228) phosphoenolpyruvate carboxylase [Zea mays]
Seq. No.	394037
Contig ID	45667_1.R1084
5'-most EST	uC-osflM202088f12a1
Method	BLASTX
NCBI GI	g1311479
BLAST score	733
E value	4.0e-97
Match length	205
% identity	89
NCBI Description	(D45890) sucrose phosphate synthase [Oryza sativa]
Seq. No.	394038
Contig ID	45679_1.R1084
5'-most EST	g2800456
Seq. No.	394039
Contig ID	45680_1.R1084
5'-most EST	g3763681
Seq. No.	394040
Contig ID	45683_1.R1084
5'-most EST	g3768170
Seq. No.	394041
Contig ID	45704_1.R1084
5'-most EST	uC-osflM202092e05b1
Seq. No.	394042
Contig ID	45744_1.R1084
5'-most EST	uC-osflM202097h01b1
Seq. No.	394043
Contig ID	45751_1.R1084
5'-most EST	uC-osflM202052a08b1
Method	BLASTX
NCBI GI	g4567201

BLAST score 790
E value 2.0e-84
Match length 190
% identity 79
NCBI Description (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]

Seq. No. 394044
Contig ID 45760_1.R1084
5'-most EST uC-osflm202102c12b1

Seq. No. 394045
Contig ID 45770_1.R1084
5'-most EST g3090633
Method BLASTX
NCBI GI g5731763
BLAST score 154
E value 4.0e-10
Match length 53
% identity 62
NCBI Description (X92419) SNAP25A protein [Arabidopsis thaliana] >gi_5731764_emb_CAB52583.1_ (X92420) SNAP25AB protein [Arabidopsis thaliana]

Seq. No. 394046
Contig ID 45782_1.R1084
5'-most EST uC-osflM202052h05b1

Seq. No. 394047
Contig ID 45784_1.R1084
5'-most EST g2428250

Seq. No. 394048
Contig ID 45785_1.R1084
5'-most EST uC-osflM202053a03b1
Method BLASTX
NCBI GI g2244884
BLAST score 197
E value 2.0e-19
Match length 127
% identity 51
NCBI Description (Z97338) glucosyltransferase [Arabidopsis thaliana]

Seq. No. 394049
Contig ID 45800_1.R1084
5'-most EST uC-osflM202053e02b1
Method BLASTX
NCBI GI g5596468
BLAST score 177
E value 1.0e-12
Match length 96
% identity 38
NCBI Description (AL096882) putative protein [Arabidopsis thaliana]

Seq. No. 394050
Contig ID 45822_1.R1084
5'-most EST g4715181

Method	BLASTX
NCBI GI	g4371285
BLAST score	153
E value	1.0e-09
Match length	38
% identity	68
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394051
Contig ID	45823_1.R1084
5'-most EST	uC-osf1M202065a04a1

Seq. No.	394052
Contig ID	45824_1.R1084
5'-most EST	uC-osf1M202065a05a1

Seq. No.	394053
Contig ID	45833_1.R1084
5'-most EST	uC-osf1M202065b03a1

Seq. No.	394054
Contig ID	45840_1.R1084
5'-most EST	g3766706
Method	BLASTX
NCBI GI	g4006877
BLAST score	205
E value	9.0e-16
Match length	69
% identity	67
NCBI Description	(Z99707) RNA-binding like protein [Arabidopsis thaliana]

Seq. No.	394055
Contig ID	45844_1.R1084
5'-most EST	g3107311

Seq. No.	394056
Contig ID	45846_1.R1084
5'-most EST	g3762342
Method	BLASTX
NCBI GI	g3861189
BLAST score	143
E value	1.0e-08
Match length	46
% identity	59
NCBI Description	(AJ235272) 50S RIBOSOMAL PROTEIN L14 (rplN) [Rickettsia prowazekii]

Seq. No.	394057
Contig ID	45848_1.R1084
5'-most EST	g3767779

Seq. No.	394058
Contig ID	45849_1.R1084
5'-most EST	g3763790
Method	BLASTX
NCBI GI	g4115925
BLAST score	159

E value	6.0e-21
Match length	115
% identity	41
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana] >gi_4959384_gb_AAD34325.1_ (AF109721) RNA-binding protein [Arabidopsis thaliana]
Seq. No.	394059
Contig ID	45864_1.R1084
5'-most EST	uC-osflM202065e01a1
Seq. No.	394060
Contig ID	45868_1.R1084
5'-most EST	uC-osflM202065e06a1
Seq. No.	394061
Contig ID	45878_1.R1084
5'-most EST	uC-osflM202065f10a1
Seq. No.	394062
Contig ID	45881_1.R1084
5'-most EST	uC-osrocyp016f08a1
Seq. No.	394063
Contig ID	45884_1.R1084
5'-most EST	uC-osflM202065f12a1
Seq. No.	394064
Contig ID	45891_1.R1084
5'-most EST	uC-osflM202065g09a1
Seq. No.	394065
Contig ID	45895_1.R1084
5'-most EST	uC-osflM202065h02a1
Seq. No.	394066
Contig ID	45904_1.R1084
5'-most EST	uC-osflM202065h12a1
Seq. No.	394067
Contig ID	45908_1.R1084
5'-most EST	g2317575
Seq. No.	394068
Contig ID	45913_1.R1084
5'-most EST	uC-osflM202066b02b1
Seq. No.	394069
Contig ID	45924_1.R1084
5'-most EST	uC-osflM202066f12b1
Method	BLASTN
NCBI GI	g6063530
BLAST score	51
E value	2.0e-19
Match length	285

% identity	81
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	394070
Contig ID	45951_1.R1084
5'-most EST	uC-osflM202115f12b1
Method	BLASTX
NCBI GI	g4490707
BLAST score	217
E value	4.0e-18
Match length	68
% identity	57
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	394071
Contig ID	45957_1.R1084
5'-most EST	uC-osflM202054a07b1
Method	BLASTX
NCBI GI	g1652601
BLAST score	153
E value	1.0e-09
Match length	132
% identity	28
NCBI Description	(D90906) hypothetical protein [Synechocystis sp.]

Seq. No.	394072
Contig ID	45972_1.R1084
5'-most EST	g427223
Method	BLASTX
NCBI GI	g2129783
BLAST score	226
E value	1.0e-18
Match length	59
% identity	75
NCBI Description	cystatin - field mustard >gi_762785 (L41355) cysteine proteinase inhibitor [Brassica campestris]

Seq. No.	394073
Contig ID	45985_1.R1084
5'-most EST	g2312594

Seq. No.	394074
Contig ID	46023_1.R1084
5'-most EST	uC-osflM202063c06a1

Seq. No.	394075
Contig ID	46025_1.R1084
5'-most EST	g3768499

Seq. No.	394076
Contig ID	46033_1.R1084
5'-most EST	g3760942

Seq. No.	394077
Contig ID	46041_1.R1084
5'-most EST	g3767891
Method	BLASTX

NCBI GI	g3258569
BLAST score	221
E value	1.0e-17
Match length	47
% identity	85
NCBI Description	(U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]

Seq. No.	394078
Contig ID	46066_1.R1084
5'-most EST	uC-osflM202063g07a1
Method	BLASTX
NCBI GI	g4455323
BLAST score	179
E value	1.0e-21
Match length	104
% identity	47
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	394079
Contig ID	46068_1.R1084
5'-most EST	uC-osflM202063g09a1

Seq. No.	394080
Contig ID	46120_1.R1084
5'-most EST	uC-osflM202069a09a1
Method	BLASTX
NCBI GI	g5531229
BLAST score	555
E value	3.0e-76
Match length	188
% identity	77
NCBI Description	(AJ243812) glutathione synthetase [Arabidopsis thaliana]

Seq. No.	394081
Contig ID	46127_1.R1084
5'-most EST	uC-osflM202069b06a1
Method	BLASTX
NCBI GI	g3935181
BLAST score	379
E value	2.0e-36
Match length	85
% identity	85
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	394082
Contig ID	46148_1.R1084
5'-most EST	uC-osflM202069d11a1

Seq. No.	394083
Contig ID	46152_1.R1084
5'-most EST	uC-osflM202069e04a1

Seq. No.	394084
Contig ID	46171_1.R1084
5'-most EST	uC-osrocyp004g08a1

Method	BLASTX
NCBI GI	g3860272
BLAST score	324
E value	9.0e-36
Match length	157
% identity	53
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	394085
Contig ID	46207_1.R1084
5'-most EST	g570024
Method	BLASTX
NCBI GI	g3915866
BLAST score	241
E value	3.0e-20
Match length	91
% identity	55
NCBI Description	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

Seq. No.	394086
Contig ID	46209_1.R1084
5'-most EST	uC-osf1M202095e07b1
Method	BLASTX
NCBI GI	g3482921
BLAST score	213
E value	7.0e-17
Match length	81
% identity	49
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana]

Seq. No.	394087
Contig ID	46217_1.R1084
5'-most EST	g4714686

Seq. No.	394088
Contig ID	46231_1.R1084
5'-most EST	g2428236

Seq. No.	394089
Contig ID	46243_1.R1084
5'-most EST	g570042
Method	BLASTX
NCBI GI	g629783
BLAST score	241
E value	3.0e-58
Match length	184
% identity	66
NCBI Description	ES43 protein - barley >gi_1345528_emb_CAA54682_ (X77575) ES43 [Hordeum vulgare]

Seq. No.	394090
Contig ID	46268_1.R1084
5'-most EST	g2428294

Method	BLASTX
NCBI GI	g4836877
BLAST score	194
E value	1.0e-14
Match length	102
% identity	38
NCBI Description	(AC007260) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	394091
Contig ID	46270_1.R1084
5'-most EST	g2428088
Method	BLASTX
NCBI GI	g548493
BLAST score	186
E value	9.0e-14
Match length	85
% identity	45
NCBI Description	EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi_629854_pir__S30067 polygalacturonase - maize >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea mays]

Seq. No.	394092
Contig ID	46274_1.R1084
5'-most EST	g572109

Seq. No.	394093
Contig ID	46303_1.R1084
5'-most EST	uC-osf1M202021e04a1
Method	BLASTX
NCBI GI	g4914460
BLAST score	263
E value	1.0e-22
Match length	86
% identity	58
NCBI Description	(AL050400) putative protein [Arabidopsis thaliana]

Seq. No.	394094
Contig ID	46306_1.R1084
5'-most EST	g5004682
Method	BLASTN
NCBI GI	g435456
BLAST score	45
E value	6.0e-16
Match length	94
% identity	95
NCBI Description	Proso millet gene for aspartate aminotransferase, complete cds

Seq. No.	394095
Contig ID	46307_1.R1084
5'-most EST	g5900667

Seq. No.	394096
Contig ID	46322_1.R1084

5'-most EST	g2427916
Seq. No.	394097
Contig ID	46354_1.R1084
5'-most EST	uC-osf1M202074e10a1
Seq. No.	394098
Contig ID	46373_1.R1084
5'-most EST	g3760568
Seq. No.	394099
Contig ID	46375_1.R1084
5'-most EST	uC-osf1M202056b11a1
Seq. No.	394100
Contig ID	46377_1.R1084
5'-most EST	uC-osf1M202056c01a1
Seq. No.	394101
Contig ID	46397_1.R1084
5'-most EST	g3760272
Seq. No.	394102
Contig ID	46407_1.R1084
5'-most EST	g4714746
Method	BLASTX
NCBI GI	g3025189
BLAST score	307
E value	2.0e-27
Match length	218
% identity	35
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]
Seq. No.	394103
Contig ID	46416_1.R1084
5'-most EST	g3768983
Seq. No.	394104
Contig ID	46417_1.R1084
5'-most EST	uC-osrocyp014g11a1
Seq. No.	394105
Contig ID	46437_1.R1084
5'-most EST	g4715011
Seq. No.	394106
Contig ID	46456_1.R1084
5'-most EST	g3107002
Method	BLASTX
NCBI GI	g3785998
BLAST score	144
E value	8.0e-09
Match length	87
% identity	36
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 394107
Contig ID 46464_1.R1084
5'-most EST g3759628

Seq. No. 394108
Contig ID 46464_2.R1084
5'-most EST g2312600
Method BLASTX
NCBI GI g2943792
BLAST score 335
E value 6.0e-49
Match length 121
% identity 73
NCBI Description (AB006809) PV72 [Cucurbita sp.]

Seq. No. 394109
Contig ID 46476_1.R1084
5'-most EST uC-osflM202058h10a1
Method BLASTX
NCBI GI g4586049
BLAST score 315
E value 2.0e-48
Match length 209
% identity 53
NCBI Description (AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No. 394110
Contig ID 46478_1.R1084
5'-most EST uC-osroM202036d10a1

Seq. No. 394111
Contig ID 46478_2.R1084
5'-most EST uC-osflM202058h12a1

Seq. No. 394112
Contig ID 46482_1.R1084
5'-most EST uC-osroM202017c07b1

Seq. No. 394113
Contig ID 46509_1.R1084
5'-most EST g569542

Seq. No. 394114
Contig ID 46523_1.R1084
5'-most EST uC-osflM202062c11b1

Seq. No. 394115
Contig ID 46534_1.R1084
5'-most EST g5002975
Method BLASTX
NCBI GI g1421730
BLAST score 486
E value 1.0e-65
Match length 173
% identity 75
NCBI Description (U43082) RF2 [Zea mays]

Seq. No.	394116
Contig ID	46541_1.R1084
5'-most EST	g4878268
Method	BLASTX
NCBI GI	g2492678
BLAST score	176
E value	1.0e-12
Match length	68
% identity	50
NCBI Description	ACTIN-LIKE PROTEIN ARP8 >gi_2132896_pir__S67026 probable membrane protein YOR141c - yeast (Saccharomyces cerevisiae) >gi_1262142_emb_CAA64058_ (X94335) YOR3348c [Saccharomyces cerevisiae] >gi_1420356_emb_CAA99341_ (Z75049) ORF YOR141c [Saccharomyces cerevisiae]

Seq. No.	394117
Contig ID	46559_1.R1084
5'-most EST	g3767783

Seq. No.	394118
Contig ID	46561_1.R1084
5'-most EST	g2431409
Method	BLASTN
NCBI GI	g6002460
BLAST score	40
E value	6.0e-13
Match length	48
% identity	96
NCBI Description	Oryza sativa poxA gene for peroxidase, complete cds

Seq. No.	394119
Contig ID	46565_1.R1084
5'-most EST	uC-osroM202016b07a1

Seq. No.	394120
Contig ID	46570_1.R1084
5'-most EST	g4880786

Seq. No.	394121
Contig ID	46575_1.R1084
5'-most EST	uC-osrocyp036e11a1

Seq. No.	394122
Contig ID	46576_1.R1084
5'-most EST	uC-osflM202070d05a1

Seq. No.	394123
Contig ID	46584_1.R1084
5'-most EST	g4880989

Seq. No.	394124
Contig ID	46591_1.R1084
5'-most EST	g700418

Seq. No.	394125
Contig ID	46592_1.R1084

5'-most EST	uC-osflM202070f04a1
Seq. No.	394126
Contig ID	46604_1.R1084
5'-most EST	uC-osrocyp037h02a1
Seq. No.	394127
Contig ID	46627_1.R1084
5'-most EST	uC-osflM202014c12b1
Seq. No.	394128
Contig ID	46639_1.R1084
5'-most EST	g4715408
Seq. No.	394129
Contig ID	46644_1.R1084
5'-most EST	g4715464
Method	BLASTX
NCBI GI	g3650037
BLAST score	262
E value	1.0e-22
Match length	56
% identity	88
NCBI Description	(AC005396) auxin-responsive GH3-like protein [Arabidopsis thaliana]
Seq. No.	394130
Contig ID	46644_2.R1084
5'-most EST	uC-osflM202073b09a1
Seq. No.	394131
Contig ID	46650_1.R1084
5'-most EST	uC-osflM202073c03a1
Seq. No.	394132
Contig ID	46655_1.R1084
5'-most EST	uC-osrocyp015e05a1
Seq. No.	394133
Contig ID	46661_1.R1084
5'-most EST	g3762613
Seq. No.	394134
Contig ID	46672_1.R1084
5'-most EST	g3767863
Method	BLASTX
NCBI GI	g1706956
BLAST score	261
E value	2.0e-22
Match length	62
% identity	76
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.	394135
Contig ID	46682_1.R1084
5'-most EST	g3763706

Seq. No.	394136
Contig ID	46739_1.R1084
5'-most EST	g3761652
Method	BLASTX
NCBI GI	g1871186
BLAST score	156
E value	7.0e-18
Match length	70
% identity	70
NCBI Description	(U90439) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	394137
Contig ID	46760_1.R1084
5'-most EST	g3768362
Method	BLASTX
NCBI GI	g5533003
BLAST score	513
E value	1.0e-51
Match length	193
% identity	55
NCBI Description	(AF157028) protein phosphatase methylesterase-1 [Homo sapiens]

Seq. No.	394138
Contig ID	46775_1.R1084
5'-most EST	g6024966

Seq. No.	394139
Contig ID	46811_1.R1084
5'-most EST	uC-osflM202016c02b1
Method	BLASTX
NCBI GI	g2565305
BLAST score	401
E value	1.0e-41
Match length	105
% identity	86
NCBI Description	(AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No.	394140
Contig ID	46816_1.R1084
5'-most EST	uC-osflm202102h07b1
Method	BLASTX
NCBI GI	g5689613
BLAST score	210
E value	2.0e-16
Match length	83
% identity	55
NCBI Description	(AJ242807) cellulase [Brassica napus]

Seq. No.	394141
Contig ID	46826_1.R1084
5'-most EST	g426572
Method	BLASTX
NCBI GI	g4760700
BLAST score	377
E value	5.0e-36

Match length	126
% identity	60
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]
Seq. No.	394142
Contig ID	46842_1.R1084
5'-most EST	uC-osflM202134b05a1
Seq. No.	394143
Contig ID	46858_1.R1084
5'-most EST	uC-osflM202135d05a1
Seq. No.	394144
Contig ID	46881_1.R1084
5'-most EST	uC-osflM202134g03a1
Seq. No.	394145
Contig ID	46886_1.R1084
5'-most EST	g3767883
Seq. No.	394146
Contig ID	46887_1.R1084
5'-most EST	uC-osflM202134g10a1
Method	BLASTX
NCBI GI	g3024501
BLAST score	594
E value	5.0e-71
Match length	213
% identity	73
NCBI Description	RAS-RELATED PROTEIN RAB11C >gi_1370146_emb_CAA98179_ (Z73951) RAB11C [Lotus japonicus]
Seq. No.	394147
Contig ID	46891_1.R1084
5'-most EST	g5039040
Seq. No.	394148
Contig ID	46905_1.R1084
5'-most EST	g2317360
Method	BLASTX
NCBI GI	g416564
BLAST score	220
E value	9.0e-18
Match length	75
% identity	69
NCBI Description	ABCISIC ACID-INDUCIBLE PROTEIN KINASE >gi_422013_pir__A46408 abscisic acid-inducible serine/threonine protein kinase homolog - wheat (fragment) >gi_170664_gb_AAA96325.1_AAA96325 (M94726) protein kinase [Triticum aestivum]
Seq. No.	394149
Contig ID	46921_1.R1084
5'-most EST	g4714097
Seq. No.	394150
Contig ID	46944_1.R1084

5'-most EST	uC-osroM202026d04b1
Method	BLASTX
NCBI GI	g5302775
BLAST score	148
E value	4.0e-09
Match length	65
% identity	43
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394151
Contig ID	46966_1.R1084
5'-most EST	g2310368

Seq. No.	394152
Contig ID	46978_1.R1084
5'-most EST	uC-osflM202016b11b1
Method	BLASTX
NCBI GI	g4680179
BLAST score	370
E value	3.0e-35
Match length	172
% identity	45
NCBI Description	(AF111709) polyprotein [Oryza sativa subsp. indica]

Seq. No.	394153
Contig ID	47009_1.R1084
5'-most EST	g2797498
Method	BLASTX
NCBI GI	g4587514
BLAST score	373
E value	1.0e-35
Match length	81
% identity	85
NCBI Description	(AC007060) Similar to WO8E3.3 gi_3880615 putative GTP-binding protein from C. elegans cosmid gb_Z92773. EST gb_AA597331 comes from this gene. [Arabidopsis thaliana]

Seq. No.	394154
Contig ID	47010_1.R1084
5'-most EST	g2312398

Seq. No.	394155
Contig ID	47013_1.R1084
5'-most EST	g4715295
Method	BLASTX
NCBI GI	g4544409
BLAST score	305
E value	1.0e-27
Match length	99
% identity	59
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana] >gi_4585920_gb_AAD25580.1_AC007211_2 (AC007211) putative scarecrow homolog [Arabidopsis thaliana]

Seq. No.	394156
Contig ID	47017_1.R1084
5'-most EST	g5607374

Seq. No.	394157
Contig ID	47020_1.R1084
5'-most EST	uC-osf1M202031b07a1

Seq. No.	394158
Contig ID	47041_1.R1084
5'-most EST	uC-osf1M202031e08a1
Method	BLASTX
NCBI GI	g1709798
BLAST score	517
E value	1.0e-52
Match length	163
% identity	72
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi_1155334 (U43398) POTATP1 [Solanum tuberosum]

Seq. No.	394159
Contig ID	47048_1.R1084
5'-most EST	uC-osf1M202031f10a1

Seq. No.	394160
Contig ID	47076_1.R1084
5'-most EST	g2427840
Method	BLASTX
NCBI GI	g4063751
BLAST score	236
E value	4.0e-21
Match length	246
% identity	31
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	394161
Contig ID	47079_1.R1084
5'-most EST	g2312317
Method	BLASTX
NCBI GI	g2827537
BLAST score	375
E value	7.0e-36
Match length	97
% identity	71
NCBI Description	(AL021633) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	394162
Contig ID	47082_1.R1084
5'-most EST	uC-osf1M202046e07b1

Seq. No.	394163
Contig ID	47093_1.R1084
5'-most EST	uC-osf1M202047a01b1
Method	BLASTX
NCBI GI	g2493494
BLAST score	650
E value	9.0e-72

Match length	162
% identity	83
NCBI Description	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase II-2 [Hordeum vulgare]

Seq. No.	394164
Contig ID	47105_1.R1084
5'-most EST	g3420885
Method	BLASTX
NCBI GI	g2852449
BLAST score	214
E value	3.0e-20
Match length	141
% identity	49
NCBI Description	(D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No.	394165
Contig ID	47113_1.R1084
5'-most EST	g569683
Method	BLASTX
NCBI GI	g3513303
BLAST score	232
E value	4.0e-19
Match length	128
% identity	40
NCBI Description	(AC005594) R26984_1 [Homo sapiens]

Seq. No.	394166
Contig ID	47160_1.R1084
5'-most EST	uC-osflM202049b01b1

Seq. No.	394167
Contig ID	47176_1.R1084
5'-most EST	uC-osrocyp021b12b1
Method	BLASTX
NCBI GI	g2245030
BLAST score	468
E value	2.0e-61
Match length	142
% identity	83
NCBI Description	(Z97341) acyl-CoA oxidase like protein [Arabidopsis thaliana]

Seq. No.	394168
Contig ID	47179_1.R1084
5'-most EST	uC-osflM202049h07b1
Method	BLASTX
NCBI GI	g3426039
BLAST score	299
E value	6.0e-27
Match length	76
% identity	71
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 394169
Contig ID 47191_1.R1084
5'-most EST g2428609

Seq. No. 394170
Contig ID 47206_1.R1084
5'-most EST uC-osflM202123b05b1
Method BLASTX
NCBI GI g3153205
BLAST score 232
E value 4.0e-19
Match length 101
% identity 53
NCBI Description (U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No. 394171
Contig ID 47223_1.R1084
5'-most EST uC-osflM202123g11b1

Seq. No. 394172
Contig ID 47224_1.R1084
5'-most EST uC-osflM202123g12b1
Method BLASTX
NCBI GI g3421413
BLAST score 328
E value 2.0e-30
Match length 71
% identity 90
NCBI Description (AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No. 394173
Contig ID 47239_1.R1084
5'-most EST g3761308

Seq. No. 394174
Contig ID 47245_1.R1084
5'-most EST uC-osflm202109b10b1
Method BLASTX
NCBI GI g5689136
BLAST score 446
E value 3.0e-44
Match length 91
% identity 46
NCBI Description (AB023479) transcription factor Ntlim1 [Nicotiana tabacum]

Seq. No. 394175
Contig ID 47246_1.R1084
5'-most EST uC-osflm202109b12b1

Seq. No. 394176
Contig ID 47261_1.R1084
5'-most EST uC-osflm202109f09b1
Method BLASTX

NCBI GI	g4584957
BLAST score	735
E value	1.0e-89
Match length	184
% identity	96
NCBI Description	(AF077337) heat shock protein 101; 101 kDa heat shock protein [Zea mays] >gi_4928488_gb_AAD33606.1_AF133840_1 (AF133840) heat shock protein HSP101 [Zea mays]

Seq. No.	394177
Contig ID	47276_1.R1084
5'-most EST	g3762507
Method	BLASTX
NCBI GI	g3046695
BLAST score	261
E value	4.0e-22
Match length	83
% identity	63
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	394178
Contig ID	47301_1.R1084
5'-most EST	uC-osflm202111b11b1
Method	BLASTN
NCBI GI	g1311478
BLAST score	186
E value	1.0e-100
Match length	224
% identity	98
NCBI Description	Oryza sativa DNA for sucrose phosphate synthase, complete cds

Seq. No.	394179
Contig ID	47305_1.R1084
5'-most EST	uC-osrocyp008g08b1

Seq. No.	394180
Contig ID	47342_1.R1084
5'-most EST	g428770
Method	BLASTX
NCBI GI	g5733874
BLAST score	305
E value	1.0e-27
Match length	129
% identity	47
NCBI Description	(AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No.	394181
Contig ID	47355_1.R1084
5'-most EST	uC-osflm202112f09b1

Seq. No.	394182
Contig ID	47393_1.R1084
5'-most EST	uC-osflm202113h05b1

Seq. No.	394183
Contig ID	47412_1.R1084

5'-most EST	g426618
Method	BLASTX
NCBI GI	g1710807
BLAST score	529
E value	7.0e-54
Match length	121
% identity	88
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_1185390 (U21105) alphacpn60 [Pisum sativum]

Seq. No.	394184
Contig ID	47423_1.R1084
5'-most EST	g5667239

Seq. No.	394185
Contig ID	47447_1.R1084
5'-most EST	uC-osflM202020g04b1
Method	BLASTX
NCBI GI	g2129921
BLAST score	165
E value	4.0e-11
Match length	34
% identity	91
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	394186
Contig ID	47459_1.R1084
5'-most EST	g2310550
Method	BLASTX
NCBI GI	g4651204
BLAST score	221
E value	9.0e-18
Match length	80
% identity	46
NCBI Description	(AB026262) ring finger protein [Cicer arietinum]

Seq. No.	394187
Contig ID	47463_1.R1084
5'-most EST	g5003033

Seq. No.	394188
Contig ID	47464_1.R1084
5'-most EST	uC-osflM202035b10b1
Method	BLASTX
NCBI GI	g4803944
BLAST score	504
E value	9.0e-51
Match length	175
% identity	57
NCBI Description	(AC006264) putative C2-domain protein (prosite: PD0C00380) [Arabidopsis thaliana]

Seq. No.	394189
Contig ID	47468_1.R1084
5'-most EST	uC-osflM202035c10b1

Method	BLASTN
NCBI GI	g4680189
BLAST score	187
E value	1.0e-100
Match length	453
% identity	99
NCBI Description	Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds

Seq. No.	394190
Contig ID	47497_1.R1084
5'-most EST	uC-osroM202034b11b1
Method	BLASTX
NCBI GI	g129881
BLAST score	321
E value	4.0e-31
Match length	154
% identity	52
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_482294_pir__A36094 pyrophosphate--fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - potato (cv. Kennebec) >gi_169538 (M55190) pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit [Solanum tuberosum]

Seq. No.	394191
Contig ID	47505_1.R1084
5'-most EST	uC-osf1M202040f09b1
Method	BLASTX
NCBI GI	g3193293
BLAST score	582
E value	8.0e-60
Match length	253
% identity	51
NCBI Description	(AF069298) contains a short region of similarity to another Arabidopsis hypothetical protein F19K23.8 (GB:AC000375) [Arabidopsis thaliana]

Seq. No.	394192
Contig ID	47515_1.R1084
5'-most EST	g2431136
Method	BLASTX
NCBI GI	g4490342
BLAST score	152
E value	3.0e-16
Match length	185
% identity	44
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	394193
Contig ID	47520_1.R1084
5'-most EST	uC-osf1M202043b07b1

Seq. No.	394194
Contig ID	47538_1.R1084
5'-most EST	g569204
Method	BLASTX
NCBI GI	g2244765
BLAST score	234
E value	2.0e-19
Match length	79
% identity	54
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394195
Contig ID	47545_1.R1084
5'-most EST	uC-osf1M202074b07a1

Seq. No.	394196
Contig ID	47550_1.R1084
5'-most EST	g2798793
Method	BLASTN
NCBI GI	g58067
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP

Seq. No.	394197
Contig ID	47558_1.R1084
5'-most EST	uC-osf1M202074c12a1
Method	BLASTX
NCBI GI	g6065749
BLAST score	207
E value	7.0e-34
Match length	158
% identity	38
NCBI Description	(AJ250341) beta-amylase enzyme [Arabidopsis thaliana]

Seq. No.	394198
Contig ID	47593_1.R1084
5'-most EST	g3767802
Method	BLASTX
NCBI GI	g421843
BLAST score	368
E value	2.0e-37
Match length	161
% identity	39
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	394199
Contig ID	47600_1.R1084
5'-most EST	g3768481

Seq. No.	394200
Contig ID	47615_1.R1084

5'-most EST	g5003817
Seq. No.	394201
Contig ID	47632_1.R1084
5'-most EST	g2427619
Method	BLASTX
NCBI GI	g4417293
BLAST score	375
E value	1.0e-47
Match length	192
% identity	53
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]
Seq. No.	394202
Contig ID	47633_1.R1084
5'-most EST	uC-osflM202082d02b1
Seq. No.	394203
Contig ID	47645_1.R1084
5'-most EST	uC-osflM202082f07b1
Method	BLASTX
NCBI GI	g3142294
BLAST score	743
E value	6.0e-79
Match length	150
% identity	94
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]
Seq. No.	394204
Contig ID	47659_1.R1084
5'-most EST	g3760093
Method	BLASTX
NCBI GI	g3413717
BLAST score	199
E value	4.0e-15
Match length	84
% identity	49
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi_3643590 (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.	394205
Contig ID	47670_1.R1084
5'-most EST	uC-osflM202085c02a1
Seq. No.	394206
Contig ID	47673_1.R1084
5'-most EST	uC-osrocyp009e06a1
Seq. No.	394207
Contig ID	47680_1.R1084
5'-most EST	uC-osflM202085d05a1
Seq. No.	394208
Contig ID	47684_1.R1084

5'-most EST	g3759876
Method	BLASTX
NCBI GI	g3426048
BLAST score	201
E value	1.0e-15
Match length	65
% identity	62
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	394209
Contig ID	47692_1.R1084
5'-most EST	g2798857
Method	BLASTN
NCBI GI	g310727
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	BlueScribe SK Plus cloning vector

Seq. No.	394210
Contig ID	47700_1.R1084
5'-most EST	uC-osflM202085f07a1

Seq. No.	394211
Contig ID	47717_1.R1084
5'-most EST	g3763542
Method	BLASTX
NCBI GI	g5596468
BLAST score	260
E value	2.0e-22
Match length	66
% identity	71
NCBI Description	(AL096882) putative protein [Arabidopsis thaliana]

Seq. No.	394212
Contig ID	47720_1.R1084
5'-most EST	uC-osflM202085h04a1

Seq. No.	394213
Contig ID	47726_1.R1084
5'-most EST	uC-osflM202085h10a1

Seq. No.	394214
Contig ID	47733_1.R1084
5'-most EST	g2310441

Seq. No.	394215
Contig ID	47737_1.R1084
5'-most EST	g286721

Seq. No.	394216
Contig ID	47737_2.R1084
5'-most EST	g568622

Seq. No.	394217

Contig ID	47746_1.R1084
5'-most EST	uC-osflM202089e11b1
Seq. No.	394218
Contig ID	47756_1.R1084
5'-most EST	uC-osflM202089h07b1
Method	BLASTX
NCBI GI	g4490737
BLAST score	309
E value	4.0e-28
Match length	140
% identity	49
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]
Seq. No.	394219
Contig ID	47778_1.R1084
5'-most EST	g3766883
Method	BLASTX
NCBI GI	g585451
BLAST score	211
E value	1.0e-27
Match length	99
% identity	64
NCBI Description	MALATE OXIDOREDUCTASE [NAD] 62 KD ISOFORM, MITOCHONDRIAL PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi_1076667_pir__B53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 62K chain precursor, mitochondrial - potato >gi_438249_emb_CAA80559_ (Z23023) malate dehydrogenase [Solanum tuberosum]
Seq. No.	394220
Contig ID	47816_1.R1084
5'-most EST	g3767018
Seq. No.	394221
Contig ID	47817_1.R1084
5'-most EST	g5002849
Seq. No.	394222
Contig ID	47825_1.R1084
5'-most EST	uC-osflM202064a06a1
Seq. No.	394223
Contig ID	47828_1.R1084
5'-most EST	g3769125
Seq. No.	394224
Contig ID	47851_1.R1084
5'-most EST	g2317418
Method	BLASTX
NCBI GI	g4337195
BLAST score	252
E value	4.0e-24
Match length	79
% identity	68
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	394225
Contig ID	47859_1.R1084
5'-most EST	uC-osflM202064d08a1
Method	BLASTX
NCBI GI	g3334133
BLAST score	238
E value	3.0e-41
Match length	119
% identity	69
NCBI Description	CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi_1432145 (U61231) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	394226
Contig ID	47873_1.R1084
5'-most EST	uC-osflM202064e10a1
Method	BLASTX
NCBI GI	g5731259
BLAST score	131
E value	1.0e-15
Match length	56
% identity	79
NCBI Description	(AF166351) alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis thaliana]

Seq. No.	394227
Contig ID	47909_1.R1084
5'-most EST	uC-osflM2020116a09a1

Seq. No.	394228
Contig ID	47920_1.R1084
5'-most EST	uC-osflM2020116d09a1

Seq. No.	394229
Contig ID	47922_1.R1084
5'-most EST	g3762870
Method	BLASTX
NCBI GI	g2462761
BLAST score	312
E value	3.0e-28
Match length	161
% identity	44
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	394230
Contig ID	47974_1.R1084
5'-most EST	uC-osroM202016d08a1

Seq. No.	394231
Contig ID	47991_1.R1084
5'-most EST	uC-osflm202002d04b1
Method	BLASTX
NCBI GI	g1737492
BLAST score	520
E value	7.0e-53
Match length	130
% identity	20

NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]
Seq. No.	394232
Contig ID	48001_1.R1084
5'-most EST	g3061181
Seq. No.	394233
Contig ID	48011_1.R1084
5'-most EST	g701507
Seq. No.	394234
Contig ID	48021_1.R1084
5'-most EST	uC-osflm202099d05b1
Seq. No.	394235
Contig ID	48040_1.R1084
5'-most EST	g3061053
Method	BLASTX
NCBI GI	g1771162
BLAST score	336
E value	4.0e-31
Match length	144
% identity	51
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000.1_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]
Seq. No.	394236
Contig ID	48053_1.R1084
5'-most EST	g2428167
Seq. No.	394237
Contig ID	48068_1.R1084
5'-most EST	g572194
Method	BLASTX
NCBI GI	g133872
BLAST score	440
E value	2.0e-43
Match length	160
% identity	54
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]
Seq. No.	394238
Contig ID	48077_1.R1084
5'-most EST	uC-osrocyp037d06b1
Method	BLASTX
NCBI GI	g3249066
BLAST score	528
E value	1.0e-53
Match length	191
% identity	60

NCBI Description	(AC004473) Similar to S. cerevisiae SIK1P protein gb_984964. ESTs gb_F15433 and gb_AA395158 come from this gene. [Arabidopsis thaliana]
Seq. No.	394239
Contig ID	48100_1.R1084
5'-most EST	uC-osflm202102f08b1
Seq. No.	394240
Contig ID	48116_1.R1084
5'-most EST	uC-osflm202103g02b1
Seq. No.	394241
Contig ID	48137_1.R1084
5'-most EST	uC-osflm202104f08b1
Method	BLASTX
NCBI GI	g4539293
BLAST score	530
E value	9.0e-54
Match length	216
% identity	48
NCBI Description	(AL049480) putative membrane transporter [Arabidopsis thaliana]
Seq. No.	394242
Contig ID	48140_1.R1084
5'-most EST	g572285
Seq. No.	394243
Contig ID	48143_1.R1084
5'-most EST	g2428663
Seq. No.	394244
Contig ID	48145_1.R1084
5'-most EST	g700279
Seq. No.	394245
Contig ID	48149_1.R1084
5'-most EST	uC-osflm202106c09b1
Seq. No.	394246
Contig ID	48182_1.R1084
5'-most EST	g571955
Method	BLASTX
NCBI GI	g4584343
BLAST score	245
E value	1.0e-20
Match length	69
% identity	68
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis thaliana]
Seq. No.	394247
Contig ID	48219_1.R1084
5'-most EST	g2312517
Method	BLASTX
NCBI GI	g4895226

BLAST score 445
E value 8.0e-57
Match length 149
% identity 78
NCBI Description (AC007660) hypothetical protein [Arabidopsis thaliana]

Seq. No. 394248
Contig ID 48223_1.R1084
5'-most EST uC-osflm202108d06b1
Method BLASTX
NCBI GI g4835767
BLAST score 233
E value 4.0e-33
Match length 146
% identity 53
NCBI Description (AC007202) T8K14.16 [Arabidopsis thaliana]

Seq. No. 394249
Contig ID 48227_2.R1084
5'-most EST g4879619

Seq. No. 394250
Contig ID 48230_1.R1084
5'-most EST g2312105
Method BLASTX
NCBI GI g3213227
BLAST score 161
E value 9.0e-11
Match length 148
% identity 26
NCBI Description (AF035209) putative v-SNARE Vti1a [Mus musculus]
>gi_3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]

Seq. No. 394251
Contig ID 48248_1.R1084
5'-most EST g2311555
Method BLASTX
NCBI GI g3738312
BLAST score 462
E value 6.0e-58
Match length 171
% identity 64
NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No. 394252
Contig ID 48260_1.R1084
5'-most EST uC-osroM202010d05b1
Method BLASTX
NCBI GI g5596996
BLAST score 148
E value 3.0e-09
Match length 65
% identity 52
NCBI Description (Y14600) putative protein serine /threonine kinase [Sorghum bicolor]

Seq. No. 394253

Contig ID	48260_2.R1084
5'-most EST	uC-osrocyp002e02b1
Seq. No.	394254
Contig ID	48262_1.R1084
5'-most EST	uC-osroM202024g08b1
Seq. No.	394255
Contig ID	48271_1.R1084
5'-most EST	uC-osrocyp002f06b1
Seq. No.	394256
Contig ID	48273_1.R1084
5'-most EST	uC-osrocyp002f10b1
Seq. No.	394257
Contig ID	48287_1.R1084
5'-most EST	uC-osrocyp033h05b1
Method	BLASTX
NCBI GI	g5823572
BLAST score	409
E value	9.0e-40
Match length	136
% identity	59
NCBI Description	(AL049730) putative protein [Arabidopsis thaliana]
Seq. No.	394258
Contig ID	48291_1.R1084
5'-most EST	g572121
Method	BLASTX
NCBI GI	g1778093
BLAST score	423
E value	3.0e-48
Match length	152
% identity	69
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]
Seq. No.	394259
Contig ID	48294_1.R1084
5'-most EST	uC-osrocyp004a03b1
Method	BLASTX
NCBI GI	g1653196
BLAST score	399
E value	2.0e-38
Match length	117
% identity	62
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]
Seq. No.	394260
Contig ID	48296_1.R1084
5'-most EST	uC-osrocyp004a10b1
Method	BLASTX
NCBI GI	g3915395
BLAST score	877
E value	2.0e-96

Match length	176
% identity	92
NCBI Description	HYPOTHETICAL 21.0 KD PROTEIN SLR0612

Seq. No.	394261
Contig ID	48297_1.R1084
5'-most EST	uC-osrocyp004a11b1
Method	BLASTX
NCBI GI	g1651876
BLAST score	688
E value	2.0e-72
Match length	139
% identity	96
NCBI Description	(D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	394262
Contig ID	48299_1.R1084
5'-most EST	uC-osrocyp004b07b1
Method	BLASTN
NCBI GI	g1652027
BLAST score	549
E value	0.0e+00
Match length	569
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 4/27, 402290-524345

Seq. No.	394263
Contig ID	48300_1.R1084
5'-most EST	uC-osrocyp004b08b1
Method	BLASTX
NCBI GI	g1006580
BLAST score	259
E value	7.0e-45
Match length	128
% identity	80
NCBI Description	(D64005) hypothetical protein [Synechocystis sp.]

Seq. No.	394264
Contig ID	48302_1.R1084
5'-most EST	uC-osrocyp004c04b1
Method	BLASTN
NCBI GI	g1001396
BLAST score	633
E value	0.0e+00
Match length	649
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 18/27, 2267260-2392728

Seq. No.	394265
Contig ID	48305_1.R1084
5'-most EST	uC-osrocyp004d09b1
Method	BLASTX
NCBI GI	g1001555
BLAST score	729
E value	4.0e-77

Match length 159
% identity 94
NCBI Description (D64000) ATP-dependent Clp protease regulatory subunit [Synechocystis sp.]

Seq. No. 394266
Contig ID 48306_1.R1084
5'-most EST uC-osrocyp004d11b1

Seq. No. 394267
Contig ID 48310_1.R1084
5'-most EST uC-osrocyp004f03b1
Method BLASTX
NCBI GI g3183135
BLAST score 582
E value 5.0e-60
Match length 118
% identity 97
NCBI Description PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) >gi_1653581_dbj_BAA18494_ (D90914) primosomal protein N [Synechocystis sp.]

Seq. No. 394268
Contig ID 48317_1.R1084
5'-most EST uC-osrocyp004h05b1
Method BLASTX
NCBI GI g1653718
BLAST score 917
E value 1.0e-102
Match length 236
% identity 77
NCBI Description (D90916) hypothetical protein [Synechocystis sp.]

Seq. No. 394269
Contig ID 48318_1.R1084
5'-most EST g2312593
Method BLASTX
NCBI GI g5733886
BLAST score 423
E value 2.0e-41
Match length 116
% identity 72
NCBI Description (AC007932) F11A17.20 [Arabidopsis thaliana]

Seq. No. 394270
Contig ID 48322_1.R1084
5'-most EST g572124
Method BLASTX
NCBI GI g5731998
BLAST score 726
E value 1.0e-76
Match length 261
% identity 57
NCBI Description (AF139532) aldehyde 5-hydroxylase [Liquidambar styraciflua]

Seq. No. 394271
Contig ID 48325_1.R1084

5'-most EST	uC-osrocyp005a11b1
Seq. No.	394272
Contig ID	48327_1.R1084
5'-most EST	uC-osrocyp005b02b1
Method	BLASTX
NCBI GI	g2842490
BLAST score	311
E value	3.0e-28
Match length	69
% identity	86
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.	394273
Contig ID	48341_1.R1084
5'-most EST	uC-osrocyp005d06b1
Method	BLASTN
NCBI GI	g5852170
BLAST score	83
E value	2.0e-38
Match length	153
% identity	49
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804
Seq. No.	394274
Contig ID	48347_1.R1084
5'-most EST	g2310450
Method	BLASTX
NCBI GI	g4914402
BLAST score	575
E value	3.0e-59
Match length	188
% identity	59
NCBI Description	(AL050352) hypothetical protein [Arabidopsis thaliana]
Seq. No.	394275
Contig ID	48362_1.R1084
5'-most EST	uC-osrocyp007g04b1
Method	BLASTX
NCBI GI	g2911300
BLAST score	288
E value	8.0e-25
Match length	765
% identity	24
NCBI Description	(AF022937) structural polyprotein [Rhopalosiphum padi virus]
Seq. No.	394276
Contig ID	48364_1.R1084
5'-most EST	g701738
Seq. No.	394277
Contig ID	48373_1.R1084
5'-most EST	uC-osrocyp005g11b1
Method	BLASTX
NCBI GI	g4538939

BLAST score 410
E value 5.0e-40
Match length 86
% identity 88
NCBI Description (AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No. 394278
Contig ID 48381_1.R1084
5'-most EST g2442628

Seq. No. 394279
Contig ID 48398_1.R1084
5'-most EST uC-osrocyp010d08b1

Seq. No. 394280
Contig ID 48401_1.R1084
5'-most EST uC-osrocyp006c04b1

Seq. No. 394281
Contig ID 48420_1.R1084
5'-most EST uC-osrocyp006e06b1
Method BLASTX
NCBI GI g5103807
BLAST score 361
E value 3.0e-34
Match length 113
% identity 58
NCBI Description (AC007591) Contains similarity to gb_AF014403 type-2 phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo sapiens. ESTs gb_T88254 and gb_AA394650 come from this gene. [Arabidopsis thaliana]

Seq. No. 394282
Contig ID 48422_1.R1084
5'-most EST uC-osrocyp006e10b1

Seq. No. 394283
Contig ID 48426_1.R1084
5'-most EST uC-osrocyp008h09b1

Seq. No. 394284
Contig ID 48456_1.R1084
5'-most EST uC-osrocyp008b01b1

Seq. No. 394285
Contig ID 48475_1.R1084
5'-most EST g5056083
Method BLASTX
NCBI GI g6007450
BLAST score 113
E value 1.0e-08
Match length 120
% identity 42
NCBI Description (AF188159) actin I [Hypotrichida sp. 'unknown F']

Seq. No. 394286

Contig ID	48477_1.R1084
5'-most EST	uC-osroM202014e08b1
Method	BLASTX
NCBI GI	g3242717
BLAST score	320
E value	2.0e-29
Match length	81
% identity	75
NCBI Description	(AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No.	394287
Contig ID	48479_1.R1084
5'-most EST	uC-osroM202019b12b1
Method	BLASTX
NCBI GI	g3395431
BLAST score	355
E value	1.0e-33
Match length	102
% identity	67
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	394288
Contig ID	48506_1.R1084
5'-most EST	uC-osrocyp008h08b1
Method	BLASTX
NCBI GI	g2981475
BLAST score	329
E value	2.0e-30
Match length	102
% identity	68
NCBI Description	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]

Seq. No.	394289
Contig ID	48531_1.R1084
5'-most EST	uC-osrocyp009c07b1
Method	BLASTX
NCBI GI	g2191135
BLAST score	387
E value	6.0e-37
Match length	241
% identity	34
NCBI Description	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]

Seq. No.	394290
Contig ID	48541_1.R1084
5'-most EST	uC-osrocyp009d08b1

Seq. No.	394291
Contig ID	48559_1.R1084
5'-most EST	uC-osrocyp009f10b1
Method	BLASTX
NCBI GI	g3377509
BLAST score	429
E value	7.0e-42
Match length	158

% identity	49
NCBI Description	(AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No.	394292
Contig ID	48564_1.R1084
5'-most EST	uC-osrocyp032b09b1

Seq. No.	394293
Contig ID	48583_1.R1084
5'-most EST	g427136
Method	BLASTX
NCBI GI	g2833375
BLAST score	349
E value	8.0e-33
Match length	71
% identity	90
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10) (RP10) (ABC10) >gi_533690 (U12133) RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]

Seq. No.	394294
Contig ID	48595_1.R1084
5'-most EST	g427516
Method	BLASTX
NCBI GI	g2492512
BLAST score	162
E value	1.0e-10
Match length	90
% identity	46
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG 3 >gi_1652556_dbj_BAA17477_ (D90906) cell division protein FtsH [Synechocystis sp.]

Seq. No.	394295
Contig ID	48597_1.R1084
5'-most EST	uC-osrocyp010d09b1

Seq. No.	394296
Contig ID	48613_1.R1084
5'-most EST	uC-osrocyp010f09b1
Method	BLASTX
NCBI GI	g913445
BLAST score	410
E value	2.0e-65
Match length	207
% identity	59
NCBI Description	(S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

Seq. No.	394297
Contig ID	48616_1.R1084
5'-most EST	uC-osrocyp010f12b1

Seq. No.	394298

Contig ID	48616_2.R1084
5'-most EST	g4878564
Seq. No.	394299
Contig ID	48621_1.R1084
5'-most EST	g2800099
Method	BLASTX
NCBI GI	g2827661
BLAST score	577
E value	3.0e-59
Match length	207
% identity	60
NCBI Description	(AL021637) hyuC-like protein [Arabidopsis thaliana]
Seq. No.	394300
Contig ID	48634_1.R1084
5'-most EST	uC-osrocyp011a04b1
Seq. No.	394301
Contig ID	48638_1.R1084
5'-most EST	g2797342
Method	BLASTX
NCBI GI	g4512685
BLAST score	523
E value	4.0e-53
Match length	173
% identity	58
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]
Seq. No.	394302
Contig ID	48654_1.R1084
5'-most EST	g2798771
Method	BLASTX
NCBI GI	g3618312
BLAST score	225
E value	2.0e-18
Match length	96
% identity	32
NCBI Description	(AB001884) zinc finger protein [Oryza sativa]
Seq. No.	394303
Contig ID	48658_1.R1084
5'-most EST	uC-osrocyp011d05b1
Method	BLASTX
NCBI GI	g6006379
BLAST score	842
E value	2.0e-90
Match length	203
% identity	84
NCBI Description	(AP000559) ESTs AU078277(S1084),AU078273(S13585), D47857(S13585) correspond to a region of the predicted gene.; Similar to Caenorhabditis elegans cosmid C15H9; hypothetical protein (U56965) [Oryza sativa]
Seq. No.	394304

Contig ID	48671_1.R1084
5'-most EST	g428183
Method	BLASTX
NCBI GI	g585661
BLAST score	303
E value	2.0e-27
Match length	124
% identity	48
NCBI Description	PEROXIDASE PRECURSOR >gi_287401_dbj_BAA03644_ (D14997) peroxidase [Oryza sativa]

Seq. No.	394305
Contig ID	48674_1.R1084
5'-most EST	uC-osrocyp017d12b1

Seq. No.	394306
Contig ID	48688_1.R1084
5'-most EST	g427761
Method	BLASTX
NCBI GI	g128592
BLAST score	428
E value	5.0e-42
Match length	99
% identity	75
NCBI Description	POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR >gi_82190_pir__S22495 pollen-specific protein precursor - common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen specific protein [Nicotiana tabacum]

Seq. No.	394307
Contig ID	48689_1.R1084
5'-most EST	uC-osrocyp011h04b1
Method	BLASTN
NCBI GI	g5441876
BLAST score	153
E value	2.0e-80
Match length	491
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	394308
Contig ID	48690_1.R1084
5'-most EST	uC-osrocyp011h05b1

Seq. No.	394309
Contig ID	48694_1.R1084
5'-most EST	uC-osrocyp012a01b1
Method	BLASTX
NCBI GI	g5902444
BLAST score	553
E value	7.0e-60
Match length	220
% identity	62
NCBI Description	(AB030283) GAG-POL precursor [Oryza sativa]

Seq. No.	394310

Contig ID	48708_1.R1084
5'-most EST	g701717
Method	BLASTX
NCBI GI	g4836876
BLAST score	540
E value	4.0e-55
Match length	190
% identity	72
NCBI Description	(AC007260) Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana]

Seq. No.	394311
Contig ID	48709_1.R1084
5'-most EST	g426044
Method	BLASTX
NCBI GI	g3395431
BLAST score	445
E value	1.0e-43
Match length	167
% identity	51
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	394312
Contig ID	48723_1.R1084
5'-most EST	uC-osrocyp012d03b1

Seq. No.	394313
Contig ID	48724_1.R1084
5'-most EST	uC-osrocyp012d04b1
Method	BLASTX
NCBI GI	g4056507
BLAST score	411
E value	8.0e-40
Match length	109
% identity	72
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	394314
Contig ID	48727_1.R1084
5'-most EST	uC-osrocyp015b12b1
Method	BLASTX
NCBI GI	g5923675
BLAST score	610
E value	3.0e-63
Match length	220
% identity	56
NCBI Description	(AC009326) putative mRNA capping enzyme, RNA guanylyltransferase [Arabidopsis thaliana]

Seq. No.	394315
Contig ID	48729_1.R1084
5'-most EST	uC-osrocyp012d09b1
Method	BLASTX
NCBI GI	g4519615
BLAST score	147
E value	5.0e-09

Match length	78
% identity	45
NCBI Description	(AB017594) RPE65 [Gallus gallus]

Seq. No.	394316
Contig ID	48740_1.R1084
5'-most EST	uC-osrocyp012f07b1
Method	BLASTX
NCBI GI	g2576361
BLAST score	427
E value	5.0e-42
Match length	116
% identity	67
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	394317
Contig ID	48743_1.R1084
5'-most EST	uC-osrocyp012f11b1
Method	BLASTX
NCBI GI	g4678268
BLAST score	365
E value	1.0e-34
Match length	77
% identity	79
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]

Seq. No.	394318
Contig ID	48747_1.R1084
5'-most EST	g5003036

Seq. No.	394319
Contig ID	48757_1.R1084
5'-most EST	uC-osrocyp012h06b1

Seq. No.	394320
Contig ID	48796_1.R1084
5'-most EST	g2428215

Seq. No.	394321
Contig ID	48804_1.R1084
5'-most EST	uC-osrocyp013f04b1
Method	BLASTX
NCBI GI	g3445201
BLAST score	166
E value	1.0e-17
Match length	105
% identity	44
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	394322
Contig ID	48805_1.R1084
5'-most EST	g2427989
Method	BLASTX
NCBI GI	g2347195
BLAST score	304
E value	2.0e-27

Match length	142
% identity	45
NCBI Description	(AC002338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394323
Contig ID	48829_1.R1084
5'-most EST	g1631499
Method	BLASTX
NCBI GI	g4587520
BLAST score	251
E value	2.0e-40
Match length	148
% identity	62
NCBI Description	(AC007060) Strong similarity to gb_X71057 protein kinase from Nicotiana tabacum and contains PF_00069 eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No.	394324
Contig ID	48846_1.R1084
5'-most EST	uC-osrocyp014c07b1
Method	BLASTX
NCBI GI	g3377820
BLAST score	342
E value	5.0e-32
Match length	98
% identity	68
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	394325
Contig ID	48856_1.R1084
5'-most EST	uC-osroM202021e01b1

Seq. No.	394326
Contig ID	48868_1.R1084
5'-most EST	uC-osrocyp014f02b1
Method	BLASTX
NCBI GI	g5019548
BLAST score	728
E value	4.0e-77
Match length	177
% identity	70
NCBI Description	(AJ242663) cathepsin Z [Mus musculus]

Seq. No.	394327
Contig ID	48879_1.R1084
5'-most EST	uC-osrocyp015g01b1

Seq. No.	394328
Contig ID	48882_1.R1084
5'-most EST	uC-osrocyp014g04b1
Method	BLASTN
NCBI GI	g5091597
BLAST score	70
E value	7.0e-31
Match length	127
% identity	89

NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.	394329
Contig ID	48883_1.R1084
5'-most EST	g700426
Method	BLASTX
NCBI GI	g4887131
BLAST score	294
E value	2.0e-26
Match length	95
% identity	62
NCBI Description	(AF134732) 60S ribosomal protein L1 [Prunus armeniaca]
Seq. No.	394330
Contig ID	48892_1.R1084
5'-most EST	g5667199
Method	BLASTX
NCBI GI	g4972075
BLAST score	211
E value	1.0e-16
Match length	82
% identity	48
NCBI Description	(AL078467) proton pump interactor [Arabidopsis thaliana]
Seq. No.	394331
Contig ID	48896_1.R1084
5'-most EST	g2428258
Seq. No.	394332
Contig ID	48898_1.R1084
5'-most EST	uC-osrocyp015b09b1
Method	BLASTX
NCBI GI	g2623297
BLAST score	258
E value	4.0e-22
Match length	171
% identity	36
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3790583 (AF079180) RING-H2 finger protein RHC1a [Arabidopsis thaliana]
Seq. No.	394333
Contig ID	48902_1.R1084
5'-most EST	uC-osrocyp015b05b1
Method	BLASTX
NCBI GI	g3980417
BLAST score	281
E value	1.0e-24
Match length	82
% identity	31
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.	394334
Contig ID	48904_1.R1084
5'-most EST	uC-osrocyp015b07b1
Seq. No.	394335

Contig ID	48905_1.R1084
5'-most EST	uC-osrocyp032d02b1
Method	BLASTX
NCBI GI	g5304837
BLAST score	321
E value	2.0e-29
Match length	137
% identity	50
NCBI Description	(AJ243483) ATP citrate lyase [Cyanophora paradoxa]

Seq. No.	394336
Contig ID	48916_1.R1084
5'-most EST	uC-osrocyp032g10b1
Method	BLASTX
NCBI GI	g300264
BLAST score	433
E value	1.0e-42
Match length	138
% identity	49
NCBI Description	(S59747) HSP68=68 kda heat-stress DnaK homolog [Solanum tuberosum=potatoes, Peptide Mitochondrial, 682 aa] [Solanum tuberosum]

Seq. No.	394337
Contig ID	48919_1.R1084
5'-most EST	g2310156
Method	BLASTX
NCBI GI	g4508079
BLAST score	397
E value	2.0e-38
Match length	143
% identity	62
NCBI Description	(AC005882) 66284 [Arabidopsis thaliana]

Seq. No.	394338
Contig ID	48922_1.R1084
5'-most EST	uC-osroM202034f08b1
Method	BLASTX
NCBI GI	g2760834
BLAST score	150
E value	2.0e-09
Match length	84
% identity	39
NCBI Description	(AC003105) putative nitrate transporter [Arabidopsis thaliana]

Seq. No.	394339
Contig ID	48923_1.R1084
5'-most EST	uC-osrocyp015d09b1

Seq. No.	394340
Contig ID	48930_1.R1084
5'-most EST	uC-osrocyp015e07b1
Method	BLASTX
NCBI GI	g4586109
BLAST score	288
E value	1.0e-25

Match length 133
% identity 44
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 394341
Contig ID 48969_1.R1084
5'-most EST uC-osrocyp016b07b1
Method BLASTX
NCBI GI g4263721
BLAST score 441
E value 1.0e-43
Match length 172
% identity 51
NCBI Description (AC006223) putative DNA repair protein RAD50 [Arabidopsis thaliana]

Seq. No. 394342
Contig ID 48979_1.R1084
5'-most EST uC-osroM202007b03a1
Method BLASTX
NCBI GI g2501555
BLAST score 364
E value 2.0e-34
Match length 71
% identity 93
NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 394343
Contig ID 48996_1.R1084
5'-most EST g2310143
Method BLASTX
NCBI GI g2190550
BLAST score 692
E value 7.0e-73
Match length 171
% identity 78
NCBI Description (AC001229) ESTs gb_T45673,gb_N37512 come from this gene. [Arabidopsis thaliana]

Seq. No. 394344
Contig ID 48999_1.R1084
5'-most EST uC-osrocyp028a05b1

Seq. No. 394345
Contig ID 49006_1.R1084
5'-most EST uC-osrocyp016g12b1
Method BLASTX
NCBI GI g2832898
BLAST score 351
E value 4.0e-33
Match length 128
% identity 59
NCBI Description (AJ000886) Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus]

Seq. No. 394346

Contig ID	49017_1.R1084
5'-most EST	g3763864
Method	BLASTX
NCBI GI	g3912917
BLAST score	807
E value	1.0e-117
Match length	295
% identity	77
NCBI Description	(AF001308) putative NAK-like ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	394347
Contig ID	49022_1.R1084
5'-most EST	uC-osrocyp017a12b1
Method	BLASTX
NCBI GI	g5103807
BLAST score	157
E value	1.0e-10
Match length	53
% identity	53
NCBI Description	(AC007591) Contains similarity to gb_AF014403 type-2 phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo sapiens. ESTs gb_T88254 and gb_AA394650 come from this gene. [Arabidopsis thaliana]

Seq. No.	394348
Contig ID	49050_1.R1084
5'-most EST	g5667602
Method	BLASTX
NCBI GI	g2618696
BLAST score	153
E value	9.0e-10
Match length	93
% identity	32
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394349
Contig ID	49054_1.R1084
5'-most EST	uC-osrocyp017f05b1

Seq. No.	394350
Contig ID	49071_1.R1084
5'-most EST	g3767106
Method	BLASTX
NCBI GI	g4835757
BLAST score	318
E value	2.0e-29
Match length	115
% identity	51
NCBI Description	(AC007202) EST gb_AA404917 comes from this gene. [Arabidopsis thaliana]

Seq. No.	394351
Contig ID	49073_1.R1084
5'-most EST	uC-osrocyp024c01b1

Seq. No. 394352

Contig ID	49104_1.R1084
5'-most EST	uC-osroM202037a09b1
Seq. No.	394353
Contig ID	49137_1.R1084
5'-most EST	g428028
Seq. No.	394354
Contig ID	49147_1.R1084
5'-most EST	g286410
Method	BLASTX
NCBI GI	g3176660
BLAST score	166
E value	2.0e-11
Match length	64
% identity	50
NCBI Description	(AC004393) Similar to ERECTA receptor protein kinase gb_U47029 from A. thaliana. [Arabidopsis thaliana]
Seq. No.	394355
Contig ID	49156_1.R1084
5'-most EST	uC-osrocyp032h04b1
Seq. No.	394356
Contig ID	49159_1.R1084
5'-most EST	g2799730
Method	BLASTX
NCBI GI	g1688233
BLAST score	208
E value	2.0e-17
Match length	101
% identity	56
NCBI Description	(U77655) DNA binding protein homolog [Solanum tuberosum]
Seq. No.	394357
Contig ID	49160_1.R1084
5'-most EST	uC-osrocyp028e08b1
Method	BLASTX
NCBI GI	g4454039
BLAST score	282
E value	5.0e-25
Match length	92
% identity	62
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]
Seq. No.	394358
Contig ID	49161_1.R1084
5'-most EST	g2429048
Method	BLASTX
NCBI GI	g4510376
BLAST score	285
E value	2.0e-25
Match length	96
% identity	53
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	394359
Contig ID	49175_1.R1084
5'-most EST	g702130
Method	BLASTX
NCBI GI	g5730134
BLAST score	185
E value	1.0e-13
Match length	90
% identity	47
NCBI Description	(AL109796) putative protein [Arabidopsis thaliana]

Seq. No.	394360
Contig ID	49180_1.R1084
5'-most EST	uC-osrocyp028h06b1

Seq. No.	394361
Contig ID	49203_1.R1084
5'-most EST	uC-osrocyp029d09b1

Seq. No.	394362
Contig ID	49205_1.R1084
5'-most EST	g4715247

Seq. No.	394363
Contig ID	49217_1.R1084
5'-most EST	uC-osrocyp029g10b1
Method	BLASTX
NCBI GI	g320130
BLAST score	301
E value	3.0e-27
Match length	90
% identity	63
NCBI Description	acetolactate synthase (EC 4.1.3.18) (clone pSOG109) - maize >gi_22141_emb_CAA45117_ (X63554) acetohydroxyacid synthase [Zea mays]

Seq. No.	394364
Contig ID	49219_1.R1084
5'-most EST	uC-osrocyp029g12b1
Method	BLASTX
NCBI GI	g3152940
BLAST score	186
E value	9.0e-14
Match length	98
% identity	42
NCBI Description	(AF065483) sorting nexin 1 [Homo sapiens]

Seq. No.	394365
Contig ID	49247_1.R1084
5'-most EST	g4715095
Method	BLASTX
NCBI GI	g2760324
BLAST score	578
E value	3.0e-59
Match length	306
% identity	43
NCBI Description	(AC002130) F1N21.9 [Arabidopsis thaliana]

Seq. No.	394366
Contig ID	49249_1.R1084
5'-most EST	g4880935
Method	BLASTX
NCBI GI	g3360289
BLAST score	1150
E value	1.0e-126
Match length	362
% identity	63
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	394367
Contig ID	49251_1.R1084
5'-most EST	uC-osrocyp030c12b1
Method	BLASTX
NCBI GI	g1703446
BLAST score	922
E value	1.0e-99
Match length	299
% identity	66
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	394368
Contig ID	49256_1.R1084
5'-most EST	uC-osrocyp030d05b1
Method	BLASTX
NCBI GI	g6094554
BLAST score	203
E value	9.0e-16
Match length	73
% identity	58
NCBI Description	(AC010676) putative protein kinase [Arabidopsis thaliana]

Seq. No.	394369
Contig ID	49272_1.R1084
5'-most EST	uC-osrocyp030f11b1

Seq. No.	394370
Contig ID	49277_1.R1084
5'-most EST	uC-osroM202033d06b1
Method	BLASTX
NCBI GI	g2459575
BLAST score	184
E value	2.0e-13
Match length	104
% identity	33
NCBI Description	(U75346) envelope protein [Chlamydomonas reinhardtii]

Seq. No.	394371
Contig ID	49278_1.R1084
5'-most EST	g2312209
Method	BLASTX

NCBI GI	g3075391
BLAST score	170
E value	9.0e-12
Match length	93
% identity	42
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	394372
Contig ID	49281_1.R1084
5'-most EST	uC-osrocyp030h05b1

Seq. No.	394373
Contig ID	49294_1.R1084
5'-most EST	uC-osrocyp031b06b1
Method	BLASTX
NCBI GI	g486849
BLAST score	251
E value	2.0e-21
Match length	168
% identity	25
NCBI Description	licheninase (EC 3.2.1.73) precursor - wheat >gi_311764_emb_CAA80493_ (Z22874) (1,3;1,4) beta glucanase [Triticum aestivum]

Seq. No.	394374
Contig ID	49302_1.R1084
5'-most EST	uC-osrocyp013c02b1
Method	BLASTX
NCBI GI	g4490309
BLAST score	381
E value	1.0e-36
Match length	117
% identity	59
NCBI Description	(AL035678) peroxidase ATP17a-like protein [Arabidopsis thaliana]

Seq. No.	394375
Contig ID	49313_1.R1084
5'-most EST	uC-osrocyp031f11b1
Method	BLASTX
NCBI GI	g3341679
BLAST score	208
E value	2.0e-16
Match length	60
% identity	70
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	394376
Contig ID	49315_1.R1084
5'-most EST	uC-osrocyp031g02b1

Seq. No.	394377
Contig ID	49317_1.R1084
5'-most EST	uC-osrocyp031g06b1
Method	BLASTX
NCBI GI	g4262167

BLAST score	144
E value	1.0e-08
Match length	35
% identity	66
NCBI Description	(AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No.	394378
Contig ID	49320_1.R1084
5'-most EST	g2311283
Method	BLASTX
NCBI GI	g4884932
BLAST score	233
E value	1.0e-39
Match length	148
% identity	58
NCBI Description	(AF141659) AtHVA22a [Arabidopsis thaliana] >gi_4884944_gb_AAD31885.1_AF141977_1 (AF141977) AtHVA22a [Arabidopsis thaliana]

Seq. No.	394379
Contig ID	49350_1.R1084
5'-most EST	uC-osrocyp032d10b1

Seq. No.	394380
Contig ID	49367_1.R1084
5'-most EST	g2312199

Seq. No.	394381
Contig ID	49378_1.R1084
5'-most EST	g2312139

Seq. No.	394382
Contig ID	49382_1.R1084
5'-most EST	uC-osrocyp033a10b1

Seq. No.	394383
Contig ID	49394_1.R1084
5'-most EST	uC-osrocyp033c07b1
Method	BLASTX
NCBI GI	g2315591
BLAST score	203
E value	1.0e-15
Match length	107
% identity	38
NCBI Description	(AF016662) No definition line found [Caenorhabditis elegans]

Seq. No.	394384
Contig ID	49415_1.R1084
5'-most EST	g3061215

Seq. No.	394385
Contig ID	49419_1.R1084
5'-most EST	g1631451

Seq. No.	394386

Contig ID	49423_1.R1084
5'-most EST	uC-osrocyp033h12b1
Seq. No.	394387
Contig ID	49438_1.R1084
5'-most EST	uC-osrocyp002b02a1
Seq. No.	394388
Contig ID	49458_1.R1084
5'-most EST	uC-osrocyp002c06a1
Seq. No.	394389
Contig ID	49461_1.R1084
5'-most EST	uC-osrocyp002c09a1
Seq. No.	394390
Contig ID	49484_1.R1084
5'-most EST	g4715842
Seq. No.	394391
Contig ID	49503_1.R1084
5'-most EST	uC-osrocyp002f04b1
Seq. No.	394392
Contig ID	49507_1.R1084
5'-most EST	g2317495
Method	BLASTX
NCBI GI	g4006829
BLAST score	307
E value	2.0e-55
Match length	152
% identity	73
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.	394393
Contig ID	49513_1.R1084
5'-most EST	uC-osrocyp002f12b1
Seq. No.	394394
Contig ID	49553_1.R1084
5'-most EST	g3768657
Seq. No.	394395
Contig ID	49555_1.R1084
5'-most EST	g2317533
Seq. No.	394396
Contig ID	49563_1.R1084
5'-most EST	uC-osrocyp003c01a1
Seq. No.	394397
Contig ID	49573_1.R1084
5'-most EST	g4968907
Method	BLASTX
NCBI GI	g3461821
BLAST score	493
E value	2.0e-49

Match length 191
% identity 55
NCBI Description (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No. 394398
Contig ID 49602_1.R1084
5'-most EST g4714134
Method BLASTX
NCBI GI g5541697
BLAST score 167
E value 2.0e-11
Match length 43
% identity 77
NCBI Description (AL096860) putative protein [Arabidopsis thaliana]

Seq. No. 394399
Contig ID 49626_1.R1084
5'-most EST uC-osrocyp036c03a1
Method BLASTX
NCBI GI g3242789
BLAST score 894
E value 1.0e-111
Match length 262
% identity 74
NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]

Seq. No. 394400
Contig ID 49644_1.R1084
5'-most EST uC-osrocyp004b03a1
Method BLASTX
NCBI GI g2500610
BLAST score 413
E value 3.0e-40
Match length 85
% identity 91
NCBI Description DNA-DIRECTED RNA POLYMERASE BETA CHAIN (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT) >gi_1652443_dbj_BAA17365_ (D90905) RNA polymerase beta subunit [Synechocystis sp.]

Seq. No. 394401
Contig ID 49648_1.R1084
5'-most EST uC-osrocyp004b05a1
Method BLASTX
NCBI GI g1652841
BLAST score 501
E value 2.0e-50
Match length 101
% identity 97
NCBI Description (D90908) sensory transduction histidine kinase [Synechocystis sp.]

Seq. No. 394402
Contig ID 49653_1.R1084
5'-most EST uC-osrocyp004b09b1

Method	BLASTN
NCBI GI	g1001291
BLAST score	363
E value	0.0e+00
Match length	479
% identity	95
NCBI Description	Synechocystis sp. PCC6803 complete genome, 25/27, 3138604-3270709

Seq. No.	394403
Contig ID	49660_1.R1084
5'-most EST	uC-osrocyp004c05a1

Seq. No.	394404
Contig ID	49663_1.R1084
5'-most EST	uC-osrocyp004c07b1
Method	BLASTX
NCBI GI	g5262759
BLAST score	454
E value	3.0e-45
Match length	115
% identity	77
NCBI Description	(AL080283) putative protein [Arabidopsis thaliana]

Seq. No.	394405
Contig ID	49665_1.R1084
5'-most EST	uC-osrocyp004c09a1
Method	BLASTX
NCBI GI	g431176
BLAST score	309
E value	2.0e-46
Match length	203
% identity	51
NCBI Description	(D21815) serine proteinase [Lilium longiflorum]

Seq. No.	394406
Contig ID	49672_1.R1084
5'-most EST	uC-osrocyp004d02b1
Method	BLASTX
NCBI GI	g1001461
BLAST score	321
E value	7.0e-34
Match length	81
% identity	9
NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]

Seq. No.	394407
Contig ID	49686_1.R1084
5'-most EST	uC-osrocyp004e02a1
Method	BLASTX
NCBI GI	g2313556
BLAST score	427
E value	1.0e-41
Match length	278
% identity	36
NCBI Description	(AE000560) conserved hypothetical protein [Helicobacter pylori 26695]

Seq. No.	394408
Contig ID	49690_1.R1084
5'-most EST	uC-osrocyp004e05b1
Method	BLASTN
NCBI GI	g1651897
BLAST score	166
E value	2.0e-88
Match length	230
% identity	94
NCBI Description	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289

Seq. No.	394409
Contig ID	49692_1.R1084
5'-most EST	uC-osrocyp004e06a1
Method	BLASTX
NCBI GI	g1001150
BLAST score	859
E value	1.0e-92
Match length	190
% identity	86
NCBI Description	(D64001) general secretion pathway protein E [Synechocystis sp.]

Seq. No.	394410
Contig ID	49694_1.R1084
5'-most EST	uC-osrocyp004e07b1
Method	BLASTX
NCBI GI	g1651911
BLAST score	341
E value	2.0e-32
Match length	69
% identity	100
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	394411
Contig ID	49699_1.R1084
5'-most EST	uC-osrocyp004e12a1
Method	BLASTX
NCBI GI	g118730
BLAST score	812
E value	9.0e-87
Match length	161
% identity	99
NCBI Description	DNAK PROTEIN 2 (HEAT SHOCK PROTEIN 70) (HSP70) >gi_97632_pir__C39025 70K heat shock protein dnaK - Synechocystis sp. (PCC 6803) >gi_154468 (M57518) putative [Synechocystis sp.] >gi_1001435_dbj_BAA10059_ (D63999) DnaK protein [Synechocystis sp.]

Seq. No.	394412
Contig ID	49702_1.R1084
5'-most EST	uC-osrocyp004f02a1
Method	BLASTX
NCBI GI	g1652136
BLAST score	471

E value	5.0e-47
Match length	92
% identity	97
NCBI Description	(D90903) hypothetical protein [Synechocystis sp.]

Seq. No.	394413
Contig ID	49709_1.R1084
5'-most EST	uC-osrocyp004f10b1
Method	BLASTN
NCBI GI	g1001484
BLAST score	255
E value	1.0e-141
Match length	255
% identity	100
NCBI Description	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999

Seq. No.	394414
Contig ID	49711_1.R1084
5'-most EST	uC-osrocyp004f12b1
Method	BLASTN
NCBI GI	g1001612
BLAST score	256
E value	1.0e-142
Match length	296
% identity	97
NCBI Description	Synechocystis sp. PCC6803 complete genome, 21/27, 2644795-2755702

Seq. No.	394415
Contig ID	49719_1.R1084
5'-most EST	uC-osrocyp004g09a1
Method	BLASTN
NCBI GI	g1653083
BLAST score	353
E value	0.0e+00
Match length	594
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643

Seq. No.	394416
Contig ID	49721_1.R1084
5'-most EST	uC-osrocyp004g10b1
Method	BLASTN
NCBI GI	g1001701
BLAST score	289
E value	1.0e-161
Match length	293
% identity	100
NCBI Description	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965

Seq. No.	394417
Contig ID	49738_1.R1084
5'-most EST	uC-osrocyp004h11a1
Method	BLASTX

NCBI GI g1653201
BLAST score 1169
E value 1.0e-128
Match length 229
% identity 99
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]

Seq. No. 394418
Contig ID 49741_1.R1084
5'-most EST uC-osrocyp005a01a1

Seq. No. 394419
Contig ID 49750_1.R1084
5'-most EST uC-osrocyp009b03a1

Seq. No. 394420
Contig ID 49766_1.R1084
5'-most EST g3769025

Seq. No. 394421
Contig ID 49767_1.R1084
5'-most EST uC-osrocyp005b08b1

Seq. No. 394422
Contig ID 49768_1.R1084
5'-most EST uC-osrocyp005b09a1
Method BLASTX
NCBI GI g3451075
BLAST score 577
E value 1.0e-59
Match length 146
% identity 69
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 394423
Contig ID 49772_1.R1084
5'-most EST g3767817
Method BLASTX
NCBI GI g3395432
BLAST score 186
E value 9.0e-14
Match length 42
% identity 71
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
>gi_5731261_gb_AAD48838.1_AF166352_1 (AF166352)
alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis
thaliana]

Seq. No. 394424
Contig ID 49780_1.R1084
5'-most EST g3761364
Method BLASTX
NCBI GI g1657855
BLAST score 284
E value 3.0e-25
Match length 107
% identity 55

NCBI Description	(U73216) cold acclimation protein WCOR413 [Triticum aestivum]
Seq. No.	394425
Contig ID	49836_1.R1084
5'-most EST	uC-osrocyp017c02a1
Method	BLASTX
NCBI GI	g836954
BLAST score	155
E value	3.0e-10
Match length	44
% identity	59
NCBI Description	(U20948) receptor protein kinase [Ipomoea trifida]
Seq. No.	394426
Contig ID	49841_1.R1084
5'-most EST	uC-osroM202016g02b1
Method	BLASTX
NCBI GI	g1076202
BLAST score	170
E value	9.0e-12
Match length	149
% identity	29
NCBI Description	calcium-stimulated protein kinase - Chlamydomonas eugametos >gi_806542_emb_CAA89202_ (Z49233) calcium-stimulated protein kinase [Chlamydomonas eugametos]
Seq. No.	394427
Contig ID	49854_1.R1084
5'-most EST	uC-osrocyp010f12a1
Seq. No.	394428
Contig ID	49865_1.R1084
5'-most EST	g3762811
Method	BLASTX
NCBI GI	g1848283
BLAST score	476
E value	2.0e-47
Match length	115
% identity	79
NCBI Description	(U87982) Sorghum bicolor aldehyde dehydrogenase (Dha1) mRNA, partial sequence
Seq. No.	394429
Contig ID	49883_1.R1084
5'-most EST	uC-osrocyp006b12a1
Seq. No.	394430
Contig ID	49895_1.R1084
5'-most EST	uC-osrocyp006c10a1
Seq. No.	394431
Contig ID	49934_1.R1084
5'-most EST	uC-osrocyp006f05a1
Method	BLASTX
NCBI GI	g3953479
BLAST score	168

E value	2.0e-11
Match length	67
% identity	54
NCBI Description	(AC002328) F22O2.24 [Arabidopsis thaliana]

Seq. No.	394432
Contig ID	49935_1.R1084
5'-most EST	g5667584
Method	BLASTX
NCBI GI	g1841468
BLAST score	217
E value	4.0e-17
Match length	106
% identity	43
NCBI Description	(Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]

Seq. No.	394433
Contig ID	49939_1.R1084
5'-most EST	g701392
Method	BLASTX
NCBI GI	g854361
BLAST score	507
E value	3.0e-51
Match length	135
% identity	79
NCBI Description	(X58877) beta-glucanase [Oryza sativa]

Seq. No.	394434
Contig ID	49940_1.R1084
5'-most EST	g3766756

Seq. No.	394435
Contig ID	49951_1.R1084
5'-most EST	uC-osrocyp006g07a1

Seq. No.	394436
Contig ID	49971_1.R1084
5'-most EST	uC-osrocyp007a02b1
Method	BLASTX
NCBI GI	g3080439
BLAST score	269
E value	4.0e-23
Match length	160
% identity	32
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	394437
Contig ID	49997_1.R1084
5'-most EST	g3768109
Method	BLASTX
NCBI GI	g2961378
BLAST score	236
E value	1.0e-29
Match length	91
% identity	36
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	394438
Contig ID	50028_1.R1084
5'-most EST	uC-osrocyp007d07b1
Method	BLASTX
NCBI GI	g3157932
BLAST score	409
E value	6.0e-48
Match length	143
% identity	69
NCBI Description	(AC002131) Similar to hypothetical protein HYP1 gb_Z97338 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	394439
Contig ID	50029_1.R1084
5'-most EST	uC-osrocyp007d08b1
Method	BLASTX
NCBI GI	g3128218
BLAST score	152
E value	1.0e-09
Match length	78
% identity	56
NCBI Description	(AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No.	394440
Contig ID	50034_1.R1084
5'-most EST	uC-osrocyp007d11a1
Method	BLASTX
NCBI GI	g5002232
BLAST score	617
E value	6.0e-64
Match length	180
% identity	65
NCBI Description	(AF145234) NADPH:quinone oxidoreductase [Arabidopsis thaliana]

Seq. No.	394441
Contig ID	50070_1.R1084
5'-most EST	g5056150
Method	BLASTX
NCBI GI	g2827661
BLAST score	130
E value	6.0e-13
Match length	83
% identity	57
NCBI Description	(AL021637) hyuC-like protein [Arabidopsis thaliana]

Seq. No.	394442
Contig ID	50072_1.R1084
5'-most EST	g426677
Method	BLASTX
NCBI GI	g4006932
BLAST score	181
E value	8.0e-13
Match length	123
% identity	37
NCBI Description	(AJ011400) NADH:ubiquinone oxidoreductase b17.2 subunit [Bos taurus]

Seq. No.	394443
Contig ID	50074_1.R1084
5'-most EST	g3761339

Seq. No.	394444
Contig ID	50082_1.R1084
5'-most EST	uC-osrocyp007g06b1
Method	BLASTX
NCBI GI	g4530585
BLAST score	159
E value	4.0e-14
Match length	75
% identity	52
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

Seq. No.	394445
Contig ID	50107_1.R1084
5'-most EST	uC-osrocyp007h11a1

Seq. No.	394446
Contig ID	50117_1.R1084
5'-most EST	uC-osrocyp028a07a1
Method	BLASTX
NCBI GI	g4587589
BLAST score	416
E value	9.0e-41
Match length	98
% identity	76
NCBI Description	(AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394447
Contig ID	50129_1.R1084
5'-most EST	uC-osrocyp008b05a1
Method	BLASTX
NCBI GI	g3242789
BLAST score	400
E value	4.0e-48
Match length	156
% identity	62
NCBI Description	(AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]

Seq. No.	394448
Contig ID	50137_1.R1084
5'-most EST	uC-osrocyp008b12a1
Method	BLASTX
NCBI GI	g2252472
BLAST score	595
E value	1.0e-61
Match length	159
% identity	74
NCBI Description	(Z97558) argininosuccinate lyase [Arabidopsis thaliana]

Seq. No.	394449
Contig ID	50166_1.R1084
5'-most EST	uC-osrocyp008d11a1

Seq. No.	394450
Contig ID	50171_1.R1084
5'-most EST	uC-osrocyp008e03a1
Method	BLASTX
NCBI GI	g4056425
BLAST score	316
E value	7.0e-29
Match length	70
% identity	79
NCBI Description	(AC005322) ESTs gb_H36249, gb_AA59732 and gb_AA651219 come from this gene. [Arabidopsis thaliana]

Seq. No.	394451
Contig ID	50173_1.R1084
5'-most EST	g3766970

Seq. No.	394452
Contig ID	50183_1.R1084
5'-most EST	g3767849

Seq. No.	394453
Contig ID	50227_1.R1084
5'-most EST	uC-osrocyp009a02b1
Method	BLASTX
NCBI GI	g5263310
BLAST score	284
E value	3.0e-25
Match length	82
% identity	67
NCBI Description	(AC007727) EST gb_N95925 comes from this gene. [Arabidopsis thaliana]

Seq. No.	394454
Contig ID	50251_1.R1084
5'-most EST	uC-osroM202017b04b1

Seq. No.	394455
Contig ID	50272_1.R1084
5'-most EST	uC-osrocyp009e09b1

Seq. No.	394456
Contig ID	50292_1.R1084
5'-most EST	uC-osrocyp009e08a1

Seq. No.	394457
Contig ID	50300_1.R1084
5'-most EST	g3763395
Method	BLASTX
NCBI GI	g4454049
BLAST score	171
E value	7.0e-12
Match length	66
% identity	50
NCBI Description	(AL035394) 98b like protein [Arabidopsis thaliana]

Seq. No.	394458

Contig ID	50309_1.R1084
5'-most EST	uC-osroM202001a11a1
Seq. No.	394459
Contig ID	50315_1.R1084
5'-most EST	uC-osrocyp009g04a1
Seq. No.	394460
Contig ID	50320_1.R1084
5'-most EST	uC-osrocyp009g07a1
Seq. No.	394461
Contig ID	50321_1.R1084
5'-most EST	uC-osrocyp033b11a1
Method	BLASTX
NCBI GI	g2541876
BLAST score	112
E value	1.0e-08
Match length	119
% identity	39
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
Seq. No.	394462
Contig ID	50329_1.R1084
5'-most EST	uC-osrocyp009h03a1
Method	BLASTX
NCBI GI	g520570
BLAST score	202
E value	1.0e-15
Match length	70
% identity	59
NCBI Description	(U12315) peroxidase [Cenchrus ciliaris]
Seq. No.	394463
Contig ID	50336_1.R1084
5'-most EST	uC-osrocyp009h07a1
Seq. No.	394464
Contig ID	50338_2.R1084
5'-most EST	uC-osroM202025b08b1
Method	BLASTX
NCBI GI	g3643088
BLAST score	193
E value	2.0e-14
Match length	52
% identity	67
NCBI Description	(AF075581) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]
Seq. No.	394465
Contig ID	50338_4.R1084
5'-most EST	g571698
Seq. No.	394466
Contig ID	50338_5.R1084
5'-most EST	uC-osroM202033e01b1

Seq. No. 394467
Contig ID 50349_1.R1084
5'-most EST uC-osrocyp010a04a1

Seq. No. 394468
Contig ID 50352_1.R1084
5'-most EST uC-osrocyp010a06a1

Seq. No. 394469
Contig ID 50366_1.R1084
5'-most EST g4715538

Seq. No. 394470
Contig ID 50369_1.R1084
5'-most EST uC-osrocyp010b09a1

Seq. No. 394471
Contig ID 50413_1.R1084
5'-most EST uC-osrocyp010e08a1
Method BLASTX
NCBI GI g5430769
BLAST score 505
E value 4.0e-51
Match length 170
% identity 57
NCBI Description (AC007504) Similar to somatic embryogenesis receptor-like kinase [Arabidopsis thaliana]

Seq. No. 394472
Contig ID 50415_1.R1084
5'-most EST uC-osrocyp010e10a1
Method BLASTX
NCBI GI g5852096
BLAST score 196
E value 7.0e-15
Match length 50
% identity 76
NCBI Description (AL117264) zwh19.1 [Oryza sativa]

Seq. No. 394473
Contig ID 50421_1.R1084
5'-most EST g4968889
Method BLASTX
NCBI GI g2398829
BLAST score 246
E value 9.0e-21
Match length 51
% identity 86
NCBI Description (Y11220) mitochondrial uncoupling protein [Solanum tuberosum]

Seq. No. 394474
Contig ID 50426_1.R1084
5'-most EST uC-osrocyp010f10a1
Method BLASTX
NCBI GI g3901268

BLAST score 189
E value 6.0e-14
Match length 125
% identity 36
NCBI Description (AF060173) SV2 related protein [Rattus norvegicus]

Seq. No. 394475
Contig ID 50427_1.R1084
5'-most EST uC-osrocyp010h01a1

Seq. No. 394476
Contig ID 50432_1.R1084
5'-most EST uC-osrocyp010g03a1

Seq. No. 394477
Contig ID 50437_1.R1084
5'-most EST g5039062
Method BLASTX
NCBI GI g2738752
BLAST score 296
E value 3.0e-26
Match length 93
% identity 80
NCBI Description (AF016306) sulfate permease [Zea mays]

Seq. No. 394478
Contig ID 50448_1.R1084
5'-most EST g3762842

Seq. No. 394479
Contig ID 50471_1.R1084
5'-most EST g5038740
Method BLASTX
NCBI GI g1710076
BLAST score 306
E value 1.0e-27
Match length 86
% identity 69
NCBI Description REHYDRIN HOMOLOG (DORMANCY-ASSOCIATED PROTEIN PBS128) >gi_82340_pir__S22499 hypothetical protein - chess bromegrass (fragment) >gi_17932_emb_CAA44884_ (X63202) ORF [Bromus secalinus]

Seq. No. 394480
Contig ID 50494_1.R1084
5'-most EST uC-osroM202033f02a1

Seq. No. 394481
Contig ID 50514_1.R1084
5'-most EST uC-osrocyp011e08b1

Seq. No. 394482
Contig ID 50518_1.R1084
5'-most EST uC-osrocyp017d12a1

Seq. No. 394483
Contig ID 50521_1.R1084

5'-most EST	g4714655
Seq. No.	394484
Contig ID	50523_1.R1084
5'-most EST	g3760123
Seq. No.	394485
Contig ID	50535_1.R1084
5'-most EST	uC-osroM202010f07a1
Seq. No.	394486
Contig ID	50538_1.R1084
5'-most EST	uC-osrocyp011g03b1
Seq. No.	394487
Contig ID	50540_1.R1084
5'-most EST	g3766572
Seq. No.	394488
Contig ID	50545_1.R1084
5'-most EST	uC-osrocyp011g11a1
Method	BLASTX
NCBI GI	g100347
BLAST score	298
E value	1.0e-26
Match length	92
% identity	63
NCBI Description	monosaccharide transport protein MST1 - common tobacco >gi_19885_emb_CAA47324_ (X66856) monosaccharid transporter [Nicotiana tabacum]
Seq. No.	394489
Contig ID	50546_1.R1084
5'-most EST	g5003158
Seq. No.	394490
Contig ID	50561_1.R1084
5'-most EST	uC-osrocyp011h11a1
Seq. No.	394491
Contig ID	50583_1.R1084
5'-most EST	uC-osrocyp016h03b1
Seq. No.	394492
Contig ID	50584_1.R1084
5'-most EST	uC-osroM202037c07a1
Seq. No.	394493
Contig ID	50601_1.R1084
5'-most EST	uC-osrocyp015b12a1
Seq. No.	394494
Contig ID	50660_1.R1084
5'-most EST	g569307
Seq. No.	394495
Contig ID	50696_1.R1084

5'-most EST	uC-osrocyp014b10a1
Seq. No.	394496
Contig ID	50699_1.R1084
5'-most EST	g3767128
Seq. No.	394497
Contig ID	50716_1.R1084
5'-most EST	uC-osrocyp014c10a1
Method	BLASTX
NCBI GI	g4454039
BLAST score	404
E value	2.0e-39
Match length	147
% identity	54
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]
Seq. No.	394498
Contig ID	50739_1.R1084
5'-most EST	uC-osrocyp017d05a1
Seq. No.	394499
Contig ID	50761_1.R1084
5'-most EST	g4715590
Method	BLASTX
NCBI GI	g5281040
BLAST score	235
E value	2.0e-19
Match length	50
% identity	84
NCBI Description	(AL080318) copper amine oxidase-like protein [Arabidopsis thaliana]
Seq. No.	394500
Contig ID	50768_1.R1084
5'-most EST	g2312669
Method	BLASTX
NCBI GI	g3036805
BLAST score	293
E value	1.0e-29
Match length	114
% identity	61
NCBI Description	(AL022373) thaumatin-like protein [Arabidopsis thaliana]
Seq. No.	394501
Contig ID	50781_1.R1084
5'-most EST	uC-osrocyp014h05a1
Seq. No.	394502
Contig ID	50803_1.R1084
5'-most EST	g5003161
Seq. No.	394503
Contig ID	50828_1.R1084
5'-most EST	g3769079

Seq. No.	394504
Contig ID	50839_1.R1084
5'-most EST	g5607372
Method	BLASTX
NCBI GI	g4982479
BLAST score	253
E value	2.0e-21
Match length	95
% identity	54
NCBI Description	(AF069441) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	394505
Contig ID	50843_1.R1084
5'-most EST	uC-osrocyp015d07a1

Seq. No.	394506
Contig ID	50862_1.R1084
5'-most EST	uC-osrocyp015e10a1
Method	BLASTX
NCBI GI	g2498731
BLAST score	492
E value	2.0e-49
Match length	156
% identity	60
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	394507
Contig ID	50876_1.R1084
5'-most EST	g426906

Seq. No.	394508
Contig ID	50880_1.R1084
5'-most EST	uC-osrocyp015f11a1
Method	BLASTX
NCBI GI	g2921823
BLAST score	257
E value	2.0e-22
Match length	97
% identity	59
NCBI Description	(AF046934) shoot-forming PKSF1 [Paulownia kawakamii]

Seq. No.	394509
Contig ID	50896_1.R1084
5'-most EST	g3762965
Method	BLASTX
NCBI GI	g6056204
BLAST score	151
E value	1.0e-09
Match length	64
% identity	47
NCBI Description	(AC009400) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394510

Contig ID	50897_1.R1084
5'-most EST	g702096
Method	BLASTX
NCBI GI	g6056204
BLAST score	309
E value	4.0e-28
Match length	139
% identity	47
NCBI Description	(AC009400) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394511
Contig ID	50902_1.R1084
5'-most EST	uC-osrocyp015h06b1
Method	BLASTX
NCBI GI	g6063552
BLAST score	1178
E value	1.0e-129
Match length	237
% identity	99
NCBI Description	(AP000615) ESTs AU065232(E60855),C23624(S1554), AU078241(E60855) correspond to a region of the predicted gene.; similar to putative adenylate kinase. (AC005896) [Oryza sativa]

Seq. No.	394512
Contig ID	50912_1.R1084
5'-most EST	g3761462

Seq. No.	394513
Contig ID	50925_1.R1084
5'-most EST	uC-osrocyp016a11a1
Method	BLASTX
NCBI GI	g3894191
BLAST score	179
E value	5.0e-13
Match length	76
% identity	49
NCBI Description	(AC005662) unknown protein [Arabidopsis thaliana]

Seq. No.	394514
Contig ID	50935_1.R1084
5'-most EST	g4716664

Seq. No.	394515
Contig ID	50936_1.R1084
5'-most EST	g3768673

Seq. No.	394516
Contig ID	50960_1.R1084
5'-most EST	g3762991

Seq. No.	394517
Contig ID	50978_1.R1084
5'-most EST	uC-osroM202028h02a1

Seq. No.	394518
Contig ID	50985_1.R1084

5'-most EST	g3761901
Method	BLASTX
NCBI GI	g4512685
BLAST score	195
E value	2.0e-30
Match length	153
% identity	46
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394519
Contig ID	50987_1.R1084
5'-most EST	uC-osrocyp028a05a1
Method	BLASTN
NCBI GI	g5042437
BLAST score	103
E value	1.0e-50
Match length	323
% identity	44
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	394520
Contig ID	50988_1.R1084
5'-most EST	uC-osrocyp016f07a1
Method	BLASTX
NCBI GI	g2462839
BLAST score	173
E value	1.0e-12
Match length	48
% identity	73
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	394521
Contig ID	50990_1.R1084
5'-most EST	g2309903

Seq. No.	394522
Contig ID	51005_1.R1084
5'-most EST	uC-osrocyp016g09a1

Seq. No.	394523
Contig ID	51009_1.R1084
5'-most EST	uC-osrocyp016g11a1

Seq. No.	394524
Contig ID	51013_1.R1084
5'-most EST	g2798232
Method	BLASTX
NCBI GI	g4107276
BLAST score	316
E value	6.0e-29
Match length	65
% identity	95
NCBI Description	(X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No. 394525

Contig ID	51025_1.R1084
5'-most EST	g2428465
Method	BLASTX
NCBI GI	g6041851
BLAST score	226
E value	3.0e-18
Match length	75
% identity	63
NCBI Description	(AC009853) unknown protein [Arabidopsis thaliana]

Seq. No.	394526
Contig ID	51030_1.R1084
5'-most EST	uC-osrocyp028h09b1

Seq. No.	394527
Contig ID	51042_1.R1084
5'-most EST	g3759095
Method	BLASTN
NCBI GI	g5441876
BLAST score	354
E value	0.0e+00
Match length	607
% identity	97
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	394528
Contig ID	51043_1.R1084
5'-most EST	uC-osrocyp017b02b1
Method	BLASTN
NCBI GI	g5441876
BLAST score	487
E value	0.0e+00
Match length	571
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	394529
Contig ID	51053_1.R1084
5'-most EST	uC-osrocyp017b09b1
Method	BLASTX
NCBI GI	g3193302
BLAST score	134
E value	8.0e-13
Match length	96
% identity	49
NCBI Description	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 139.32) [Arabidopsis thaliana]

Seq. No.	394530
Contig ID	51063_1.R1084
5'-most EST	g3766868
Method	BLASTX
NCBI GI	g4741198

BLAST score 264
E value 2.0e-25
Match length 105
% identity 69
NCBI Description (AL049746) putative protein [Arabidopsis thaliana]

Seq. No. 394531
Contig ID 51076_1.R1084
5'-most EST uC-osroM202041d02b1
Method BLASTX
NCBI GI g4836950
BLAST score 500
E value 3.0e-50
Match length 227
% identity 47
NCBI Description (AC006085) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 394532
Contig ID 51079_1.R1084
5'-most EST g3763588

Seq. No. 394533
Contig ID 51083_1.R1084
5'-most EST uC-osrocyp017d09a1

Seq. No. 394534
Contig ID 51086_1.R1084
5'-most EST g3761237

Seq. No. 394535
Contig ID 51099_1.R1084
5'-most EST uC-osrocyp017e10a1

Seq. No. 394536
Contig ID 51104_1.R1084
5'-most EST g3760561

Seq. No. 394537
Contig ID 51113_1.R1084
5'-most EST uC-osrocyp017f10a1
Method BLASTX
NCBI GI g4220481
BLAST score 356
E value 2.0e-33
Match length 158
% identity 46
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 394538
Contig ID 51118_1.R1084
5'-most EST uC-osrocyp017g01a1

Seq. No. 394539
Contig ID 51141_1.R1084
5'-most EST uC-osrocyp017h04a1

Seq. No. 394540

Contig ID 51149_1.R1084
5'-most EST uC-osrocyp017h09b1

Seq. No. 394541
Contig ID 51156_1.R1084
5'-most EST uC-osrocyp032h05b1
Method BLASTX
NCBI GI g2651313
BLAST score 214
E value 6.0e-17
Match length 96
% identity 51
NCBI Description (AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 394542
Contig ID 51163_1.R1084
5'-most EST g4714139
Method BLASTX
NCBI GI g3548801
BLAST score 173
E value 4.0e-12
Match length 85
% identity 38
NCBI Description (AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No. 394543
Contig ID 51205_1.R1084
5'-most EST g2798351
Method BLASTX
NCBI GI g3212871
BLAST score 774
E value 2.0e-82
Match length 175
% identity 81
NCBI Description (AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No. 394544
Contig ID 51213_1.R1084
5'-most EST uC-osrocyp024h08b1

Seq. No. 394545
Contig ID 51218_1.R1084
5'-most EST g3762469
Method BLASTX
NCBI GI g1853975
BLAST score 204
E value 5.0e-22
Match length 134
% identity 49
NCBI Description (D14482) putative peroxidase [Oryza sativa]

Seq. No. 394546
Contig ID 51243_1.R1084
5'-most EST g4714660

Seq. No. 394547
Contig ID 51276_1.R1084
5'-most EST uC-osrocyp025f12a1

Seq. No. 394548
Contig ID 51283_1.R1084
5'-most EST g4880576
Method BLASTX
NCBI GI g6041858
BLAST score 308
E value 4.0e-28
Match length 106
% identity 56
NCBI Description (AC009853) unknown protein [Arabidopsis thaliana]

Seq. No. 394549
Contig ID 51283_3.R1084
5'-most EST uC-osrocyp037g09a1
Method BLASTX
NCBI GI g6041858
BLAST score 299
E value 1.0e-26
Match length 120
% identity 57
NCBI Description (AC009853) unknown protein [Arabidopsis thaliana]

Seq. No. 394550
Contig ID 51285_1.R1084
5'-most EST g287024

Seq. No. 394551
Contig ID 51286_1.R1084
5'-most EST uC-osrocyp025g10a1
Method BLASTN
NCBI GI g5670155
BLAST score 134
E value 4.0e-69
Match length 245
% identity 45
NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete sequence

Seq. No. 394552
Contig ID 51299_1.R1084
5'-most EST uC-osrocyp026a01a1

Seq. No. 394553
Contig ID 51308_1.R1084
5'-most EST g5667368

Seq. No. 394554
Contig ID 51311_1.R1084
5'-most EST uC-osroM202019a03a1

Seq. No. 394555
Contig ID 51324_1.R1084

5'-most EST	uC-osrocyp026c08a1
Method	BLASTX
NCBI GI	g535454
BLAST score	246
E value	6.0e-21
Match length	56
% identity	73
NCBI Description	(U13940) cysteine proteinase [Alnus glutinosa]

Seq. No.	394556
Contig ID	51338_1.R1084
5'-most EST	uC-osrocyp026d11a1
Method	BLASTX
NCBI GI	g5231210
BLAST score	597
E value	8.0e-62
Match length	110
% identity	97
NCBI Description	(AF159061) serine/threonine protein phosphatase PP2A-3 catalytic subunit [Oryza sativa subsp. indica]

Seq. No.	394557
Contig ID	51372_1.R1084
5'-most EST	g3769098

Seq. No.	394558
Contig ID	51374_1.R1084
5'-most EST	g5039147

Seq. No.	394559
Contig ID	51376_1.R1084
5'-most EST	uC-osroM202030g03a1

Seq. No.	394560
Contig ID	51386_1.R1084
5'-most EST	uC-osrocyp027a08a1
Method	BLASTX
NCBI GI	g5263337
BLAST score	254
E value	9.0e-22
Match length	68
% identity	69
NCBI Description	(AC007727) Strong similarity to gb_X96932 ascorbate oxidase-related protein PS60 from Nicotiana tabacum and is a member of the PF_00394 Multicopper oxidase family. This gene is cut off. [Arabidopsis thaliana]

Seq. No.	394561
Contig ID	51389_1.R1084
5'-most EST	uC-osroM202006e05b1

Seq. No.	394562
Contig ID	51390_1.R1084
5'-most EST	g3759848

Seq. No.	394563
Contig ID	51400_1.R1084

5'-most EST uC-osrocyp027b08a1
Method BLASTX
NCBI GI g4519936
BLAST score 165
E value 3.0e-11
Match length 111
% identity 37
NCBI Description (AB019186) RPR1 [Oryza sativa]

Seq. No. 394564
Contig ID 51416_1.R1084
5'-most EST uC-osrocyp027c10a1

Seq. No. 394565
Contig ID 51418_1.R1084
5'-most EST g2317566

Seq. No. 394566
Contig ID 51422_1.R1084
5'-most EST uC-osrocyp027d04a1

Seq. No. 394567
Contig ID 51428_1.R1084
5'-most EST uC-osrocyp027d09b1

Seq. No. 394568
Contig ID 51454_1.R1084
5'-most EST uC-osrocyp027f09a1

Seq. No. 394569
Contig ID 51470_1.R1084
5'-most EST g2800550

Seq. No. 394570
Contig ID 51490_1.R1084
5'-most EST g4715515
Method BLASTX
NCBI GI g5679843
BLAST score 513
E value 6.0e-52
Match length 101
% identity 100
NCBI Description (AJ243961) Putitive Ser/Thr protein kinase [Oryza sativa]

Seq. No. 394571
Contig ID 51503_1.R1084
5'-most EST uC-osroM202021f01b1

Seq. No. 394572
Contig ID 51546_1.R1084
5'-most EST g4880910

Seq. No. 394573
Contig ID 51551_1.R1084
5'-most EST g5002745

Seq. No. 394574

Contig ID	51564_1.R1084
5'-most EST	uC-osrocyp028f04a1
Method	BLASTX
NCBI GI	g3142298
BLAST score	229
E value	8.0e-19
Match length	143
% identity	40
NCBI Description	(AC002411) Strong similarity to protein SBT1 gb_X98929 from Lycopersicum esculentum. [Arabidopsis thaliana]

Seq. No.	394575
Contig ID	51566_1.R1084
5'-most EST	g5055944
Method	BLASTN
NCBI GI	g5295936
BLAST score	373
E value	0.0e+00
Match length	627
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	394576
Contig ID	51587_1.R1084
5'-most EST	g3767733

Seq. No.	394577
Contig ID	51588_1.R1084
5'-most EST	uC-osrocyp028h01a1

Seq. No.	394578
Contig ID	51631_1.R1084
5'-most EST	g3106637
Method	BLASTX
NCBI GI	g5453379
BLAST score	311
E value	2.0e-28
Match length	91
% identity	64
NCBI Description	(AF155124) bacterial-induced peroxidase precursor [Gossypium hirsutum]

Seq. No.	394579
Contig ID	51647_1.R1084
5'-most EST	uC-osrocyp029e01a1

Seq. No.	394580
Contig ID	51653_1.R1084
5'-most EST	g2311605
Method	BLASTX
NCBI GI	g3924599
BLAST score	204
E value	2.0e-17
Match length	125
% identity	40
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	394581
Contig ID	51654_1.R1084
5'-most EST	uC-osrocyp029e10a1
Method	BLASTX
NCBI GI	g2290772
BLAST score	186
E value	1.0e-13
Match length	87
% identity	43
NCBI Description	(AF002164) AP-3 delta-adaptin subunit [Drosophila melanogaster]

Seq. No.	394582
Contig ID	51659_1.R1084
5'-most EST	uC-osrocyp029f02a1

Seq. No.	394583
Contig ID	51664_1.R1084
5'-most EST	g2311713

Seq. No.	394584
Contig ID	51728_1.R1084
5'-most EST	uC-osrocyp031a08a1

Seq. No.	394585
Contig ID	51750_1.R1084
5'-most EST	uC-osrocyp031c05b1
Method	BLASTX
NCBI GI	g5803272
BLAST score	343
E value	1.0e-37
Match length	134
% identity	67
NCBI Description	(AP000399) ESTs AU055950(S20175),C73125(E2952), AU055951(S20175) correspond to a region of the predicted gene; similar to acyl-ACP thioesterase (U92878) [Oryza sativa]

Seq. No.	394586
Contig ID	51779_1.R1084
5'-most EST	g5038775

Seq. No.	394587
Contig ID	51794_1.R1084
5'-most EST	g5607364
Method	BLASTX
NCBI GI	g4926868
BLAST score	220
E value	1.0e-17
Match length	50
% identity	88
NCBI Description	(AC007509) putative phosphoserine aminotransferase precursor [Arabidopsis thaliana]

Seq. No.	394588
Contig ID	51858_1.R1084

5'-most EST	uC-osrocyp033a02a1
Seq. No.	394589
Contig ID	51859_1.R1084
5'-most EST	uC-osroM202028a02b1
Seq. No.	394590
Contig ID	51860_1.R1084
5'-most EST	uC-osrocyp033a03a1
Seq. No.	394591
Contig ID	51865_1.R1084
5'-most EST	uC-osrocyp033a07a1
Seq. No.	394592
Contig ID	51877_1.R1084
5'-most EST	uC-osrocyp033b10a1
Seq. No.	394593
Contig ID	51881_1.R1084
5'-most EST	uC-osrocyp033c01a1
Method	BLASTX
NCBI GI	g3249098
BLAST score	151
E value	1.0e-09
Match length	38
% identity	79
NCBI Description	(AC003114) ESTs gb_T04610, gb_N38459, gb_T45174, gb_R30481 and gb_N64971 come from this gene. [Arabidopsis thaliana]
Seq. No.	394594
Contig ID	51889_1.R1084
5'-most EST	g3767292
Seq. No.	394595
Contig ID	51891_1.R1084
5'-most EST	g2799188
Method	BLASTN
NCBI GI	g310732
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	BlueScribe SK Minus cloning vector
Seq. No.	394596
Contig ID	51931_1.R1084
5'-most EST	g4714501
Seq. No.	394597
Contig ID	51932_1.R1084
5'-most EST	g428145
Method	BLASTX
NCBI GI	g1781328
BLAST score	192
E value	1.0e-14
Match length	77

% identity	49
NCBI Description	(Y10465) peroxidase [Spinacia oleracea]

Seq. No.	394598
Contig ID	51993_1.R1084
5'-most EST	g5056071
Method	BLASTX
NCBI GI	g3157951
BLAST score	399
E value	1.0e-38
Match length	99
% identity	85
NCBI Description	(AC002131) Contains similarity to vesicle trafficking protein gb_U91538 from Mus musculus. ESTs gb_F15494 and gb_F14097 come from this gene. [Arabidopsis thaliana]

Seq. No.	394599
Contig ID	51997_1.R1084
5'-most EST	uC-osrocyp034e02a1
Method	BLASTN
NCBI GI	g6063530
BLAST score	408
E value	0.0e+00
Match length	408
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	394600
Contig ID	51999_1.R1084
5'-most EST	g5667353

Seq. No.	394601
Contig ID	52036_1.R1084
5'-most EST	g4715946

Seq. No.	394602
Contig ID	52040_1.R1084
5'-most EST	uC-osroM202003a09a2

Seq. No.	394603
Contig ID	52042_1.R1084
5'-most EST	uC-osrocyp037h08a1

Seq. No.	394604
Contig ID	52062_1.R1084
5'-most EST	uC-osrocyp036b04b1

Seq. No.	394605
Contig ID	52065_1.R1084
5'-most EST	g4715061

Seq. No.	394606
Contig ID	52066_1.R1084
5'-most EST	uC-osrocyp036b07a1

Seq. No.	394607
Contig ID	52090_1.R1084

5'-most EST	g3763581
Method	BLASTX
NCBI GI	g5031981
BLAST score	585
E value	3.0e-60
Match length	177
% identity	66
NCBI Description	26S proteasome-associated pad1 homolog >gi_1923256 (U86782) 26S proteasome-associated pad1 homolog [Homo sapiens]

Seq. No.	394608
Contig ID	52102_1.R1084
5'-most EST	g700033
Method	BLASTX
NCBI GI	g5453379
BLAST score	233
E value	2.0e-19
Match length	75
% identity	57
NCBI Description	(AF155124) bacterial-induced peroxidase precursor [Gossypium hirsutum]

Seq. No.	394609
Contig ID	52103_1.R1084
5'-most EST	g4715270
Method	BLASTX
NCBI GI	g4337195
BLAST score	190
E value	5.0e-14
Match length	76
% identity	51
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	394610
Contig ID	52104_1.R1084
5'-most EST	uC-osroM202021c08b1

Seq. No.	394611
Contig ID	52117_1.R1084
5'-most EST	uC-osrocyp036e12b1

Seq. No.	394612
Contig ID	52121_1.R1084
5'-most EST	uC-osrocyp036e03a1

Seq. No.	394613
Contig ID	52121_2.R1084
5'-most EST	g2442593

Seq. No.	394614
Contig ID	52129_1.R1084
5'-most EST	g3760352
Method	BLASTX
NCBI GI	g2760323
BLAST score	222
E value	1.0e-18
Match length	215

% identity	16
NCBI Description	(AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No.	394615
Contig ID	52163_1.R1084
5'-most EST	uC-osrocyp036g04a1
Method	BLASTN
NCBI GI	g5852170
BLAST score	58
E value	1.0e-23
Match length	137
% identity	37
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No.	394616
Contig ID	52168_1.R1084
5'-most EST	uC-osrocyp036g07a1
Method	BLASTX
NCBI GI	g2245394
BLAST score	180
E value	8.0e-13
Match length	54
% identity	65
NCBI Description	(U89771) ARF1-binding protein [Arabidopsis thaliana]

Seq. No.	394617
Contig ID	52184_1.R1084
5'-most EST	uC-osrocyp036h07a1

Seq. No.	394618
Contig ID	52196_1.R1084
5'-most EST	g6025041

Seq. No.	394619
Contig ID	52198_1.R1084
5'-most EST	uC-osrocyp037a03a1

Seq. No.	394620
Contig ID	52217_1.R1084
5'-most EST	uC-osroM202027h11a1
Method	BLASTX
NCBI GI	g3688528
BLAST score	193
E value	1.0e-14
Match length	49
% identity	67
NCBI Description	(AJ004958) pre-pro-TPE4A protein [Pisum sativum]

Seq. No.	394621
Contig ID	52263_1.R1084
5'-most EST	g4716818

Seq. No.	394622
Contig ID	52267_1.R1084
5'-most EST	uC-osrocyp037d11a1
Method	BLASTX

NCBI GI	g2983997
BLAST score	273
E value	9.0e-24
Match length	92
% identity	57
NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	394623
Contig ID	52269_1.R1084
5'-most EST	uC-osrocyp037d12b1
Method	BLASTX
NCBI GI	g5430771
BLAST score	160
E value	1.0e-10
Match length	65
% identity	45
NCBI Description	(AC007504) Unknown Protein [Arabidopsis thaliana]

Seq. No.	394624
Contig ID	52271_1.R1084
5'-most EST	g5455489
Method	BLASTN
NCBI GI	g5042437
BLAST score	42
E value	5.0e-14
Match length	182
% identity	63
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	394625
Contig ID	52287_1.R1084
5'-most EST	g5005375
Method	BLASTX
NCBI GI	g2909583
BLAST score	353
E value	3.0e-33
Match length	129
% identity	53
NCBI Description	(AL021926) oxcA [Mycobacterium tuberculosis]

Seq. No.	394626
Contig ID	52301_1.R1084
5'-most EST	uC-osroM202013g10b1
Method	BLASTX
NCBI GI	g4220518
BLAST score	360
E value	9.0e-34
Match length	173
% identity	43
NCBI Description	(AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394627
Contig ID	52326_1.R1084
5'-most EST	g4968841
Method	BLASTX
NCBI GI	g3334756
BLAST score	460

E value	6.0e-46
Match length	105
% identity	82
NCBI Description	(Y16672) putative arginine/serine-rich splicing factor [Medicago sativa]

Seq. No.	394628
Contig ID	52340_1.R1084
5'-most EST	uC-osrocyp037h09b1

Seq. No.	394629
Contig ID	52345_1.R1084
5'-most EST	uC-osrocyp037h12a1

Seq. No.	394630
Contig ID	52346_1.R1084
5'-most EST	g2311028
Method	BLASTX
NCBI GI	g1871526
BLAST score	393
E value	7.0e-38
Match length	177
% identity	49
NCBI Description	(X81997) leucine-rich-repeat protein [Helianthus annuus]

Seq. No.	394631
Contig ID	52366_1.R1084
5'-most EST	uC-osroM202001c09b1

Seq. No.	394632
Contig ID	52368_1.R1084
5'-most EST	uC-osroM202001c12b1

Seq. No.	394633
Contig ID	52376_1.R1084
5'-most EST	g2427439
Method	BLASTX
NCBI GI	g1731146
BLAST score	237
E value	1.0e-19
Match length	86
% identity	51
NCBI Description	HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III >gi_3881615_emb_CAA87435.1_ (Z47358) similar to YJU2 protein; cDNA EST yk645d5.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	394634
Contig ID	52378_1.R1084
5'-most EST	uC-osroM202001e03b1
Method	BLASTX
NCBI GI	g4063746
BLAST score	511
E value	4.0e-53
Match length	148
% identity	72
NCBI Description	(AC005851) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	394635
Contig ID	52384_1.R1084
5'-most EST	uC-osroM202001f10b1

Seq. No.	394636
Contig ID	52388_1.R1084
5'-most EST	uC-osroM202001f11b1
Method	BLASTX
NCBI GI	g3413511
BLAST score	215
E value	4.0e-17
Match length	64
% identity	58
NCBI Description	(AJ000265) glucose-6-phosphate isomerase [Spinacia oleracea]

Seq. No.	394637
Contig ID	52413_1.R1084
5'-most EST	g2312093
Method	BLASTX
NCBI GI	g4775270
BLAST score	379
E value	6.0e-49
Match length	114
% identity	86
NCBI Description	(AJ131214) SF2/ASF-like splicing modulator Srp30 [Arabidopsis thaliana]

Seq. No.	394638
Contig ID	52419_1.R1084
5'-most EST	uC-osroM202004c07b1
Method	BLASTX
NCBI GI	g4490704
BLAST score	571
E value	8.0e-59
Match length	140
% identity	76
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	394639
Contig ID	52442_1.R1084
5'-most EST	uC-osroM202004f10a2

Seq. No.	394640
Contig ID	52477_1.R1084
5'-most EST	g431840
Method	BLASTX
NCBI GI	g4097948
BLAST score	366
E value	8.0e-35
Match length	127
% identity	59
NCBI Description	(U72255) beta-1,3-glucanase precursor [Oryza sativa]

Seq. No.	394641
Contig ID	52485_1.R1084

5'-most EST	uC-osroM202005g09b1
Seq. No.	394642
Contig ID	52487_1.R1084
5'-most EST	uC-osroM202005g11b1
Method	BLASTX
NCBI GI	g3738324
BLAST score	206
E value	4.0e-16
Match length	68
% identity	54
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]
Seq. No.	394643
Contig ID	52491_1.R1084
5'-most EST	uC-osroM202006a07b1
Method	BLASTX
NCBI GI	g2244899
BLAST score	146
E value	3.0e-19
Match length	80
% identity	75
NCBI Description	(Z97338) UFD1 like protein [Arabidopsis thaliana]
Seq. No.	394644
Contig ID	52495_1.R1084
5'-most EST	g2428259
Seq. No.	394645
Contig ID	52498_1.R1084
5'-most EST	uC-osroM202005g03b1
Seq. No.	394646
Contig ID	52504_1.R1084
5'-most EST	g3761443
Seq. No.	394647
Contig ID	52517_1.R1084
5'-most EST	uC-osroM202006f11b1
Method	BLASTX
NCBI GI	g6056193
BLAST score	404
E value	3.0e-46
Match length	110
% identity	82
NCBI Description	(AC009400) transcription initiation factor IIB (TFIIB) [Arabidopsis thaliana]
Seq. No.	394648
Contig ID	52519_1.R1084
5'-most EST	uC-osroM202006g06b1
Seq. No.	394649
Contig ID	52527_1.R1084
5'-most EST	g427747
Method	BLASTX
NCBI GI	g4417286

BLAST score 300
E value 4.0e-30
Match length 117
% identity 62
NCBI Description (AC007019) putative shikimate kinase [Arabidopsis thaliana]

Seq. No. 394650
Contig ID 52534_1.R1084
5'-most EST uC-osroM202007a11b1
Method BLASTX
NCBI GI g4160280
BLAST score 234
E value 7.0e-23
Match length 99
% identity 53
NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No. 394651
Contig ID 52557_1.R1084
5'-most EST uC-osroM202007e08b1

Seq. No. 394652
Contig ID 52573_1.R1084
5'-most EST uC-osroM202007h06b1
Method BLASTX
NCBI GI g5915838
BLAST score 264
E value 6.0e-23
Match length 125
% identity 42
NCBI Description CYTOCHROME P450 71D9 (P450 CP3) >gi_3334661_emb_CAA71514_ (Y10490) putative cytochrome P450 [Glycine max]

Seq. No. 394653
Contig ID 52574_1.R1084
5'-most EST g702312
Method BLASTX
NCBI GI g5051780
BLAST score 360
E value 4.0e-34
Match length 123
% identity 54
NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 394654
Contig ID 52581_1.R1084
5'-most EST uC-osroM202005c10b1

Seq. No. 394655
Contig ID 52591_1.R1084
5'-most EST uC-osroM202024b10b1
Method BLASTX
NCBI GI g5453379
BLAST score 530
E value 7.0e-54
Match length 168
% identity 61

NCBI Description	(AF155124) bacterial-induced peroxidase precursor [Gossypium hirsutum]

Seq. No.	394656
Contig ID	52597_1.R1084
5'-most EST	uC-osroM202008d02b1
Method	BLASTX
NCBI GI	g4850342
BLAST score	179
E value	1.0e-12
Match length	77
% identity	43
NCBI Description	(AB003331) RNA binding protein [Anabaena variabilis]

Seq. No.	394657
Contig ID	52610_1.R1084
5'-most EST	uC-osroM202035b01a1
Method	BLASTX
NCBI GI	g3355533
BLAST score	187
E value	9.0e-14
Match length	125
% identity	33
NCBI Description	(AL021331) dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F11.1) LIKE protein) [Homo sapiens]

Seq. No.	394658
Contig ID	52613_1.R1084
5'-most EST	g2310008
Method	BLASTX
NCBI GI	g1854443
BLAST score	335
E value	3.0e-32
Match length	102
% identity	71
NCBI Description	(D83970) CPRD8 protein [Vigna unguiculata]

Seq. No.	394659
Contig ID	52637_1.R1084
5'-most EST	g3768304

Seq. No.	394660
Contig ID	52645_1.R1084
5'-most EST	uC-osroM202024a07b1
Method	BLASTX
NCBI GI	g4240305
BLAST score	364
E value	2.0e-34
Match length	205
% identity	40
NCBI Description	(AB020715) KIAA0908 protein [Homo sapiens]

Seq. No.	394661
Contig ID	52649_1.R1084
5'-most EST	g3760301

Seq. No.	394662

Contig ID 52655_1.R1084
5'-most EST uC-osroM202010f03b1

Seq. No. 394663
Contig ID 52668_1.R1084
5'-most EST g2280668

Seq. No. 394664
Contig ID 52677_1.R1084
5'-most EST g701133

Seq. No. 394665
Contig ID 52689_1.R1084
5'-most EST g3763055

Seq. No. 394666
Contig ID 52693_1.R1084
5'-most EST g2309736

Seq. No. 394667
Contig ID 52711_1.R1084
5'-most EST uC-osroM202011h06b1
Method BLASTX
NCBI GI g349379
BLAST score 155
E value 5.0e-10
Match length 142
% identity 37
NCBI Description (L22847) HAHB-1 [Helianthus annuus]

Seq. No. 394668
Contig ID 52732_1.R1084
5'-most EST g2312405

Seq. No. 394669
Contig ID 52740_2.R1084
5'-most EST g700993
Method BLASTX
NCBI GI g1931641
BLAST score 211
E value 5.0e-30
Match length 127
% identity 57
NCBI Description (U95973) unknown protein [Arabidopsis thaliana]

Seq. No. 394670
Contig ID 52741_1.R1084
5'-most EST uC-osroM202013c06b1
Method BLASTX
NCBI GI g3687235
BLAST score 510
E value 1.0e-51
Match length 128
% identity 81
NCBI Description (AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	394671
Contig ID	52748_1.R1084
5'-most EST	uC-osroM202013d05b1
Seq. No.	394672
Contig ID	52761_1.R1084
5'-most EST	uC-osroM202030e09a1
Method	BLASTX
NCBI GI	g4586107
BLAST score	572
E value	9.0e-59
Match length	240
% identity	15
NCBI Description	(AL049638) putative disease resistance protein [Arabidopsis thaliana]
Seq. No.	394673
Contig ID	52762_1.R1084
5'-most EST	uC-osroM202013f03b1
Seq. No.	394674
Contig ID	52768_1.R1084
5'-most EST	uC-osroM202013g02b1
Method	BLASTX
NCBI GI	g5545339
BLAST score	464
E value	2.0e-46
Match length	131
% identity	66
NCBI Description	(AB030083) lectin-like protein kinase [Populus nigra]
Seq. No.	394675
Contig ID	52779_1.R1084
5'-most EST	uC-osroM202013h10b1
Method	BLASTX
NCBI GI	g3360289
BLAST score	478
E value	4.0e-49
Match length	204
% identity	54
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]
Seq. No.	394676
Contig ID	52805_1.R1084
5'-most EST	uC-osroM202014d04b1
Method	BLASTX
NCBI GI	g6016737
BLAST score	148
E value	4.0e-09
Match length	171
% identity	35
NCBI Description	(AC009325) hypothetical protein [Arabidopsis thaliana] >gi_6091741_gb_AAF03453.1_AC010797_29 (AC010797) hypothetical protein [Arabidopsis thaliana]
Seq. No.	394677

Contig ID	52838_1.R1084
5'-most EST	g286539
Method	BLASTX
NCBI GI	g3355632
BLAST score	264
E value	2.0e-27
Match length	88
% identity	72
NCBI Description	(AJ006957) stearoyl-acyl carrier protein desaturase [Linum usitatissimum]

Seq. No.	394678
Contig ID	52840_1.R1084
5'-most EST	uC-osroM202016a03b1

Seq. No.	394679
Contig ID	52846_1.R1084
5'-most EST	g2312310

Seq. No.	394680
Contig ID	52852_1.R1084
5'-most EST	g426559

Seq. No.	394681
Contig ID	52854_1.R1084
5'-most EST	uC-osroM202016c02b1
Method	BLASTX
NCBI GI	g4235430
BLAST score	412
E value	3.0e-40
Match length	142
% identity	58
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	394682
Contig ID	52863_1.R1084
5'-most EST	uC-osroM202030b04b1

Seq. No.	394683
Contig ID	52867_1.R1084
5'-most EST	uC-osroM202016d10b1
Method	BLASTX
NCBI GI	g3023817
BLAST score	624
E value	7.0e-65
Match length	170
% identity	72
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	394684
Contig ID	52869_1.R1084
5'-most EST	uC-osroM202016d12b1
Method	BLASTX
NCBI GI	g5734619
BLAST score	718

E value	7.0e-76
Match length	175
% identity	73
NCBI Description	(AP000391) Similar to Arabidopsis thaliana BAC F15P23 (AF128392) [Oryza sativa]

Seq. No.	394685
Contig ID	52870_1.R1084
5'-most EST	uC-osroM202016e02b1

Seq. No.	394686
Contig ID	52891_1.R1084
5'-most EST	uC-osroM202016h04b1

Seq. No.	394687
Contig ID	52898_1.R1084
5'-most EST	g4715431
Method	BLASTX
NCBI GI	g4678310
BLAST score	198
E value	2.0e-31
Match length	153
% identity	43
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	394688
Contig ID	52906_1.R1084
5'-most EST	g428440
Method	BLASTX
NCBI GI	g2827708
BLAST score	573
E value	4.0e-59
Match length	118
% identity	85
NCBI Description	(AL021684) myb - related protein [Arabidopsis thaliana]

Seq. No.	394689
Contig ID	52908_1.R1084
5'-most EST	uC-osroM202017c04b1

Seq. No.	394690
Contig ID	52910_1.R1084
5'-most EST	g3769060
Method	BLASTX
NCBI GI	g5091622
BLAST score	221
E value	3.0e-26
Match length	163
% identity	39
NCBI Description	(AC007454) F23M19.10 [Arabidopsis thaliana]

Seq. No.	394691
Contig ID	52913_1.R1084
5'-most EST	uC-osroM202017c09b1
Method	BLASTX
NCBI GI	g4097690
BLAST score	595

E value	1.0e-61
Match length	136
% identity	82
NCBI Description	(U66592) prohibitin 2 [Arabidopsis thaliana] >gi_4099801 (U89791) prohibitin-like protein [Arabidopsis thaliana] >gi_4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]

Seq. No.	394692
Contig ID	52914_1.R1084
5'-most EST	uC-osroM202017c10b1
Method	BLASTX
NCBI GI	g2058504
BLAST score	154
E value	5.0e-10
Match length	116
% identity	30
NCBI Description	(U76554) zinc-finger protein-1 [Brassica rapa]

Seq. No.	394693
Contig ID	52923_1.R1084
5'-most EST	g2427771
Method	BLASTX
NCBI GI	g5823554
BLAST score	156
E value	4.0e-10
Match length	49
% identity	57
NCBI Description	(AF180920) cyclin ania-6a [Homo sapiens]

Seq. No.	394694
Contig ID	52927_1.R1084
5'-most EST	uC-osroM202017e02b1

Seq. No.	394695
Contig ID	52928_1.R1084
5'-most EST	uC-osroM202017e03b1
Method	BLASTX
NCBI GI	g4512685
BLAST score	122
E value	1.0e-08
Match length	46
% identity	53
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394696
Contig ID	52931_1.R1084
5'-most EST	g571894

Seq. No.	394697
Contig ID	52932_1.R1084
5'-most EST	uC-osroM202020e02b1
Method	BLASTX
NCBI GI	g2392895
BLAST score	694
E value	4.0e-73

Match length	223
% identity	11
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana] >gi_5042156_emb_CAB44675.1_ (AL078620) brassinosteroid insensitive 1 gene (BRI1) [Arabidopsis thaliana]

Seq. No.	394698
Contig ID	52939_1.R1084
5'-most EST	uC-osroM202017f08b1

Seq. No.	394699
Contig ID	52940_1.R1084
5'-most EST	uC-osroM202033a10b1
Method	BLASTX
NCBI GI	g3176690
BLAST score	208
E value	7.0e-23
Match length	162
% identity	48
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	394700
Contig ID	52955_1.R1084
5'-most EST	uC-osroM202032a09b1
Method	BLASTX
NCBI GI	g3608364
BLAST score	222
E value	7.0e-26
Match length	101
% identity	59
NCBI Description	(AF019749) high-affinity nitrate transporter ACH2 [Arabidopsis thaliana]

Seq. No.	394701
Contig ID	52983_1.R1084
5'-most EST	uC-osroM202018f06b1
Method	BLASTX
NCBI GI	g6063549
BLAST score	322
E value	1.0e-29
Match length	149
% identity	48
NCBI Description	(AP000615) EST AU070346(S12172) corresponds to a region of the predicted gene.; similar to AMP-binding protein. (X94625) [Oryza sativa]

Seq. No.	394702
Contig ID	52992_1.R1084
5'-most EST	g5607569

Seq. No.	394703
Contig ID	52996_1.R1084
5'-most EST	g3107289
Method	BLASTX

NCBI GI	g5725442
BLAST score	627
E value	3.0e-65
Match length	244
% identity	54
NCBI Description	(AL109787) putative protein [Arabidopsis thaliana]

Seq. No.	394704
Contig ID	53003_1.R1084
5'-most EST	g4714234

Seq. No.	394705
Contig ID	53008_1.R1084
5'-most EST	uC-osroM202019b06b1
Method	BLASTX
NCBI GI	g3790581
BLAST score	220
E value	2.0e-17
Match length	52
% identity	65
NCBI Description	(AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana]

Seq. No.	394706
Contig ID	53025_1.R1084
5'-most EST	uC-osroM202019e04a1
Method	BLASTX
NCBI GI	g2688822
BLAST score	394
E value	5.0e-38
Match length	104
% identity	72
NCBI Description	(U93272) pyrophosphate-dependent phosphofructo-1-kinase [Prunus armeniaca]

Seq. No.	394707
Contig ID	53027_1.R1084
5'-most EST	uC-osroM202019e06b1
Method	BLASTX
NCBI GI	g4914402
BLAST score	509
E value	2.0e-51
Match length	173
% identity	58
NCBI Description	(AL050352) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394708
Contig ID	53035_1.R1084
5'-most EST	g2428255

Seq. No.	394709
Contig ID	53041_1.R1084
5'-most EST	uC-osroM202019g09b1
Method	BLASTX
NCBI GI	g4938491
BLAST score	159
E value	1.0e-10

Match length	137
% identity	31
NCBI Description	(AL078464) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394710
Contig ID	53069_1.R1084
5'-most EST	g4715785
Method	BLASTX
NCBI GI	g5541709
BLAST score	794
E value	2.0e-84
Match length	269
% identity	62
NCBI Description	(AL096860) putative protein [Arabidopsis thaliana]

Seq. No.	394711
Contig ID	53070_1.R1084
5'-most EST	g570158

Seq. No.	394712
Contig ID	53072_1.R1084
5'-most EST	uC-osroM202020c09b1

Seq. No.	394713
Contig ID	53075_1.R1084
5'-most EST	g2312338
Method	BLASTX
NCBI GI	g2262159
BLAST score	190
E value	3.0e-14
Match length	51
% identity	71
NCBI Description	(AC002329) predicted protein similar to S.pombe protein C5H10.03 [Arabidopsis thaliana]

Seq. No.	394714
Contig ID	53087_1.R1084
5'-most EST	uC-osroM202020e09b1
Method	BLASTX
NCBI GI	g1361979
BLAST score	152
E value	3.0e-16
Match length	97
% identity	47
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) - watermelon >gi_1350550_dbj_BAA12843_ (D85624) serine acetyltransferase [Citrullus lanatus] >gi_1841312_dbj_BAA08479_ (D49535) serine acetyltransferase. [Citrullus lanatus] >gi_2337772_dbj_BAA21827_ (AB006530) serine acetyltransferase [Citrullus lanatus]

Seq. No.	394715
Contig ID	53101_1.R1084
5'-most EST	uC-osroM202020h03b1
Method	BLASTX
NCBI GI	g5732035
BLAST score	205

E value	4.0e-23
Match length	138
% identity	50
NCBI Description	(AF160760) contains similarity to Pfam family PF0040 - WD domain, G-beta repeat; score=10.8, E=3.2, N-2 [Arabidopsis thaliana]

Seq. No.	394716
Contig ID	53111_1.R1084
5'-most EST	uC-osroM202021a04b1

Seq. No.	394717
Contig ID	53116_1.R1084
5'-most EST	g1632053

Seq. No.	394718
Contig ID	53127_1.R1084
5'-most EST	uC-osroM202021c10b1
Method	BLASTX
NCBI GI	g1752734
BLAST score	383
E value	1.0e-36
Match length	193
% identity	42
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No.	394719
Contig ID	53131_1.R1084
5'-most EST	uC-osroM202021d06b1

Seq. No.	394720
Contig ID	53137_1.R1084
5'-most EST	g702352
Method	BLASTX
NCBI GI	g3746431
BLAST score	597
E value	5.0e-88
Match length	210
% identity	79
NCBI Description	(AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1 [Zea mays]

Seq. No.	394721
Contig ID	53146_1.R1084
5'-most EST	uC-osroM202021g01b1

Seq. No.	394722
Contig ID	53153_1.R1084
5'-most EST	uC-osroM202021g11b1

Seq. No.	394723
Contig ID	53156_1.R1084
5'-most EST	uC-osroM202022h11b1

Seq. No.	394724
Contig ID	53161_1.R1084
5'-most EST	uC-osroM202021h08b1

09604605.050698

Method	BLASTX
NCBI GI	g100001
BLAST score	381
E value	1.0e-36
Match length	115
% identity	58
NCBI Description	endopeptidase C1 - kidney bean >gi_1345573_emb_CAA40073_ (X56753) endopeptidase (EP-C1) [Phaseolus vulgaris]

Seq. No.	394725
Contig ID	53164_1.R1084
5'-most EST	uC-osroM202022a06b1
Method	BLASTX
NCBI GI	g2493321
BLAST score	321
E value	1.0e-29
Match length	72
% identity	78
NCBI Description	L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO) >gi_2129952_pir__S66353 L-ascorbate oxidase (EC 1.10.3.3) precursor - common tobacco >gi_599594_dbj_BAA07734_ (D43624) ascorbate oxidase precursor [Nicotiana tabacum]

Seq. No.	394726
Contig ID	53165_1.R1084
5'-most EST	uC-osroM202021e11b1
Method	BLASTX
NCBI GI	g3894168
BLAST score	136
E value	8.0e-14
Match length	102
% identity	43
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	394727
Contig ID	53176_1.R1084
5'-most EST	g427860

Seq. No.	394728
Contig ID	53179_1.R1084
5'-most EST	g5455564
Method	BLASTX
NCBI GI	g4406759
BLAST score	274
E value	6.0e-24
Match length	111
% identity	47
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394729
Contig ID	53191_1.R1084
5'-most EST	g569952

Seq. No.	394730
Contig ID	53195_1.R1084
5'-most EST	uC-osroM202022f08b1

Method	BLASTX
NCBI GI	g115829
BLAST score	436
E value	3.0e-54
Match length	136
% identity	58
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_99364_pir__JW0040 light-harvesting chlorophyll 28.5K apoprotein (photosystem II) - green alga (Dunaliella tertiolecta) >gi_167985 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella tertiolecta]

Seq. No.	394731
Contig ID	53203_1.R1084
5'-most EST	g568483

Seq. No.	394732
Contig ID	53211_1.R1084
5'-most EST	uC-osroM202030e09b1

Seq. No.	394733
Contig ID	53221_1.R1084
5'-most EST	g2311079

Seq. No.	394734
Contig ID	53223_1.R1084
5'-most EST	g4878818
Method	BLASTN
NCBI GI	g5734616
BLAST score	517
E value	0.0e+00
Match length	909
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No.	394735
Contig ID	53224_1.R1084
5'-most EST	g2442736
Method	BLASTX
NCBI GI	g2832643
BLAST score	180
E value	4.0e-13
Match length	66
% identity	55
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394736
Contig ID	53234_1.R1084
5'-most EST	uC-osroM202023d12b1

Seq. No.	394737
Contig ID	53241_1.R1084
5'-most EST	g5607348
Method	BLASTX
NCBI GI	g5668762
BLAST score	259
E value	3.0e-22

Match length	77
% identity	60
NCBI Description	(AC005916) EST gb_N65787 comes from this gene. [Arabidopsis thaliana]

Seq. No.	394738
Contig ID	53251_1.R1084
5'-most EST	uC-osroM202023f07b1
Method	BLASTN
NCBI GI	g2114206
BLAST score	283
E value	1.0e-158
Match length	356
% identity	96
NCBI Description	Oryza sativa DNA for glutaredoxin, complete cds

Seq. No.	394739
Contig ID	53274_1.R1084
5'-most EST	uC-osroM202024h07b1
Method	BLASTX
NCBI GI	g2979553
BLAST score	140
E value	8.0e-10
Match length	61
% identity	55
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394740
Contig ID	53279_1.R1084
5'-most EST	uC-osroM202024c06b1
Method	BLASTX
NCBI GI	g2497953
BLAST score	422
E value	2.0e-41
Match length	102
% identity	79
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No.	394741
Contig ID	53281_1.R1084
5'-most EST	uC-osroM202024d02b1

Seq. No.	394742
Contig ID	53287_1.R1084
5'-most EST	uC-osroM202024e04b1
Method	BLASTX
NCBI GI	g4467153
BLAST score	467
E value	2.0e-46
Match length	135
% identity	65
NCBI Description	(AL035540) putative thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	394743
Contig ID	53292_1.R1084
5'-most EST	g428139
Method	BLASTX
NCBI GI	g2459447
BLAST score	627
E value	3.0e-65
Match length	166
% identity	69
NCBI Description	(AC002332) putative Mlo protein [Arabidopsis thaliana]

Seq. No.	394744
Contig ID	53303_1.R1084
5'-most EST	uC-osroM202024h01b1

Seq. No.	394745
Contig ID	53305_1.R1084
5'-most EST	uC-osroM202024h03b1
Method	BLASTX
NCBI GI	g3882018
BLAST score	215
E value	4.0e-17
Match length	88
% identity	50
NCBI Description	(Y18377) cytokinin oxidase [Zea mays]

Seq. No.	394746
Contig ID	53307_1.R1084
5'-most EST	uC-osroM202024h06b1
Method	BLASTX
NCBI GI	g3786011
BLAST score	189
E value	5.0e-24
Match length	158
% identity	37
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	394747
Contig ID	53312_1.R1084
5'-most EST	uC-osroM202036g12b1

Seq. No.	394748
Contig ID	53319_1.R1084
5'-most EST	uC-osroM202025d03b1

Seq. No.	394749
Contig ID	53325_1.R1084
5'-most EST	g2428878
Method	BLASTX
NCBI GI	g4454018
BLAST score	268
E value	3.0e-23
Match length	115
% identity	42
NCBI Description	(AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No.	394750
Contig ID	53339_1.R1084
5'-most EST	g3768583
Method	BLASTX
NCBI GI	g419789
BLAST score	207
E value	2.0e-25
Match length	96
% identity	64
NCBI Description	hypothetical protein - potato

Seq. No.	394751
Contig ID	53349_1.R1084
5'-most EST	uC-osroM202025g05b1
Method	BLASTX
NCBI GI	g3924603
BLAST score	207
E value	3.0e-16
Match length	60
% identity	60
NCBI Description	(AF069442) putative WD-repeat protein [Arabidopsis thaliana]

Seq. No.	394752
Contig ID	53377_1.R1084
5'-most EST	uC-osroM202026f11b1

Seq. No.	394753
Contig ID	53382_1.R1084
5'-most EST	uC-osroM202026g06b1
Method	BLASTX
NCBI GI	g1655536
BLAST score	192
E value	3.0e-20
Match length	109
% identity	51
NCBI Description	(Y09095) chloride channel [Arabidopsis thaliana] >gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel protein [Arabidopsis thaliana]

Seq. No.	394754
Contig ID	53395_1.R1084
5'-most EST	g2310379
Method	BLASTN
NCBI GI	g5734616
BLAST score	389
E value	0.0e+00
Match length	393
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No.	394755
Contig ID	53397_1.R1084
5'-most EST	uC-osroM202028a06b1

Seq. No.	394756

Contig ID	53400_1.R1084
5'-most EST	g699910
Seq. No.	394757
Contig ID	53415_1.R1084
5'-most EST	uC-osroM202037b07b1
Seq. No.	394758
Contig ID	53416_2.R1084
5'-most EST	uC-osroM202028d10b1
Seq. No.	394759
Contig ID	53424_1.R1084
5'-most EST	g700365
Method	BLASTX
NCBI GI	g4455244
BLAST score	193
E value	1.0e-20
Match length	166
% identity	42
NCBI Description	(AL035523) MtN3-like protein [Arabidopsis thaliana]
Seq. No.	394760
Contig ID	53426_1.R1084
5'-most EST	uC-osroM202032b07b1
Seq. No.	394761
Contig ID	53456_1.R1084
5'-most EST	uC-osroM202029b05b1
Method	BLASTX
NCBI GI	g4874306
BLAST score	319
E value	2.0e-29
Match length	113
% identity	60
NCBI Description	(AC006053) hypothetical protein [Arabidopsis thaliana]
Seq. No.	394762
Contig ID	53460_1.R1084
5'-most EST	g2312608
Seq. No.	394763
Contig ID	53461_1.R1084
5'-most EST	uC-osroM202030c02b1
Seq. No.	394764
Contig ID	53472_1.R1084
5'-most EST	uC-osroM202029f01b1
Seq. No.	394765
Contig ID	53473_1.R1084
5'-most EST	uC-osroM202029e03b1
Seq. No.	394766
Contig ID	53476_1.R1084
5'-most EST	g2312965

Seq. No.	394767
Contig ID	53477_1.R1084
5'-most EST	uC-osroM202029f09b1

Seq. No.	394768
Contig ID	53493_1.R1084
5'-most EST	uC-osroM202029g07b1

Seq. No.	394769
Contig ID	53496_1.R1084
5'-most EST	uC-osroM202029g11b1
Method	BLASTX
NCBI GI	g3128208
BLAST score	271
E value	2.0e-23
Match length	109
% identity	44
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394770
Contig ID	53499_1.R1084
5'-most EST	uC-osroM202029h04b1
Method	BLASTX
NCBI GI	g5081612
BLAST score	418
E value	9.0e-48
Match length	207
% identity	46
NCBI Description	(AF136152) PUR alpha-1 [Arabidopsis thaliana]

Seq. No.	394771
Contig ID	53524_1.R1084
5'-most EST	g2442806

Seq. No.	394772
Contig ID	53528_1.R1084
5'-most EST	uC-osroM202024a05b1
Method	BLASTX
NCBI GI	g6094242
BLAST score	371
E value	2.0e-35
Match length	93
% identity	71
NCBI Description	PUTATIVE SELENIUM-BINDING PROTEIN >gi_2244759_emb_CAB10182.1_ (Z97335) selenium-binding protein like [Arabidopsis thaliana]

Seq. No.	394773
Contig ID	53540_1.R1084
5'-most EST	uC-osroM202030e03b1

Seq. No.	394774
Contig ID	53546_1.R1084
5'-most EST	g2311406
Method	BLASTX
NCBI GI	g5729707
BLAST score	146

E value	4.0e-09
Match length	73
% identity	44
NCBI Description	(AC007927) unknown protein [Arabidopsis thaliana]

Seq. No.	394775
Contig ID	53553_1.R1084
5'-most EST	uC-osroM202030g05b1

Seq. No.	394776
Contig ID	53562_1.R1084
5'-most EST	uC-osroM202030h08b1
Method	BLASTX
NCBI GI	g4467359
BLAST score	389
E value	7.0e-38
Match length	209
% identity	45
NCBI Description	(AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

Seq. No.	394777
Contig ID	53564_1.R1084
5'-most EST	uC-osroM202030h11b1
Method	BLASTX
NCBI GI	g5262218
BLAST score	155
E value	3.0e-10
Match length	101
% identity	36
NCBI Description	(AL080254) calcium-binding protein-like [Arabidopsis thaliana]

Seq. No.	394778
Contig ID	53566_1.R1084
5'-most EST	uC-osroM202031a01b1
Method	BLASTX
NCBI GI	g2632254
BLAST score	338
E value	8.0e-50
Match length	113
% identity	93
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	394779
Contig ID	53567_1.R1084
5'-most EST	g428821
Method	BLASTX
NCBI GI	g4760700
BLAST score	216
E value	2.0e-22
Match length	106
% identity	63
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]

Seq. No.	394780
Contig ID	53570_1.R1084

5'-most EST	uC-osroM202031a09b1
Method	BLASTX
NCBI GI	g4455190
BLAST score	462
E value	8.0e-46
Match length	162
% identity	63
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	394781
Contig ID	53573_1.R1084
5'-most EST	uC-osroM202031b11b1
Method	BLASTX
NCBI GI	g4006829
BLAST score	430
E value	3.0e-42
Match length	126
% identity	67
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	394782
Contig ID	53585_1.R1084
5'-most EST	uC-osroM202031d06b1
Method	BLASTX
NCBI GI	g5051789
BLAST score	207
E value	3.0e-16
Match length	133
% identity	45
NCBI Description	(AL078637) putative protein [Arabidopsis thaliana]

Seq. No.	394783
Contig ID	53587_1.R1084
5'-most EST	uC-osroM202031d09b1
Method	BLASTX
NCBI GI	g4432860
BLAST score	594
E value	1.0e-63
Match length	297
% identity	23
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	394784
Contig ID	53595_1.R1084
5'-most EST	g568589
Method	BLASTX
NCBI GI	g2160177
BLAST score	383
E value	1.0e-36
Match length	144
% identity	53
NCBI Description	(AC000132) EST gb_R64758 comes from this gene. [Arabidopsis thaliana]

Seq. No.	394785
Contig ID	53598_1.R1084

5'-most EST	g2431379
Seq. No.	394786
Contig ID	53608_1.R1084
5'-most EST	uC-osroM202031g07b1
Seq. No.	394787
Contig ID	53621_1.R1084
5'-most EST	uC-osroM202031h11b1
Seq. No.	394788
Contig ID	53627_1.R1084
5'-most EST	uC-osroM202032b05b1
Seq. No.	394789
Contig ID	53633_1.R1084
5'-most EST	uC-osroM202032c02b1
Seq. No.	394790
Contig ID	53636_1.R1084
5'-most EST	uC-osroM202032c05b1
Method	BLASTX
NCBI GI	g4263827
BLAST score	390
E value	1.0e-37
Match length	181
% identity	49
NCBI Description	(AC006067) putative receptor protein kinase [Arabidopsis thaliana]
Seq. No.	394791
Contig ID	53642_1.R1084
5'-most EST	uC-osroM202032d02b1
Seq. No.	394792
Contig ID	53645_1.R1084
5'-most EST	uC-osroM202032d07b1
Method	BLASTX
NCBI GI	g3204108
BLAST score	768
E value	1.0e-81
Match length	180
% identity	79
NCBI Description	(AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]
Seq. No.	394793
Contig ID	53651_1.R1084
5'-most EST	uC-osroM202032e01b1
Seq. No.	394794
Contig ID	53655_1.R1084
5'-most EST	g5900712
Method	BLASTX
NCBI GI	g3688185
BLAST score	151
E value	9.0e-10

Match length	47
% identity	60
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	394795
Contig ID	53658_1.R1084
5'-most EST	uC-osroM202032e12b1

Seq. No.	394796
Contig ID	53659_1.R1084
5'-most EST	uC-osroM202032f01b1
Method	BLASTX
NCBI GI	g4006865
BLAST score	319
E value	2.0e-29
Match length	120
% identity	55
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	394797
Contig ID	53681_1.R1084
5'-most EST	g572065

Seq. No.	394798
Contig ID	53682_1.R1084
5'-most EST	uC-osroM202032h08b1

Seq. No.	394799
Contig ID	53684_1.R1084
5'-most EST	g700643
Method	BLASTX
NCBI GI	g4432845
BLAST score	182
E value	6.0e-13
Match length	112
% identity	36
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	394800
Contig ID	53685_1.R1084
5'-most EST	g569563
Method	BLASTX
NCBI GI	g5002344
BLAST score	207
E value	1.0e-20
Match length	110
% identity	48
NCBI Description	(AF149278) peroxidase 3 precursor [Phaseolus vulgaris]

Seq. No.	394801
Contig ID	53699_1.R1084
5'-most EST	g4715617

Seq. No.	394802
Contig ID	53703_1.R1084
5'-most EST	uC-osroM202033d02b1
Method	BLASTX

NCBI GI	g6056371
BLAST score	481
E value	2.0e-48
Match length	126
% identity	72
NCBI Description	(AC009894) nucleolar protein [Arabidopsis thaliana]

Seq. No.	394803
Contig ID	53705_1.R1084
5'-most EST	uC-osroM202033c03b1
Method	BLASTX
NCBI GI	g5281051
BLAST score	284
E value	2.0e-25
Match length	97
% identity	29
NCBI Description	(AL080318) stress-induced protein sti1-like protein [Arabidopsis thaliana]

Seq. No.	394804
Contig ID	53707_1.R1084
5'-most EST	uC-osroM202033d08b1

Seq. No.	394805
Contig ID	53716_1.R1084
5'-most EST	g2427884

Seq. No.	394806
Contig ID	53729_1.R1084
5'-most EST	g1631995
Method	BLASTX
NCBI GI	g2104691
BLAST score	160
E value	2.0e-10
Match length	62
% identity	44
NCBI Description	(U92794) alpha glucosidase II, beta subunit [Mus musculus]

Seq. No.	394807
Contig ID	53733_1.R1084
5'-most EST	uC-osroM202034a02b1
Method	BLASTX
NCBI GI	g6056189
BLAST score	282
E value	3.0e-31
Match length	133
% identity	56
NCBI Description	(AC009400) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394808
Contig ID	53745_1.R1084
5'-most EST	g2800657

Seq. No.	394809
Contig ID	53754_1.R1084
5'-most EST	uC-osroM202034c10b1

Seq. No.	394810
Contig ID	53756_1.R1084
5'-most EST	uC-osroM202034c12b1

Seq. No.	394811
Contig ID	53758_1.R1084
5'-most EST	uC-osroM202033d03b1
Method	BLASTX
NCBI GI	g4314378
BLAST score	156
E value	9.0e-13
Match length	89
% identity	45
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana] >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative lipase [Arabidopsis thaliana]

Seq. No.	394812
Contig ID	53763_1.R1084
5'-most EST	g426068

Seq. No.	394813
Contig ID	53764_1.R1084
5'-most EST	uC-osroM202034d11b1

Seq. No.	394814
Contig ID	53784_1.R1084
5'-most EST	uC-osroM202034h10b1
Method	BLASTX
NCBI GI	g4588012
BLAST score	541
E value	2.0e-55
Match length	146
% identity	72
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	394815
Contig ID	53788_1.R1084
5'-most EST	g2310906

Seq. No.	394816
Contig ID	53812_1.R1084
5'-most EST	uC-osroM202035d07b1
Method	BLASTX
NCBI GI	g3935137
BLAST score	419
E value	5.0e-41
Match length	125
% identity	65
NCBI Description	(AC005106) T25N20.1 [Arabidopsis thaliana]

Seq. No.	394817
Contig ID	53817_1.R1084
5'-most EST	uC-osroM202036b03b1

Seq. No.	394818

Contig ID	53818_1.R1084
5'-most EST	g569995
Method	BLASTX
NCBI GI	g4587518
BLAST score	239
E value	7.0e-20
Match length	90
% identity	59
NCBI Description	(AC007060) Strong similarity to F19I3.8 gi_3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb_AC004238 and is a member of PF_01370 the NAD dependent epimerase/dehydratase family. EST gb_AA59

Seq. No.	394819
Contig ID	53821_1.R1084
5'-most EST	uC-osroM202035f08b1

Seq. No.	394820
Contig ID	53827_1.R1084
5'-most EST	uC-osroM202035g03b1
Method	BLASTX
NCBI GI	g4220527
BLAST score	175
E value	1.0e-12
Match length	53
% identity	62
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	394821
Contig ID	53833_1.R1084
5'-most EST	g3061036
Method	BLASTX
NCBI GI	g4103635
BLAST score	201
E value	2.0e-15
Match length	78
% identity	47
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	394822
Contig ID	53834_1.R1084
5'-most EST	uC-osroM202035h01b1
Method	BLASTX
NCBI GI	g4835771
BLAST score	163
E value	5.0e-11
Match length	70
% identity	51
NCBI Description	(AC007202) Similar to gi_3844599 F31D5.2 gene product from Caenorhabditis elegans cosmid gb_U28941 and contains PF_00097 Zinc (Ring) finger C3HC4 domain. ESTs gb_F19963 and gb_T42582 come from this gene. [Arabidops

Seq. No.	394823
Contig ID	53839_1.R1084
5'-most EST	g568790
Method	BLASTX

NCBI GI	g6056375
BLAST score	345
E value	2.0e-32
Match length	114
% identity	59
NCBI Description	(AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	394824
Contig ID	53842_1.R1084
5'-most EST	uC-osroM202035h12b1
Method	BLASTX
NCBI GI	g3128176
BLAST score	267
E value	7.0e-25
Match length	109
% identity	54
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	394825
Contig ID	53853_1.R1084
5'-most EST	uC-osroM202017a09a1
Method	BLASTX
NCBI GI	g1839188
BLAST score	638
E value	1.0e-66
Match length	149
% identity	81
NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No.	394826
Contig ID	53856_1.R1084
5'-most EST	uC-osroM202022f02b1
Method	BLASTX
NCBI GI	g1203832
BLAST score	307
E value	2.0e-28
Match length	90
% identity	79
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No.	394827
Contig ID	53866_1.R1084
5'-most EST	uC-osroM202036d02b1
Method	BLASTX
NCBI GI	g4835227
BLAST score	258
E value	4.0e-22
Match length	95
% identity	54
NCBI Description	(AL049862) glycosyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	394828
Contig ID	53869_1.R1084

5'-most EST	g5004418
Seq. No.	394829
Contig ID	53872_1.R1084
5'-most EST	g2310639
Method	BLASTX
NCBI GI	g4503521
BLAST score	346
E value	1.0e-39
Match length	184
% identity	48
NCBI Description	murine mammary tumor integration site 6 (oncogene homolog) >gi_2498490_sp_Q64252_INT6_MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens]
Seq. No.	394830
Contig ID	53885_1.R1084
5'-most EST	uC-osroM202036f09b1
Method	BLASTX
NCBI GI	g3399767
BLAST score	253
E value	1.0e-21
Match length	92
% identity	46
NCBI Description	(U76298) uclacyanin I [Arabidopsis thaliana] >gi_3831466 (AC005700) uclacyanin I [Arabidopsis thaliana]
Seq. No.	394831
Contig ID	53890_1.R1084
5'-most EST	uC-osroM202036g04b1
Method	BLASTX
NCBI GI	g4874269
BLAST score	254
E value	2.0e-21
Match length	169
% identity	37
NCBI Description	(AC007354) T16B5.7 [Arabidopsis thaliana]
Seq. No.	394832
Contig ID	53893_1.R1084
5'-most EST	uC-osroM202036g09b1
Method	BLASTX
NCBI GI	g4468979
BLAST score	423
E value	1.0e-41
Match length	111
% identity	65
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]
Seq. No.	394833
Contig ID	53921_1.R1084
5'-most EST	uC-osroM202037d01b1
Method	BLASTX

NCBI GI g4894963
BLAST score 479
E value 4.0e-48
Match length 131
% identity 84
NCBI Description (AF140553) DNA-binding protein WRKY3 [Avena sativa]

Seq. No. 394834
Contig ID 53955_1.R1084
5'-most EST uC-osroM202037h10b1

Seq. No. 394835
Contig ID 53960_1.R1084
5'-most EST uC-osroM202038a06b1

Seq. No. 394836
Contig ID 53961_1.R1084
5'-most EST g5004792
Method BLASTX
NCBI GI g2708737
BLAST score 421
E value 5.0e-41
Match length 175
% identity 24
NCBI Description (AC003952) putative nuclear protein [Arabidopsis thaliana]

Seq. No. 394837
Contig ID 53969_1.R1084
5'-most EST uC-osroM202038b12b1

Seq. No. 394838
Contig ID 53981_1.R1084
5'-most EST g286674
Method BLASTX
NCBI GI g2792155
BLAST score 296
E value 6.0e-33
Match length 153
% identity 50
NCBI Description (AJ223291) chalcone reductase [Sesbania rostrata]

Seq. No. 394839
Contig ID 53982_1.R1084
5'-most EST uC-osroM202038c12b1

Seq. No. 394840
Contig ID 53984_1.R1084
5'-most EST uC-osroM202038d02b1
Method BLASTX
NCBI GI g6006895
BLAST score 458
E value 8.0e-56
Match length 223
% identity 48
NCBI Description (AC008153) hypothetical protein [Arabidopsis thaliana]

Seq. No. 394841

Contig ID	53991_1.R1084
5'-most EST	uC-osroM202038e08b1
Method	BLASTX
NCBI GI	g2494034
BLAST score	478
E value	8.0e-52
Match length	158
% identity	62
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	394842
Contig ID	53992_1.R1084
5'-most EST	g699876
Method	BLASTX
NCBI GI	g4467122
BLAST score	308
E value	4.0e-28
Match length	110
% identity	52
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	394843
Contig ID	54017_1.R1084
5'-most EST	uC-osroM202038h09b1

Seq. No.	394844
Contig ID	54019_1.R1084
5'-most EST	uC-osroM202039a01b1
Method	BLASTX
NCBI GI	g1502430
BLAST score	309
E value	1.0e-37
Match length	126
% identity	69
NCBI Description	(U62331) phosphate transporter [Arabidopsis thaliana] >gi_2564661 (AF022872) phosphate transporter [Arabidopsis thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770) phosphate transporter, AtPT2 [Arabidopsis thaliana]

Seq. No.	394845
Contig ID	54021_1.R1084
5'-most EST	uC-osroM202040b04b1

Seq. No.	394846
Contig ID	54034_1.R1084
5'-most EST	g4881017
Method	BLASTX
NCBI GI	g4056568
BLAST score	452
E value	5.0e-45
Match length	132
% identity	27
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	394847
Contig ID	54050_1.R1084
5'-most EST	uC-osroM202039e12b1
Method	BLASTX
NCBI GI	g1588281
BLAST score	199
E value	2.0e-15
Match length	165
% identity	23
NCBI Description	RING3 protein [Homo sapiens]

Seq. No.	394848
Contig ID	54053_1.R1084
5'-most EST	uC-osroM202039f07b1

Seq. No.	394849
Contig ID	54054_1.R1084
5'-most EST	uC-osroM202039f10b1
Method	BLASTX
NCBI GI	g3395425
BLAST score	300
E value	1.0e-33
Match length	156
% identity	41
NCBI Description	(AC004683) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	394850
Contig ID	54069_1.R1084
5'-most EST	uC-osroM202039h10b1
Method	BLASTX
NCBI GI	g3044218
BLAST score	488
E value	6.0e-50
Match length	133
% identity	76
NCBI Description	(AF057144) signal peptidase [Arabidopsis thaliana]

Seq. No.	394851
Contig ID	54071_1.R1084
5'-most EST	uC-osroM202040a05b1
Method	BLASTX
NCBI GI	g2911042
BLAST score	561
E value	2.0e-57
Match length	180
% identity	62
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	394852
Contig ID	54088_1.R1084
5'-most EST	g5003163

Seq. No.	394853
Contig ID	54090_1.R1084

5'-most EST	uC-osroM202040d07b1
Method	BLASTX
NCBI GI	g1706956
BLAST score	1050
E value	1.0e-115
Match length	249
% identity	78
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	394854
Contig ID	54091_1.R1084
5'-most EST	g2442365

Seq. No.	394855
Contig ID	54092_1.R1084
5'-most EST	g286738

Seq. No.	394856
Contig ID	54100_1.R1084
5'-most EST	uC-osroM202037b01b1
Method	BLASTX
NCBI GI	g3643611
BLAST score	162
E value	3.0e-24
Match length	77
% identity	71
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	394857
Contig ID	54101_1.R1084
5'-most EST	g5003802
Method	BLASTX
NCBI GI	g2708750
BLAST score	471
E value	7.0e-47
Match length	136
% identity	61
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	394858
Contig ID	54107_1.R1084
5'-most EST	uC-osroM202040g02b1
Method	BLASTX
NCBI GI	g1651890
BLAST score	338
E value	2.0e-31
Match length	171
% identity	15
NCBI Description	(D90900) mitochondrial outer membrane 72K protein [Synechocystis sp.]

Seq. No.	394859
Contig ID	54162_1.R1084
5'-most EST	uC-osroM202041f12b1
Method	BLASTX
NCBI GI	g4371296

BLAST score	430
E value	4.0e-42
Match length	184
% identity	56
NCBI Description	(AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	394860
Contig ID	54165_1.R1084
5'-most EST	g571734
Method	BLASTX
NCBI GI	g3928088
BLAST score	209
E value	2.0e-16
Match length	69
% identity	58
NCBI Description	(AC005770) putative peroxidase [Arabidopsis thaliana]

Seq. No.	394861
Contig ID	54183_1.R1084
5'-most EST	uC-osroM202001a03a1
Method	BLASTX
NCBI GI	g4972071
BLAST score	200
E value	3.0e-15
Match length	122
% identity	39
NCBI Description	(AL078467) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394862
Contig ID	54187_1.R1084
5'-most EST	uC-osroM202001a07a1

Seq. No.	394863
Contig ID	54197_1.R1084
5'-most EST	uC-osroM202001b04b1

Seq. No.	394864
Contig ID	54225_1.R1084
5'-most EST	uC-osroM202001c12a1

Seq. No.	394865
Contig ID	54240_1.R1084
5'-most EST	g702085
Method	BLASTX
NCBI GI	g4454019
BLAST score	205
E value	6.0e-16
Match length	122
% identity	37
NCBI Description	(AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No.	394866
Contig ID	54250_1.R1084
5'-most EST	g5056077

Seq. No.	394867

Contig ID	54259_1.R1084
5'-most EST	g2798217
Seq. No.	394868
Contig ID	54260_1.R1084
5'-most EST	g2799209
Method	BLASTN
NCBI GI	g58067
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP
Seq. No.	394869
Contig ID	54271_1.R1084
5'-most EST	g3769150
Method	BLASTX
NCBI GI	g3413511
BLAST score	173
E value	3.0e-13
Match length	46
% identity	67
NCBI Description	(AJ000265) glucose-6-phosphate isomerase [Spinacia oleracea]
Seq. No.	394870
Contig ID	54276_1.R1084
5'-most EST	g4715633
Seq. No.	394871
Contig ID	54284_1.R1084
5'-most EST	uC-osroM202001g09b1
Seq. No.	394872
Contig ID	54291_1.R1084
5'-most EST	uC-osroM202001h02a1
Method	BLASTX
NCBI GI	g6006867
BLAST score	445
E value	4.0e-44
Match length	122
% identity	72
NCBI Description	(AC009540) unknown protein [Arabidopsis thaliana]
Seq. No.	394873
Contig ID	54293_1.R1084
5'-most EST	uC-osroM202001h05a1
Seq. No.	394874
Contig ID	54300_1.R1084
5'-most EST	g4715276
Method	BLASTX
NCBI GI	g584892
BLAST score	792
E value	1.0e-84

09604.0004.PCUS00

Match length	244
% identity	82
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) >gi_629805_pir__S43516 serine carboxypeptidase I - rice >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I [Oryza sativa]

Seq. No.	394875
Contig ID	54318_1.R1084
5'-most EST	g4715959
Method	BLASTX
NCBI GI	g4680207
BLAST score	142
E value	1.0e-08
Match length	102
% identity	33
NCBI Description	(AF114171) disease resistance protein RPM1 homolog [Sorghum bicolor]

Seq. No.	394876
Contig ID	54352_1.R1084
5'-most EST	g4714959

Seq. No.	394877
Contig ID	54367_1.R1084
5'-most EST	g3760159
Method	BLASTX
NCBI GI	g2065531
BLAST score	203
E value	2.0e-15
Match length	136
% identity	25
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	394878
Contig ID	54371_1.R1084
5'-most EST	uC-osroM202007f06a1

Seq. No.	394879
Contig ID	54372_1.R1084
5'-most EST	uC-osroM202003g11a2

Seq. No.	394880
Contig ID	54397_1.R1084
5'-most EST	g3760335

Seq. No.	394881
Contig ID	54397_2.R1084
5'-most EST	g427522

Seq. No.	394882
Contig ID	54401_1.R1084
5'-most EST	uC-osroM202004b07a2

Seq. No.	394883
Contig ID	54413_1.R1084
5'-most EST	g5039150

Seq. No.	394884
Contig ID	54434_1.R1084
5'-most EST	g3766608
Method	BLASTX
NCBI GI	g4406756
BLAST score	209
E value	3.0e-16
Match length	48
% identity	90
NCBI Description	(AC006836) putative integral membrane protein A3 [Arabidopsis thaliana]

Seq. No.	394885
Contig ID	54443_1.R1084
5'-most EST	uC-osroM202004e01a2

Seq. No.	394886
Contig ID	54450_1.R1084
5'-most EST	g4716569
Method	BLASTX
NCBI GI	g4006865
BLAST score	431
E value	3.0e-42
Match length	160
% identity	53
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	394887
Contig ID	54453_1.R1084
5'-most EST	g5039156

Seq. No.	394888
Contig ID	54462_1.R1084
5'-most EST	uC-osroM202004f04a2

Seq. No.	394889
Contig ID	54479_1.R1084
5'-most EST	uC-osroM202004g09a2

Seq. No.	394890
Contig ID	54497_1.R1084
5'-most EST	uC-osroM202005a01b1
Method	BLASTX
NCBI GI	g4099921
BLAST score	150
E value	2.0e-10
Match length	42
% identity	86
NCBI Description	(U91982) EREBP-3 homolog [Stylosanthes hamata]

Seq. No.	394891
Contig ID	54499_1.R1084
5'-most EST	uC-osroM202005a03b1
Method	BLASTX
NCBI GI	g2245131
BLAST score	151

E value	1.0e-09
Match length	80
% identity	51
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394892
Contig ID	54510_1.R1084
5'-most EST	g3107272
Method	BLASTX
NCBI GI	g4914319
BLAST score	270
E value	2.0e-23
Match length	177
% identity	50
NCBI Description	(AC005489) F14N23.5 [Arabidopsis thaliana]

Seq. No.	394893
Contig ID	54538_1.R1084
5'-most EST	g426069
Method	BLASTX
NCBI GI	g3522945
BLAST score	181
E value	4.0e-13
Match length	86
% identity	43
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	394894
Contig ID	54546_1.R1084
5'-most EST	uC-osroM202006b01b1

Seq. No.	394895
Contig ID	54550_1.R1084
5'-most EST	g2275851

Seq. No.	394896
Contig ID	54554_1.R1084
5'-most EST	uC-osroM202006c11b1

Seq. No.	394897
Contig ID	54565_1.R1084
5'-most EST	uC-osroM202006f07b1
Method	BLASTX
NCBI GI	g4314370
BLAST score	146
E value	1.0e-10
Match length	68
% identity	54
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	394898
Contig ID	54575_1.R1084
5'-most EST	g3762841

Seq. No.	394899
Contig ID	54594_1.R1084
5'-most EST	uC-osroM202007b01a1

Seq. No.	394900
Contig ID	54617_1.R1084
5'-most EST	g3758918
Method	BLASTX
NCBI GI	g4469022
BLAST score	183
E value	2.0e-13
Match length	84
% identity	46
NCBI Description	(AL035602) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	394901
Contig ID	54642_1.R1084
5'-most EST	uC-osroM202007e09a1
Method	BLASTX
NCBI GI	g4097942
BLAST score	435
E value	6.0e-43
Match length	83
% identity	98
NCBI Description	(U72252) beta-1,3-glucanase precursor [Oryza sativa]

Seq. No.	394902
Contig ID	54653_1.R1084
5'-most EST	g4968640
Method	BLASTX
NCBI GI	g3687237
BLAST score	253
E value	1.0e-21
Match length	71
% identity	63
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	394903
Contig ID	54678_1.R1084
5'-most EST	uC-osroM202007h02a1
Method	BLASTN
NCBI GI	g5852077
BLAST score	115
E value	7.0e-58
Match length	226
% identity	93
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone: b6015

Seq. No.	394904
Contig ID	54683_1.R1084
5'-most EST	g4715725
Method	BLASTX
NCBI GI	g4927259
BLAST score	251
E value	4.0e-21
Match length	149
% identity	42

NCBI Description	(AF142322) putative transcription repressor maize TRM protein [Zea mays]

Seq. No.	394905
Contig ID	54717_1.R1084
5'-most EST	g2443062

Seq. No.	394906
Contig ID	54721_1.R1084
5'-most EST	g3767749

Seq. No.	394907
Contig ID	54721_2.R1084
5'-most EST	g4714709

Seq. No.	394908
Contig ID	54722_1.R1084
5'-most EST	uC-osroM202008c04a1

Seq. No.	394909
Contig ID	54758_1.R1084
5'-most EST	uC-osroM202008f06a1

Seq. No.	394910
Contig ID	54770_1.R1084
5'-most EST	g3759797

Seq. No.	394911
Contig ID	54779_1.R1084
5'-most EST	g2428345

Seq. No.	394912
Contig ID	54791_1.R1084
5'-most EST	g2801113

Seq. No.	394913
Contig ID	54795_1.R1084
5'-most EST	uC-osroM202010a10b1
Method	BLASTX
NCBI GI	g1085952
BLAST score	231
E value	3.0e-30
Match length	165
% identity	45
NCBI Description	hypothetical protein S1 - Phalaris coerulescens

Seq. No.	394914
Contig ID	54821_1.R1084
5'-most EST	uC-osroM202010c12a1
Method	BLASTX
NCBI GI	g4586246
BLAST score	469
E value	6.0e-47
Match length	111
% identity	75
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	394915
Contig ID	54822_1.R1084
5'-most EST	uC-osroM202010c11b1
Method	BLASTX
NCBI GI	g4689474
BLAST score	343
E value	6.0e-32
Match length	84
% identity	70
NCBI Description	(AC007213) unknown protein [Arabidopsis thaliana]

Seq. No.	394916
Contig ID	54842_1.R1084
5'-most EST	g3760302
Method	BLASTX
NCBI GI	g1565223
BLAST score	394
E value	1.0e-37
Match length	132
% identity	64
NCBI Description	(Y08301) MCM2-related protein [Arabidopsis thaliana]

Seq. No.	394917
Contig ID	54852_1.R1084
5'-most EST	g2312987
Method	BLASTN
NCBI GI	g6006355
BLAST score	361
E value	0.0e+00
Match length	665
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	394918
Contig ID	54853_1.R1084
5'-most EST	g428470

Seq. No.	394919
Contig ID	54859_1.R1084
5'-most EST	g4715410
Method	BLASTX
NCBI GI	g4038030
BLAST score	164
E value	7.0e-23
Match length	100
% identity	59
NCBI Description	(AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No.	394920
Contig ID	54863_1.R1084
5'-most EST	uC-osroM202010f08b1
Method	BLASTX
NCBI GI	g3548810
BLAST score	314
E value	9.0e-29
Match length	161

% identity	46
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	394921
Contig ID	54889_1.R1084
5'-most EST	g2800417
Method	BLASTX
NCBI GI	g2853039
BLAST score	209
E value	1.0e-20
Match length	76
% identity	68
NCBI Description	(X94289) phosphoinositide-specific phospholipase C [Solanum tuberosum]

Seq. No.	394922
Contig ID	54902_1.R1084
5'-most EST	uC-osroM202011a10a1

Seq. No.	394923
Contig ID	54903_1.R1084
5'-most EST	uC-osroM202011a10b1

Seq. No.	394924
Contig ID	54915_1.R1084
5'-most EST	g3761286
Method	BLASTX
NCBI GI	g2160185
BLAST score	257
E value	2.0e-28
Match length	90
% identity	69
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	394925
Contig ID	54917_1.R1084
5'-most EST	g4716309

Seq. No.	394926
Contig ID	54919_1.R1084
5'-most EST	uC-osroM202011b09a1

Seq. No.	394927
Contig ID	54949_1.R1084
5'-most EST	g3763056

Seq. No.	394928
Contig ID	54955_1.R1084
5'-most EST	g3768603

Seq. No.	394929
Contig ID	54958_1.R1084
5'-most EST	uC-osroM202034c03b1

Seq. No.	394930

Contig ID	54960_1.R1084
5'-most EST	uC-osroM202039e10a1
Method	BLASTX
NCBI GI	g3548808
BLAST score	344
E value	3.0e-32
Match length	130
% identity	49
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	394931
Contig ID	54962_1.R1084
5'-most EST	uC-osroM202011e06a1
Method	BLASTX
NCBI GI	g4220535
BLAST score	309
E value	4.0e-28
Match length	67
% identity	85
NCBI Description	(AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No.	394932
Contig ID	54973_1.R1084
5'-most EST	g3761218

Seq. No.	394933
Contig ID	55005_1.R1084
5'-most EST	g3760441

Seq. No.	394934
Contig ID	55012_1.R1084
5'-most EST	g4879398

Seq. No.	394935
Contig ID	55035_1.R1084
5'-most EST	uC-osroM202012f06a1
Method	BLASTX
NCBI GI	g3892054
BLAST score	209
E value	2.0e-16
Match length	152
% identity	35
NCBI Description	(AC002330) putative glycosyltransferase [Arabidopsis thaliana]

Seq. No.	394936
Contig ID	55073_1.R1084
5'-most EST	g569113

Seq. No.	394937
Contig ID	55083_1.R1084
5'-most EST	g3760490

Seq. No.	394938
Contig ID	55131_1.R1084
5'-most EST	uC-osroM202016a09a1

Seq. No. 394939
Contig ID 55132_1.R1084
5'-most EST uC-osroM202017b10b1

Seq. No. 394940
Contig ID 55166_1.R1084
5'-most EST uC-osroM202030b04a1

Seq. No. 394941
Contig ID 55169_1.R1084
5'-most EST uC-osroM202016d05b1

Seq. No. 394942
Contig ID 55172_1.R1084
5'-most EST uC-osroM202016d07b1
Method BLASTX
NCBI GI g1710401
BLAST score 497
E value 3.0e-50
Match length 119
% identity 80
NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No. 394943
Contig ID 55172_2.R1084
5'-most EST uC-osroM202018b11b1
Method BLASTX
NCBI GI g1710401
BLAST score 518
E value 1.0e-52
Match length 122
% identity 82
NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No. 394944
Contig ID 55195_1.R1084
5'-most EST g2312196

Seq. No. 394945
Contig ID 55196_1.R1084
5'-most EST uC-osroM202016f05a1
Method BLASTX
NCBI GI g3746060
BLAST score 156
E value 4.0e-10
Match length 36
% identity 83
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 394946

Contig ID	55220_1.R1084
5'-most EST	uC-osroM202016h07a1

Seq. No.	394947
Contig ID	55248_1.R1084
5'-most EST	g2800511

Seq. No.	394948
Contig ID	55249_1.R1084
5'-most EST	g2310301
Method	BLASTX
NCBI GI	g5902363
BLAST score	472
E value	2.0e-50
Match length	164
% identity	59
NCBI Description	(AC009322) Putative coatomer protein complex, subunit beta 2 (beta prime) [Arabidopsis thaliana]

Seq. No.	394949
Contig ID	55273_1.R1084
5'-most EST	g2799193
Method	BLASTN
NCBI GI	g310775
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	PhageScript SK cloning vector

Seq. No.	394950
Contig ID	55277_1.R1084
5'-most EST	uC-osroM202017c10a1

Seq. No.	394951
Contig ID	55290_1.R1084
5'-most EST	g3760693

Seq. No.	394952
Contig ID	55293_1.R1084
5'-most EST	uC-osroM202017e02a1

Seq. No.	394953
Contig ID	55295_1.R1084
5'-most EST	g3767810

Seq. No.	394954
Contig ID	55305_1.R1084
5'-most EST	uC-osroM202017e11a1

Seq. No.	394955
Contig ID	55306_1.R1084
5'-most EST	g2317507

Seq. No.	394956
Contig ID	55307_1.R1084
5'-most EST	g4714115

Seq. No.	394957
Contig ID	55337_1.R1084
5'-most EST	g3761179
Seq. No.	394958
Contig ID	55338_1.R1084
5'-most EST	uC-osroM202017h03b1
Seq. No.	394959
Contig ID	55343_1.R1084
5'-most EST	g3768076
Seq. No.	394960
Contig ID	55355_1.R1084
5'-most EST	uC-osroM202018b03b1
Seq. No.	394961
Contig ID	55365_1.R1084
5'-most EST	uC-osroM202018c10b1
Seq. No.	394962
Contig ID	55371_1.R1084
5'-most EST	uC-osroM202018d11b1
Seq. No.	394963
Contig ID	55378_1.R1084
5'-most EST	uC-osroM202018f01b1
Seq. No.	394964
Contig ID	55383_1.R1084
5'-most EST	uC-osroM202018f11b1
Method	BLASTX
NCBI GI	g4874273
BLAST score	607
E value	1.0e-100
Match length	320
% identity	56
NCBI Description	(AC007354) Similar to gi_3128199 F4I1.5 putative proteinase from Arabidopsis thaliana BAC gb_AC004521
Seq. No.	394965
Contig ID	55400_1.R1084
5'-most EST	uC-osroM202019a07a1
Method	BLASTX
NCBI GI	g3702332
BLAST score	235
E value	4.0e-19
Match length	166
% identity	33
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	394966
Contig ID	55407_1.R1084
5'-most EST	uC-osroM202019a11a1
Seq. No.	394967

Contig ID	55444_1.R1084
5'-most EST	uC-osroM202019d09a1
Method	BLASTX
NCBI GI	g6006874
BLAST score	395
E value	5.0e-38
Match length	142
% identity	54
NCBI Description	(AC008153) putative UDP-glucuronosyltransferase, 5' partial [Arabidopsis thaliana]

Seq. No.	394968
Contig ID	55458_1.R1084
5'-most EST	uC-osroM202019e10a1

Seq. No.	394969
Contig ID	55476_1.R1084
5'-most EST	g5771056
Method	BLASTX
NCBI GI	g836954
BLAST score	400
E value	8.0e-39
Match length	139
% identity	57
NCBI Description	(U20948) receptor protein kinase [Ipomoea trifida]

Seq. No.	394970
Contig ID	55477_1.R1084
5'-most EST	uC-osroM202019g01a1

Seq. No.	394971
Contig ID	55480_1.R1084
5'-most EST	g3759160

Seq. No.	394972
Contig ID	55483_1.R1084
5'-most EST	uC-osroM202019g05a1

Seq. No.	394973
Contig ID	55494_1.R1084
5'-most EST	g4715582
Method	BLASTX
NCBI GI	g5042155
BLAST score	131
E value	1.0e-12
Match length	97
% identity	40
NCBI Description	(AL078620) putative protein [Arabidopsis thaliana]

Seq. No.	394974
Contig ID	55504_1.R1084
5'-most EST	g3761596

Seq. No.	394975
Contig ID	55507_1.R1084
5'-most EST	uC-osroM202020a01b1
Method	BLASTN

NCBI GI	g5042437
BLAST score	46
E value	1.0e-16
Match length	90
% identity	44
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	394976
Contig ID	55514_1.R1084
5'-most EST	g5039054

Seq. No.	394977
Contig ID	55546_1.R1084
5'-most EST	uC-osroM202020c10b1
Method	BLASTX
NCBI GI	g1402920
BLAST score	202
E value	2.0e-24
Match length	99
% identity	53
NCBI Description	(X98321) peroxidase [Arabidopsis thaliana]

Seq. No.	394978
Contig ID	55570_1.R1084
5'-most EST	g3761277

Seq. No.	394979
Contig ID	55573_1.R1084
5'-most EST	uC-osroM202020e10a1

Seq. No.	394980
Contig ID	55611_1.R1084
5'-most EST	uC-osroM202020h07b1

Seq. No.	394981
Contig ID	55634_1.R1084
5'-most EST	g3767932
Method	BLASTX
NCBI GI	g4587992
BLAST score	273
E value	1.0e-23
Match length	86
% identity	56
NCBI Description	(AF085279) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	394982
Contig ID	55662_1.R1084
5'-most EST	g2801204

Seq. No.	394983
Contig ID	55672_1.R1084
5'-most EST	g2442776
Method	BLASTX
NCBI GI	g4097547
BLAST score	460
E value	9.0e-46
Match length	168

% identity	41
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	394984
Contig ID	55677_1.R1084
5'-most EST	g571553
Method	BLASTX
NCBI GI	g4510430
BLAST score	461
E value	6.0e-46
Match length	112
% identity	78
NCBI Description	(AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	394985
Contig ID	55683_1.R1084
5'-most EST	g3763047

Seq. No.	394986
Contig ID	55698_1.R1084
5'-most EST	uC-osroM202023b12b1
Method	BLASTX
NCBI GI	g135640
BLAST score	541
E value	3.0e-55
Match length	121
% identity	56
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA SEQUENCE-BINDING PROTEIN) (TBP) >gi_72901_pir__TWPO2D transcription initiation factor IID - potato >gi_21581_emb_CAA44360_ (X62494) TATA-binding protein [Solanum tuberosum]

Seq. No.	394987
Contig ID	55713_1.R1084
5'-most EST	uC-osroM202023f10b1
Method	BLASTX
NCBI GI	g3142292
BLAST score	525
E value	2.0e-53
Match length	135
% identity	77
NCBI Description	(AC002411) Contains similarity to tetratricopeptide repeat protein gb_U46571 from home sapiens. EST gb_Z47802 and gb_Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No.	394988
Contig ID	55714_1.R1084
5'-most EST	uC-osroM202023g01b1

Seq. No.	394989
Contig ID	55758_1.R1084
5'-most EST	uC-osroM202024c12b1

Seq. No.	394990
Contig ID	55796_1.R1084

5'-most EST	uC-osroM202024f11a1
Method	BLASTX
NCBI GI	g5852089
BLAST score	202
E value	1.0e-15
Match length	43
% identity	79
NCBI Description	(AL117264) zwh12.1 [Oryza sativa]

Seq. No.	394991
Contig ID	55798_1.R1084
5'-most EST	g4969183

Seq. No.	394992
Contig ID	55802_1.R1084
5'-most EST	g3761549

Seq. No.	394993
Contig ID	55803_1.R1084
5'-most EST	g2311996
Method	BLASTX
NCBI GI	g2281631
BLAST score	167
E value	7.0e-12
Match length	82
% identity	51
NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No.	394994
Contig ID	55814_1.R1084
5'-most EST	g3762996
Method	BLASTX
NCBI GI	g3341511
BLAST score	361
E value	3.0e-34
Match length	104
% identity	75
NCBI Description	(AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]

Seq. No.	394995
Contig ID	55842_1.R1084
5'-most EST	uC-osroM202025a11a1

Seq. No.	394996
Contig ID	55847_1.R1084
5'-most EST	g4716267

Seq. No.	394997
Contig ID	55850_1.R1084
5'-most EST	g3768957
Method	BLASTX
NCBI GI	g1236961
BLAST score	346
E value	2.0e-32
Match length	89
% identity	66

NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]
Seq. No.	394998
Contig ID	55866_1.R1084
5'-most EST	uC-osroM202025c06a1
Seq. No.	394999
Contig ID	55901_1.R1084
5'-most EST	uC-osroM202025f03b1
Method	BLASTX
NCBI GI	g1504012
BLAST score	214
E value	6.0e-17
Match length	124
% identity	36
NCBI Description	(D86969) similar to Human zinc-finger protein, BR140(P1:JC2069) [Homo sapiens] >gi_5805248_gb_AAD51905.1_ (AF127774) unknown [Homo sapiens]
Seq. No.	395000
Contig ID	55926_1.R1084
5'-most EST	uC-osroM202025g12b1
Method	BLASTX
NCBI GI	g425685
BLAST score	224
E value	3.0e-18
Match length	146
% identity	36
NCBI Description	thimet oligopeptidase=soluble angiotensin II-binding protein homolog {EC 3.4.24.15} [rats, testis, Peptide, 687 aa]
Seq. No.	395001
Contig ID	55965_1.R1084
5'-most EST	g3767840
Method	BLASTN
NCBI GI	g5091597
BLAST score	37
E value	3.0e-11
Match length	120
% identity	46
NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.	395002
Contig ID	55974_1.R1084
5'-most EST	g1632398
Seq. No.	395003
Contig ID	55998_1.R1084
5'-most EST	uC-osroM202027d07a1
Seq. No.	395004
Contig ID	56021_1.R1084
5'-most EST	uC-osroM202027f11a1
Seq. No.	395005
Contig ID	56027_1.R1084

5'-most EST	uC-osroM202027h03a1
Method	BLASTX
NCBI GI	g3252868
BLAST score	319
E value	3.0e-29
Match length	98
% identity	61
NCBI Description	(AF033536) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	395006
Contig ID	56057_1.R1084
5'-most EST	uC-osroM202028a10b1
Method	BLASTX
NCBI GI	g1076580
BLAST score	291
E value	1.0e-29
Match length	85
% identity	69
NCBI Description	alcohol dehydrogenase homolog ADH3b - tomato >gi_913446_bbs_160508 (S75487) alcohol dehydrogenase ADH {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 390 aa] [Lycopersicon esculentum]

Seq. No.	395007
Contig ID	56058_1.R1084
5'-most EST	g4879905

Seq. No.	395008
Contig ID	56059_1.R1084
5'-most EST	g568140
Method	BLASTX
NCBI GI	g4835761
BLAST score	210
E value	3.0e-16
Match length	78
% identity	45
NCBI Description	(AC007202) T8K14.10 [Arabidopsis thaliana]

Seq. No.	395009
Contig ID	56070_1.R1084
5'-most EST	uC-osroM202029g05a1
Method	BLASTX
NCBI GI	g2182267
BLAST score	277
E value	2.0e-24
Match length	69
% identity	80
NCBI Description	(L37359) lipoxygenase [Hordeum vulgare]

Seq. No.	395010
Contig ID	56074_1.R1084
5'-most EST	uC-osroM202028b11b1

Seq. No.	395011
Contig ID	56112_1.R1084
5'-most EST	g3766993

Seq. No.	395012
Contig ID	56128_1.R1084
5'-most EST	g5005437
Method	BLASTX
NCBI GI	g4836452
BLAST score	153
E value	7.0e-10
Match length	89
% identity	39
NCBI Description	(AF121878) cytidine deaminase [Arabidopsis thaliana]

Seq. No.	395013
Contig ID	56137_1.R1084
5'-most EST	uC-osroM202028f08a1

Seq. No.	395014
Contig ID	56139_1.R1084
5'-most EST	uC-osroM202028f09b1
Method	BLASTX
NCBI GI	g4887741
BLAST score	276
E value	1.0e-24
Match length	71
% identity	76
NCBI Description	(AC006533) molybdopterin biosynthesis cnx2 protein [Arabidopsis thaliana]

Seq. No.	395015
Contig ID	56159_1.R1084
5'-most EST	uC-osroM202028h07a1

Seq. No.	395016
Contig ID	56163_1.R1084
5'-most EST	g5038996
Method	BLASTX
NCBI GI	g2618699
BLAST score	145
E value	3.0e-09
Match length	88
% identity	32
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	395017
Contig ID	56181_1.R1084
5'-most EST	uC-osroM202029a10a1
Method	BLASTX
NCBI GI	g2493123
BLAST score	200
E value	2.0e-15
Match length	41
% identity	93
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_1051258 (U36939) vacuolar ATPase catalytic subunit [Hordeum vulgare]

Seq. No.	395018
Contig ID	56198_1.R1084

5'-most EST	uC-osroM202029b06a1
Method	BLASTX
NCBI GI	g4874306
BLAST score	236
E value	1.0e-19
Match length	78
% identity	59
NCBI Description	(AC006053) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395019
Contig ID	56221_1.R1084
5'-most EST	uC-osroM202029c10b1
Method	BLASTX
NCBI GI	g4262167
BLAST score	274
E value	7.0e-24
Match length	148
% identity	31
NCBI Description	(AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No.	395020
Contig ID	56242_1.R1084
5'-most EST	uC-osroM202029f01a1

Seq. No.	395021
Contig ID	56253_1.R1084
5'-most EST	uC-osroM202029f09a1

Seq. No.	395022
Contig ID	56295_1.R1084
5'-most EST	g3762361
Method	BLASTX
NCBI GI	g3913181
BLAST score	384
E value	6.0e-37
Match length	97
% identity	80
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_2388662 (AF010290) cinnamyl alcohol dehydrogenase [Lolium perenne]

Seq. No.	395023
Contig ID	56327_1.R1084
5'-most EST	uC-osroM202030c01a1

Seq. No.	395024
Contig ID	56333_1.R1084
5'-most EST	uC-osroM202030c06a1
Method	BLASTX
NCBI GI	g4559333
BLAST score	219
E value	2.0e-17
Match length	87
% identity	53
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	395025

Contig ID	56393_1.R1084
5'-most EST	g3766693
Method	BLASTX
NCBI GI	g2160166
BLAST score	253
E value	2.0e-21
Match length	95
% identity	57
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	395026
Contig ID	56400_1.R1084
5'-most EST	uC-osroM202030h02a1

Seq. No.	395027
Contig ID	56410_1.R1084
5'-most EST	uC-osroM202033c03a1

Seq. No.	395028
Contig ID	56414_1.R1084
5'-most EST	uC-osroM202031a06b1
Method	BLASTX
NCBI GI	g1685003
BLAST score	207
E value	3.0e-16
Match length	127
% identity	39
NCBI Description	(U32643) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq. No.	395029
Contig ID	56420_1.R1084
5'-most EST	g2827172
Method	BLASTX
NCBI GI	g2979562
BLAST score	210
E value	2.0e-16
Match length	57
% identity	70
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana] >gi_3386623 (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	395030
Contig ID	56444_1.R1084
5'-most EST	uC-osroM202032a01a1

Seq. No.	395031
Contig ID	56445_1.R1084
5'-most EST	uC-osroM202033b01b1
Method	BLASTX
NCBI GI	g3445201
BLAST score	214
E value	2.0e-17
Match length	67
% identity	64
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	395032
Contig ID	56463_1.R1084
5'-most EST	g5038810

Seq. No.	395033
Contig ID	56513_1.R1084
5'-most EST	uC-osroM202032e09a1

Seq. No.	395034
Contig ID	56528_1.R1084
5'-most EST	g3767933

Seq. No.	395035
Contig ID	56531_1.R1084
5'-most EST	uC-osroM202032f11b1

Seq. No.	395036
Contig ID	56563_1.R1084
5'-most EST	uC-osroM202033a03a1

Seq. No.	395037
Contig ID	56568_1.R1084
5'-most EST	uC-osroM202033a07a1

Seq. No.	395038
Contig ID	56594_1.R1084
5'-most EST	g571599
Method	BLASTX
NCBI GI	g3063455
BLAST score	415
E value	1.0e-40
Match length	101
% identity	75
NCBI Description	(AC003981) F22013.17 [Arabidopsis thaliana]

Seq. No.	395039
Contig ID	56595_1.R1084
5'-most EST	uC-osroM202033c01a1
Method	BLASTX
NCBI GI	g4314378
BLAST score	251
E value	2.0e-21
Match length	112
% identity	41
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana] >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative lipase [Arabidopsis thaliana]

Seq. No.	395040
Contig ID	56616_1.R1084
5'-most EST	g2312368
Method	BLASTX
NCBI GI	g6056371
BLAST score	426
E value	7.0e-42
Match length	165

% identity	54
NCBI Description	(AC009894) nucleolar protein [Arabidopsis thaliana]

Seq. No.	395041
Contig ID	56638_1.R1084
5'-most EST	uC-osroM202033h04a1

Seq. No.	395042
Contig ID	56651_1.R1084
5'-most EST	uC-osroM202036d08b1
Method	BLASTX
NCBI GI	g2352492
BLAST score	409
E value	1.0e-44
Match length	155
% identity	59
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	395043
Contig ID	56673_1.R1084
5'-most EST	uC-osroM202033g07a1
Method	BLASTX
NCBI GI	g1497987
BLAST score	152
E value	7.0e-10
Match length	40
% identity	72
NCBI Description	(U62798) SCARECROW [Arabidopsis thaliana]

Seq. No.	395044
Contig ID	56730_1.R1084
5'-most EST	g3760072

Seq. No.	395045
Contig ID	56734_1.R1084
5'-most EST	uC-osroM202034f07a1
Method	BLASTX
NCBI GI	g3341693
BLAST score	223
E value	3.0e-18
Match length	69
% identity	59
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	395046
Contig ID	56755_1.R1084
5'-most EST	g4714822

Seq. No.	395047
Contig ID	56768_1.R1084
5'-most EST	uC-osroM202034h09a1

Seq. No.	395048
Contig ID	56775_1.R1084
5'-most EST	uC-osroM202034h06a1

Seq. No. 395049
Contig ID 56776_1.R1084
5'-most EST uC-osroM202034h06b1

Seq. No. 395050
Contig ID 56783_1.R1084
5'-most EST uC-osroM202035a02b1
Method BLASTX
NCBI GI g4680197
BLAST score 379
E value 4.0e-36
Match length 94
% identity 78
NCBI Description (AF114171) putative beta-ketoacyl-CoA synthase [Sorghum bicolor]

Seq. No. 395051
Contig ID 56788_1.R1084
5'-most EST uC-osroM202035b03a1

Seq. No. 395052
Contig ID 56793_1.R1084
5'-most EST g5004608
Method BLASTX
NCBI GI g3395432
BLAST score 836
E value 9.0e-90
Match length 195
% identity 78
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana] >gi_5731261_gb_AAD48838.1_AF166352_1 (AF166352) alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis thaliana]

Seq. No. 395053
Contig ID 56831_1.R1084
5'-most EST uC-osroM202035d02a1
Method BLASTX
NCBI GI g2982283
BLAST score 184
E value 2.0e-13
Match length 51
% identity 69
NCBI Description (AF051226) PREG-like protein [Picea mariana]

Seq. No. 395054
Contig ID 56837_1.R1084
5'-most EST g3762766

Seq. No. 395055
Contig ID 56838_1.R1084
5'-most EST uC-osroM202035d11a1

Seq. No. 395056
Contig ID 56840_1.R1084
5'-most EST uC-osroM202035e01a1

Method	BLASTX
NCBI GI	g2827143
BLAST score	336
E value	3.0e-31
Match length	136
% identity	48
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	395057
Contig ID	56847_1.R1084
5'-most EST	g4715966
Method	BLASTX
NCBI GI	g2459419
BLAST score	236
E value	3.0e-28
Match length	233
% identity	38
NCBI Description	(AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395058
Contig ID	56848_1.R1084
5'-most EST	uC-osroM202035e06b1

Seq. No.	395059
Contig ID	56852_1.R1084
5'-most EST	g3766972

Seq. No.	395060
Contig ID	56861_1.R1084
5'-most EST	uC-osroM202035f03a1

Seq. No.	395061
Contig ID	56866_1.R1084
5'-most EST	g3759158

Seq. No.	395062
Contig ID	56875_1.R1084
5'-most EST	uC-osroM202035f12b1
Method	BLASTX
NCBI GI	g6041853
BLAST score	499
E value	4.0e-50
Match length	215
% identity	50
NCBI Description	(AC009853) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395063
Contig ID	56926_1.R1084
5'-most EST	g5004515

Seq. No.	395064
Contig ID	56954_1.R1084
5'-most EST	uC-osroM202036f04a1
Method	BLASTX
NCBI GI	g3548810
BLAST score	237

E value	2.0e-19
Match length	153
% identity	34
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	395065
Contig ID	56968_1.R1084
5'-most EST	g4714321

Seq. No.	395066
Contig ID	56970_1.R1084
5'-most EST	uC-osroM202037h08a1
Method	BLASTN
NCBI GI	g5042437
BLAST score	40
E value	6.0e-13
Match length	74
% identity	79
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	395067
Contig ID	56979_1.R1084
5'-most EST	uC-osroM202036h06a1

Seq. No.	395068
Contig ID	57024_1.R1084
5'-most EST	uC-osroM202037c08a1

Seq. No.	395069
Contig ID	57041_1.R1084
5'-most EST	uC-osroM202037d10a1
Method	BLASTX
NCBI GI	g2642448
BLAST score	107
E value	8.0e-12
Match length	187
% identity	34
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187_gb_AAC17830.1_ (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395070
Contig ID	57046_1.R1084
5'-most EST	uC-osroM202037e07a1
Method	BLASTX
NCBI GI	g2541876
BLAST score	278
E value	1.0e-26
Match length	114
% identity	56
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	395071
Contig ID	57047_1.R1084
5'-most EST	g3760315

Method	BLASTX
NCBI GI	g3702323
BLAST score	249
E value	4.0e-21
Match length	98
% identity	63
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	395072
Contig ID	57067_1.R1084
5'-most EST	uC-osroM202037f04b1

Seq. No.	395073
Contig ID	57072_1.R1084
5'-most EST	uC-osroM202037f09a1
Method	BLASTN
NCBI GI	g5441876
BLAST score	115
E value	2.0e-57
Match length	207
% identity	89
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	395074
Contig ID	57072_2.R1084
5'-most EST	g5005210
Method	BLASTN
NCBI GI	g5441876
BLAST score	285
E value	1.0e-159
Match length	352
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	395075
Contig ID	57077_1.R1084
5'-most EST	uC-osroM202037f12b1

Seq. No.	395076
Contig ID	57088_1.R1084
5'-most EST	g3763499
Method	BLASTX
NCBI GI	g3123130
BLAST score	404
E value	3.0e-39
Match length	123
% identity	16
NCBI Description	HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN T32G6.2 IN CHROMOSOME II >gi_2618685 (AC002510) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] >gi_3241948 (AC004625) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana]

Seq. No.	395077
Contig ID	57092_1.R1084

5'-most EST	uC-osroM202037h07a1
Method	BLASTX
NCBI GI	g282994
BLAST score	572
E value	8.0e-60
Match length	161
% identity	76
NCBI Description	Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No.	395078
Contig ID	57095_1.R1084
5'-most EST	uC-osroM202037h04a1

Seq. No.	395079
Contig ID	57109_1.R1084
5'-most EST	uC-osroM202038a02b1
Method	BLASTX
NCBI GI	g3738331
BLAST score	206
E value	6.0e-16
Match length	51
% identity	69
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	395080
Contig ID	57163_1.R1084
5'-most EST	uC-osroM202038e05a1
Method	BLASTX
NCBI GI	g4467122
BLAST score	134
E value	3.0e-09
Match length	148
% identity	24
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	395081
Contig ID	57176_1.R1084
5'-most EST	uC-osroM202038f04b1

Seq. No.	395082
Contig ID	57187_1.R1084
5'-most EST	g4715917
Method	BLASTX
NCBI GI	g3218550
BLAST score	227
E value	3.0e-18
Match length	199
% identity	37
NCBI Description	(AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana] >gi_4972044_emb_CAB43912.1_ (AL078470) Cdk-activating kinase CAK1At [Arabidopsis thaliana]

Seq. No.	395083
Contig ID	57193_1.R1084
5'-most EST	g5005169
Method	BLASTX

NCBI GI g3738302
BLAST score 459
E value 9.0e-46
Match length 150
% identity 58
NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No. 395084
Contig ID 57195_1.R1084
5'-most EST uC-osroM202038g10a1
Method BLASTX
NCBI GI g2244866
BLAST score 315
E value 1.0e-28
Match length 108
% identity 53
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 395085
Contig ID 57198_1.R1084
5'-most EST uC-osroM202038g11b1

Seq. No. 395086
Contig ID 57218_1.R1084
5'-most EST uC-osroM202039a05a1

Seq. No. 395087
Contig ID 57222_1.R1084
5'-most EST g1631799

Seq. No. 395088
Contig ID 57287_1.R1084
5'-most EST uC-osroM202039f05a1
Method BLASTX
NCBI GI g3822036
BLAST score 201
E value 2.0e-29
Match length 104
% identity 65
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No. 395089
Contig ID 57396_1.R1084
5'-most EST uC-osroM202041h09b1
Method BLASTX
NCBI GI g2160174
BLAST score 508
E value 3.0e-51
Match length 138
% identity 67
NCBI Description (AC000132) Identical to A. thaliana PUR2 (gb_X74766). ESTs gb_ATTS3927,gb_N96446 come from this gene. [Arabidopsis thaliana]

Seq. No. 395090

Contig ID 57397_1.R1084
5'-most EST g5667307

Seq. No. 395091
Contig ID 57401_1.R1084
5'-most EST g286272
Method BLASTN
NCBI GI g6016845
BLAST score 35
E value 9.0e-10
Match length 51
% identity 34
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 395092
Contig ID 57402_1.R1084
5'-most EST g286273
Method BLASTX
NCBI GI g4220524
BLAST score 163
E value 3.0e-18
Match length 87
% identity 57
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 395093
Contig ID 57406_1.R1084
5'-most EST g2312708

Seq. No. 395094
Contig ID 57406_2.R1084
5'-most EST g2311664

Seq. No. 395095
Contig ID 57411_1.R1084
5'-most EST g4714989

Seq. No. 395096
Contig ID 57414_1.R1084
5'-most EST g286285
Method BLASTX
NCBI GI g3135273
BLAST score 161
E value 1.0e-10
Match length 106
% identity 35
NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]
>gi_4191773 (AC005917) putative WD-40 repeat protein
[Arabidopsis thaliana]

Seq. No. 395097
Contig ID 57415_1.R1084
5'-most EST g286286

Seq. No. 395098
Contig ID 57419_1.R1084
5'-most EST g286291

Method	BLASTX
NCBI GI	g4263519
BLAST score	446
E value	2.0e-44
Match length	95
% identity	92
NCBI Description	(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]

Seq. No.	395099
Contig ID	57425_1.R1084
5'-most EST	g286298

Seq. No.	395100
Contig ID	57429_1.R1084
5'-most EST	g286303
Method	BLASTX
NCBI GI	g2583121
BLAST score	303
E value	2.0e-27
Match length	77
% identity	70
NCBI Description	(AC002387) putative phosphotransferase [Arabidopsis thaliana]

Seq. No.	395101
Contig ID	57430_1.R1084
5'-most EST	g286304

Seq. No.	395102
Contig ID	57432_1.R1084
5'-most EST	g286306

Seq. No.	395103
Contig ID	57438_1.R1084
5'-most EST	g2442755

Seq. No.	395104
Contig ID	57439_1.R1084
5'-most EST	g286314
Method	BLASTX
NCBI GI	g140474
BLAST score	141
E value	6.0e-11
Match length	130
% identity	31
NCBI Description	HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC REGION >gi_83212_pir__S19434 probable transport protein YCR023c - yeast (Saccharomyces cerevisiae) >gi_1907167_emb_CAA42315_ (X59720) YCR023c, len:611 [Saccharomyces cerevisiae]

Seq. No.	395105
Contig ID	57441_1.R1084
5'-most EST	g2275907
Method	BLASTX
NCBI GI	g2129752

BLAST score 310
E value 5.0e-28
Match length 99
% identity 59
NCBI Description thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_ (Z35475) thioredoxin [Arabidopsis thaliana]

Seq. No. 395106
Contig ID 57450_1.R1084
5'-most EST g286325

Seq. No. 395107
Contig ID 57451_1.R1084
5'-most EST g3760673

Seq. No. 395108
Contig ID 57471_1.R1084
5'-most EST g286347

Seq. No. 395109
Contig ID 57475_1.R1084
5'-most EST g286352

Seq. No. 395110
Contig ID 57476_1.R1084
5'-most EST g427123

Seq. No. 395111
Contig ID 57477_1.R1084
5'-most EST g286354

Seq. No. 395112
Contig ID 57478_1.R1084
5'-most EST g286355
Method BLASTX
NCBI GI g6006850
BLAST score 159
E value 1.0e-10
Match length 35
% identity 83
NCBI Description (AC009540) putative GAR1 protein [Arabidopsis thaliana]

Seq. No. 395113
Contig ID 57487_1.R1084
5'-most EST g4968914
Method BLASTX
NCBI GI g882341
BLAST score 245
E value 1.0e-20
Match length 90
% identity 56
NCBI Description (U24702) LRP1 [Arabidopsis thaliana]

Seq. No. 395114
Contig ID 57493_1.R1084
5'-most EST g286370
Method BLASTX

NCBI GI	g4210330
BLAST score	493
E value	1.0e-56
Match length	144
% identity	74
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	395115
Contig ID	57499_1.R1084
5'-most EST	g286376

Seq. No.	395116
Contig ID	57500_1.R1084
5'-most EST	g286377
Method	BLASTX
NCBI GI	g5669634
BLAST score	239
E value	5.0e-25
Match length	119
% identity	60
NCBI Description	(AF096246) ethylene-responsive transcriptional coactivator [Lycopersicon esculentum]

Seq. No.	395117
Contig ID	57500_2.R1084
5'-most EST	g5004245

Seq. No.	395118
Contig ID	57512_1.R1084
5'-most EST	g286389
Method	BLASTN
NCBI GI	g4680189
BLAST score	233
E value	1.0e-128
Match length	579
% identity	98
NCBI Description	Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds

Seq. No.	395119
Contig ID	57513_1.R1084
5'-most EST	g286390
Method	BLASTX
NCBI GI	g4191791
BLAST score	434
E value	1.0e-42
Match length	171
% identity	60
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

Seq. No.	395120
Contig ID	57518_1.R1084
5'-most EST	g2431351

Method	BLASTX
NCBI GI	g3236259
BLAST score	520
E value	8.0e-53
Match length	129
% identity	75
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana] >gi_4895207_gb_AAD32794.1_AC007661_31 (AC007661) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	395121
Contig ID	57530_1.R1084
5'-most EST	g6024995

Seq. No.	395122
Contig ID	57534_1.R1084
5'-most EST	g286412

Seq. No.	395123
Contig ID	57535_1.R1084
5'-most EST	g286413

Seq. No.	395124
Contig ID	57542_1.R1084
5'-most EST	g5667316
Method	BLASTX
NCBI GI	g4263509
BLAST score	567
E value	1.0e-58
Match length	169
% identity	70
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395125
Contig ID	57549_1.R1084
5'-most EST	g5038770

Seq. No.	395126
Contig ID	57553_1.R1084
5'-most EST	g286433

Seq. No.	395127
Contig ID	57565_1.R1084
5'-most EST	g1036898
Method	BLASTX
NCBI GI	g3080738
BLAST score	530
E value	3.0e-54
Match length	125
% identity	74
NCBI Description	(U77365) pasticcino 1-A [Arabidopsis thaliana]

Seq. No.	395128
Contig ID	57566_1.R1084
5'-most EST	g286448
Method	BLASTX
NCBI GI	g2414617

BLAST score	127
E value	2.0e-13
Match length	194
% identity	32
NCBI Description	(Z99259) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	395129
Contig ID	57568_1.R1084
5'-most EST	g286450
Method	BLASTX
NCBI GI	g4759180
BLAST score	160
E value	2.0e-10
Match length	121
% identity	35
NCBI Description	serine/threonine kinase 19 >gi_1082305_pir__A53439 complement C4A 5'-region protein RP - human >gi_452067 (L26261) RP1 [Homo sapiens] >gi_500622 (L26260) MHC HLA-RP-complement system protein [Homo sapiens]

Seq. No.	395130
Contig ID	57571_1.R1084
5'-most EST	g3760758

Seq. No.	395131
Contig ID	57574_1.R1084
5'-most EST	g286456

Seq. No.	395132
Contig ID	57576_1.R1084
5'-most EST	g286458

Seq. No.	395133
Contig ID	57581_1.R1084
5'-most EST	g5004005
Method	BLASTN
NCBI GI	g342661
BLAST score	377
E value	0.0e+00
Match length	604
% identity	99
NCBI Description	Maize mitochondrial 26S rRNA gene and flanks

Seq. No.	395134
Contig ID	57581_2.R1084
5'-most EST	g431836
Method	BLASTN
NCBI GI	g343690
BLAST score	365
E value	0.0e+00
Match length	379
% identity	99
NCBI Description	Wheat mitochondrial 26S rRNA gene, complete cds

Seq. No.	395135
Contig ID	57602_1.R1084
5'-most EST	g572001

Method	BLASTX
NCBI GI	g4803956
BLAST score	193
E value	1.0e-14
Match length	157
% identity	34
NCBI Description	(AC006202) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	395136
Contig ID	57616_1.R1084
5'-most EST	g1632293
Method	BLASTN
NCBI GI	g559342
BLAST score	106
E value	3.0e-52
Match length	158
% identity	94
NCBI Description	Human TBXAS1 gene for thromboxane synthase, exon

Seq. No.	395137
Contig ID	57617_1.R1084
5'-most EST	g3760787
Method	BLASTX
NCBI GI	g2960364
BLAST score	462
E value	2.0e-68
Match length	233
% identity	58
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	395138
Contig ID	57617_2.R1084
5'-most EST	g5038894
Method	BLASTX
NCBI GI	g2960364
BLAST score	260
E value	3.0e-22
Match length	101
% identity	55
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	395139
Contig ID	57619_1.R1084
5'-most EST	g3760788

Seq. No.	395140
Contig ID	57621_1.R1084
5'-most EST	g3760790
Method	BLASTN
NCBI GI	g5091597
BLAST score	376
E value	0.0e+00
Match length	461
% identity	99

NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No. 395141
Contig ID 57627_1.R1084
5'-most EST g4968784

Seq. No. 395142
Contig ID 57634_1.R1084
5'-most EST g3760797

Seq. No. 395143
Contig ID 57639_1.R1084
5'-most EST g4881174

Seq. No. 395144
Contig ID 57653_1.R1084
5'-most EST g286548
Method BLASTX
NCBI GI g4539389
BLAST score 304
E value 2.0e-28
Match length 116
% identity 57
NCBI Description (AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No. 395145
Contig ID 57657_1.R1084
5'-most EST g286552
Method BLASTX
NCBI GI g4539383
BLAST score 292
E value 5.0e-26
Match length 113
% identity 47
NCBI Description (AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 395146
Contig ID 57660_1.R1084
5'-most EST g3760814
Method BLASTX
NCBI GI g6094211
BLAST score 369
E value 3.0e-35
Match length 79
% identity 89
NCBI Description PROBABLE SMALL NUCLEAR RIBONUCLEOPROTEIN G (SNRNP-G) (SM PROTEIN G) >gi_3738322 (AC005170) putative small nuclear ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 395147
Contig ID 57671_1.R1084
5'-most EST g286568
Method BLASTX
NCBI GI g4803938
BLAST score 104
E value 1.0e-10

Match length	44
% identity	80
NCBI Description	(AC006264) putative aromatic amino acid permease [Arabidopsis thaliana] >gi_5139337_emb_CAB45643.1_ (AJ243221) putative AUX1-like permease [Arabidopsis thaliana]

Seq. No.	395148
Contig ID	57677_1.R1084
5'-most EST	g286574
Method	BLASTX
NCBI GI	g3287944
BLAST score	233
E value	3.0e-19
Match length	76
% identity	57
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN C3D6.08C IN CHROMOSOME II >gi_2117304_emb_CAB09117.1_ (Z95620) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	395149
Contig ID	57678_1.R1084
5'-most EST	g286577
Method	BLASTX
NCBI GI	g2500380
BLAST score	508
E value	2.0e-51
Match length	105
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No.	395150
Contig ID	57686_1.R1084
5'-most EST	g286585

Seq. No.	395151
Contig ID	57687_1.R1084
5'-most EST	g3759717

Seq. No.	395152
Contig ID	57703_1.R1084
5'-most EST	g286602
Method	BLASTN
NCBI GI	g2342495
BLAST score	61
E value	3.0e-25
Match length	153
% identity	85
NCBI Description	Ananas comosus mRNA for bromelain, complete cds

Seq. No.	395153
Contig ID	57711_1.R1084
5'-most EST	g3090575

Method	BLASTX
NCBI GI	g3015621
BLAST score	139
E value	2.0e-14
Match length	87
% identity	56
NCBI Description	(AF035460) low molecular weight heat shock protein precursor [Zea mays]

Seq. No.	395154
Contig ID	57713_1.R1084
5'-most EST	g287005

Seq. No.	395155
Contig ID	57713_2.R1084
5'-most EST	g4878880

Seq. No.	395156
Contig ID	57713_4.R1084
5'-most EST	g2312902

Seq. No.	395157
Contig ID	57713_5.R1084
5'-most EST	g427014

Seq. No.	395158
Contig ID	57713_6.R1084
5'-most EST	g2311220

Seq. No.	395159
Contig ID	57713_7.R1084
5'-most EST	g425830

Seq. No.	395160
Contig ID	57722_1.R1084
5'-most EST	g286622

Seq. No.	395161
Contig ID	57728_1.R1084
5'-most EST	g286628

Seq. No.	395162
Contig ID	57737_1.R1084
5'-most EST	g286637

Seq. No.	395163
Contig ID	57749_1.R1084
5'-most EST	g1631765
Method	BLASTX
NCBI GI	g100535
BLAST score	268
E value	6.0e-23
Match length	80
% identity	64
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	395164
Contig ID	57757_1.R1084
5'-most EST	g2311259
Method	BLASTX
NCBI GI	g4325369
BLAST score	173
E value	4.0e-15
Match length	130
% identity	45
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	395165
Contig ID	57758_1.R1084
5'-most EST	g2866660
Method	BLASTX
NCBI GI	g5262856
BLAST score	316
E value	3.0e-29
Match length	72
% identity	83
NCBI Description	(AJ238095) Lsm3 protein [Homo sapiens] >gi_5919147_gb_AAD56227.1_AF182289_1 (AF182289) U6 snRNA-associated Sm-like protein LSm3 [Homo sapiens]

Seq. No.	395166
Contig ID	57759_1.R1084
5'-most EST	g5039050
Method	BLASTX
NCBI GI	g2129648
BLAST score	448
E value	2.0e-44
Match length	158
% identity	61
NCBI Description	MYB-related protein 33,3K - Arabidopsis thaliana >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein [Arabidopsis thaliana]

Seq. No.	395167
Contig ID	57765_1.R1084
5'-most EST	g5004006

Seq. No.	395168
Contig ID	57766_1.R1084
5'-most EST	g2866669
Method	BLASTX
NCBI GI	g4262162
BLAST score	283
E value	6.0e-28
Match length	114
% identity	59
NCBI Description	(AC005275) putative glycosylation enzyme [Arabidopsis thaliana]

Seq. No.	395169
Contig ID	57767_1.R1084
5'-most EST	g2866670

Seq. No.	395170
Contig ID	57772_1.R1084
5'-most EST	g286675
Seq. No.	395171
Contig ID	57773_1.R1084
5'-most EST	g286676
Seq. No.	395172
Contig ID	57774_1.R1084
5'-most EST	g286717
Method	BLASTX
NCBI GI	g6094168
BLAST score	223
E value	6.0e-33
Match length	101
% identity	64
NCBI Description	40S RIBOSOMAL PROTEIN S20 >gi_3687464_emb_CAA21188_ (AL031798) 40s ribosomal protein s20. [Schizosaccharomyces pombe]
Seq. No.	395173
Contig ID	57775_1.R1084
5'-most EST	g286678
Seq. No.	395174
Contig ID	57776_1.R1084
5'-most EST	g286679
Seq. No.	395175
Contig ID	57777_1.R1084
5'-most EST	g286680
Method	BLASTX
NCBI GI	g6091738
BLAST score	166
E value	3.0e-11
Match length	34
% identity	94
NCBI Description	(AC010797) putative glutaredoxin [Arabidopsis thaliana]
Seq. No.	395176
Contig ID	57781_1.R1084
5'-most EST	g286684
Seq. No.	395177
Contig ID	57783_1.R1084
5'-most EST	g286687
Method	BLASTX
NCBI GI	g3080443
BLAST score	253
E value	2.0e-21
Match length	81
% identity	54
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]
Seq. No.	395178

Contig ID	57787_1.R1084
5'-most EST	g286692
Method	BLASTX
NCBI GI	g4588007
BLAST score	182
E value	5.0e-13
Match length	75
% identity	48
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395179
Contig ID	57799_1.R1084
5'-most EST	g286704

Seq. No.	395180
Contig ID	57806_1.R1084
5'-most EST	g2798174

Seq. No.	395181
Contig ID	57815_1.R1084
5'-most EST	g286722

Seq. No.	395182
Contig ID	57835_1.R1084
5'-most EST	g286748
Method	BLASTX
NCBI GI	g6056191
BLAST score	227
E value	2.0e-18
Match length	58
% identity	74
NCBI Description	(AC009400) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	395183
Contig ID	57845_1.R1084
5'-most EST	g286762
Method	BLASTX
NCBI GI	g1346057
BLAST score	564
E value	6.0e-58
Match length	132
% identity	80
NCBI Description	PROTEIN KINASE G11A >gi_100705_pir__B30311 protein kinase C (EC 2.7.1.-) homolog - rice (fragment) >gi_169788 (J04556) G11A protein [Oryza sativa]

Seq. No.	395184
Contig ID	57868_1.R1084
5'-most EST	g3767037
Method	BLASTX
NCBI GI	g4337195
BLAST score	448
E value	2.0e-44
Match length	136
% identity	68
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	395185
Contig ID	57871_1.R1084
5'-most EST	g286794
Seq. No.	395186
Contig ID	57881_1.R1084
5'-most EST	g2431365
Method	BLASTX
NCBI GI	g3355483
BLAST score	257
E value	8.0e-22
Match length	59
% identity	68
NCBI Description	(AC004218) gibberellin-regulated protein (GASA5)-like [Arabidopsis thaliana]
Seq. No.	395187
Contig ID	57882_1.R1084
5'-most EST	g5038608
Seq. No.	395188
Contig ID	57895_1.R1084
5'-most EST	g702887
Seq. No.	395189
Contig ID	57900_1.R1084
5'-most EST	g286825
Method	BLASTX
NCBI GI	g4314361
BLAST score	174
E value	4.0e-12
Match length	46
% identity	78
NCBI Description	(AC006340) unknown protein [Arabidopsis thaliana]
Seq. No.	395190
Contig ID	57905_1.R1084
5'-most EST	g286834
Seq. No.	395191
Contig ID	57919_1.R1084
5'-most EST	g286848
Seq. No.	395192
Contig ID	57930_1.R1084
5'-most EST	g286860
Method	BLASTX
NCBI GI	g5734747
BLAST score	164
E value	5.0e-11
Match length	72
% identity	56
NCBI Description	(AC007651) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	395193
Contig ID	57937_1.R1084

5'-most EST g3760947

Seq. No. 395194
Contig ID 57944_1.R1084
5'-most EST g427296

Seq. No. 395195
Contig ID 57966_1.R1084
5'-most EST g2311565

Seq. No. 395196
Contig ID 57971_1.R1084
5'-most EST g2796563

Seq. No. 395197
Contig ID 57972_1.R1084
5'-most EST g286919

Seq. No. 395198
Contig ID 57980_1.R1084
5'-most EST g3760961
Method BLASTN
NCBI GI g5714761
BLAST score 215
E value 1.0e-117
Match length 263
% identity 94
NCBI Description Oryza sativa subsp. indica serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete cds

Seq. No. 395199
Contig ID 57994_1.R1084
5'-most EST g2310077
Method BLASTX
NCBI GI g3522945
BLAST score 194
E value 1.0e-24
Match length 217
% identity 38
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 395200
Contig ID 58016_1.R1084
5'-most EST g286967
Method BLASTX
NCBI GI g1076715
BLAST score 166
E value 2.0e-11
Match length 39
% identity 77
NCBI Description abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No. 395201
Contig ID 58020_1.R1084
5'-most EST g286974

Seq. No.	395202
Contig ID	58028_1.R1084
5'-most EST	g5005061
Method	BLASTX
NCBI GI	g3878342
BLAST score	165
E value	1.0e-11
Match length	60
% identity	53
NCBI Description	(Z81097) Similarity to Drosophila chromatin assembly factor 1 P55 subunit (TR:Q24572); cDNA EST EMBL:C07605 comes from this gene; cDNA EST EMBL:C09018 comes from this gene; cDNA EST EMBL:C10119 comes from this gene; cDNA EST ... >gi_3880742_emb_CAA19477.1_ (AL023833) Similarity to Drosophila chromatin assembly factor 1 P55 subunit (TR:Q24572); cDNA EST EMBL:C07605 comes from this gene; cDNA EST EMBL:C09018 comes from this gene; cDNA EST EMBL:C10119 comes from this gene; cDNA ES... >gi_4164608 (AF116530) synthetic multivulva protein LIN-53 p48 [Caenorhabditis elegans]

Seq. No.	395203
Contig ID	58038_1.R1084
5'-most EST	g287000
Method	BLASTX
NCBI GI	g3549666
BLAST score	336
E value	4.0e-31
Match length	86
% identity	76
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	395204
Contig ID	58044_1.R1084
5'-most EST	g287006
Method	BLASTX
NCBI GI	g3445397
BLAST score	224
E value	4.0e-23
Match length	101
% identity	57
NCBI Description	(AJ010166) S-domain receptor-like protein kinase [Zea mays]

Seq. No.	395205
Contig ID	58045_1.R1084
5'-most EST	g287007
Method	BLASTN
NCBI GI	g984904
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Plasmid pBSL142 cloning vector, complete sequence

Seq. No.	395206
Contig ID	58045_2.R1084

5'-most EST	g426517
Method	BLASTX
NCBI GI	g2224899
BLAST score	286
E value	3.0e-25
Match length	202
% identity	37
NCBI Description	(U67133) DNA-binding protein PcMYB1 [Petroselinum crispum]

Seq. No.	395207
Contig ID	58051_1.R1084
5'-most EST	g287015
Method	BLASTX
NCBI GI	g6016330
BLAST score	208
E value	6.0e-24
Match length	83
% identity	70
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) >gi_3355311_emb_CAA08809_ (AJ009737) eukaryotic translation initiation factor 6 [Beta vulgaris]

Seq. No.	395208
Contig ID	58053_1.R1084
5'-most EST	g287017

Seq. No.	395209
Contig ID	58055_1.R1084
5'-most EST	g287020

Seq. No.	395210
Contig ID	58063_1.R1084
5'-most EST	g3761018

Seq. No.	395211
Contig ID	58064_1.R1084
5'-most EST	g4968618
Method	BLASTX
NCBI GI	g586901
BLAST score	209
E value	1.0e-16
Match length	106
% identity	50
NCBI Description	DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS HOMOLOG) >gi_2127055_pir__S66116 hypothetical protein - Bacillus subtilis >gi_467475_dbj_BAA05321_ (D26185) unknown [Bacillus subtilis] >gi_2632354_emb_CAB11863_ (Z99104) DNA repair protein homolog [Bacillus subtilis]

Seq. No.	395212
Contig ID	58074_1.R1084
5'-most EST	g287042

Seq. No.	395213
Contig ID	58076_1.R1084
5'-most EST	g2312969

Seq. No.	395214
Contig ID	58081_1.R1084
5'-most EST	g3767803

Seq. No.	395215
Contig ID	58082_1.R1084
5'-most EST	g287051
Method	BLASTX
NCBI GI	g4895187
BLAST score	270
E value	6.0e-24
Match length	76
% identity	64
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No.	395216
Contig ID	58083_1.R1084
5'-most EST	g287052

Seq. No.	395217
Contig ID	58088_1.R1084
5'-most EST	g700982
Method	BLASTX
NCBI GI	g3201626
BLAST score	539
E value	4.0e-62
Match length	182
% identity	71
NCBI Description	(AC004669) putative protein kinase MAP3K [Arabidopsis thaliana]

Seq. No.	395218
Contig ID	58105_1.R1084
5'-most EST	g287075
Method	BLASTX
NCBI GI	g4586107
BLAST score	319
E value	6.0e-34
Match length	134
% identity	11
NCBI Description	(AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	395219
Contig ID	58108_1.R1084
5'-most EST	g5900633
Method	BLASTN
NCBI GI	g6016845
BLAST score	48
E value	1.0e-17
Match length	130
% identity	89
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	395220
Contig ID	58118_1.R1084
5'-most EST	g287088

Seq. No. 395221
Contig ID 58119_1.R1084
5'-most EST g3761044

Seq. No. 395222
Contig ID 58126_1.R1084
5'-most EST g287096
Method BLASTX
NCBI GI g4914458
BLAST score 252
E value 1.0e-21
Match length 82
% identity 50
NCBI Description (AL050400) putative protein [Arabidopsis thaliana]

Seq. No. 395223
Contig ID 58130_1.R1084
5'-most EST g1854337
Method BLASTX
NCBI GI g5091552
BLAST score 394
E value 2.0e-38
Match length 87
% identity 80
NCBI Description (AC007067) T10O24.21 [Arabidopsis thaliana]

Seq. No. 395224
Contig ID 58135_1.R1084
5'-most EST g2428199

Seq. No. 395225
Contig ID 58145_1.R1084
5'-most EST g4880407

Seq. No. 395226
Contig ID 58148_1.R1084
5'-most EST g3761010
Method BLASTX
NCBI GI g3372230
BLAST score 353
E value 3.0e-39
Match length 145
% identity 61
NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6 (AC005287) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana]

Seq. No. 395227
Contig ID 58152_1.R1084
5'-most EST g287122
Method BLASTX
NCBI GI g1362192
BLAST score 268
E value 4.0e-23
Match length 61

% identity	82
NCBI Description	ferredoxin--thioredoxin reductase (EC 1.18.-.-) variable chain - maize
Seq. No.	395228
Contig ID	58155_1.R1084
5'-most EST	g3106840
Seq. No.	395229
Contig ID	58163_1.R1084
5'-most EST	g4968622
Seq. No.	395230
Contig ID	58221_1.R1084
5'-most EST	g426205
Seq. No.	395231
Contig ID	58229_1.R1084
5'-most EST	g3761507
Seq. No.	395232
Contig ID	58240_1.R1084
5'-most EST	g4715191
Seq. No.	395233
Contig ID	58243_1.R1084
5'-most EST	g3759850
Seq. No.	395234
Contig ID	58275_1.R1084
5'-most EST	g5003856
Method	BLASTX
NCBI GI	g121631
BLAST score	202
E value	8.0e-21
Match length	93
% identity	66
NCBI Description	GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR >gi_72323_pir__KNNT2S glycine-rich protein 2 - wood tobacco >gi_19743_emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana sylvestris]
Seq. No.	395235
Contig ID	58287_1.R1084
5'-most EST	g287264
Method	BLASTX
NCBI GI	g2493650
BLAST score	388
E value	2.0e-37
Match length	129
% identity	67
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale cereale]
Seq. No.	395236

Contig ID	58297_1.R1084
5'-most EST	g427564
Method	BLASTX
NCBI GI	g6094048
BLAST score	462
E value	5.0e-46
Match length	98
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L30 >gi_2879811_emb_CAA11256_ (AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	395237
Contig ID	58312_1.R1084
5'-most EST	g287289
Method	BLASTX
NCBI GI	g1708993
BLAST score	442
E value	1.0e-43
Match length	106
% identity	80
NCBI Description	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE) >gi_2129567_pir__S61429 cystathionine beta-lyase (EC 4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511) cystathionine beta-lyase [Arabidopsis thaliana]

Seq. No.	395238
Contig ID	58320_1.R1084
5'-most EST	g426025

Seq. No.	395239
Contig ID	58328_1.R1084
5'-most EST	g568070

Seq. No.	395240
Contig ID	58331_1.R1084
5'-most EST	g5607304
Method	BLASTX
NCBI GI	g4741194
BLAST score	379
E value	2.0e-36
Match length	131
% identity	56
NCBI Description	(AL049746) ABC transporter-like protein [Arabidopsis thaliana]

Seq. No.	395241
Contig ID	58334_1.R1084
5'-most EST	g426041
Method	BLASTN
NCBI GI	g1724113
BLAST score	51
E value	1.0e-19
Match length	303
% identity	82
NCBI Description	Avena fatua Af10-protein mRNA, complete cds

Seq. No.	395242
Contig ID	58335_1.R1084
5'-most EST	g3768936
Method	BLASTX
NCBI GI	g4262250
BLAST score	165
E value	2.0e-11
Match length	39
% identity	82
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	395243
Contig ID	58339_1.R1084
5'-most EST	g2309672
Method	BLASTX
NCBI GI	g2062389
BLAST score	119
E value	2.0e-15
Match length	84
% identity	58
NCBI Description	(U77657) pathogenesis-related thaumatin-like protein [Oryza sativa]

Seq. No.	395244
Contig ID	58346_1.R1084
5'-most EST	g2310549

Seq. No.	395245
Contig ID	58358_1.R1084
5'-most EST	g426065
Method	BLASTX
NCBI GI	g4585988
BLAST score	480
E value	2.0e-48
Match length	103
% identity	82
NCBI Description	(AC005287) Similar to phosphoprotein phosphatase 2A regulatory subunit [Arabidopsis thaliana]

Seq. No.	395246
Contig ID	58360_1.R1084
5'-most EST	g426066
Method	BLASTX
NCBI GI	g2529675
BLAST score	275
E value	4.0e-24
Match length	128
% identity	45
NCBI Description	(AC002535) putative AP2 domain containing protein [Arabidopsis thaliana]

Seq. No.	395247
Contig ID	58365_1.R1084
5'-most EST	g569075

Seq. No.	395248
Contig ID	58370_1.R1084

5'-most EST	g4715707
Method	BLASTX
NCBI GI	g3236247
BLAST score	116
E value	5.0e-09
Match length	158
% identity	35
NCBI Description	(AC004684) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No.	395249
Contig ID	58375_1.R1084
5'-most EST	g2311468

Seq. No.	395250
Contig ID	58401_1.R1084
5'-most EST	g571801
Method	BLASTX
NCBI GI	g1944132
BLAST score	570
E value	2.0e-58
Match length	151
% identity	74
NCBI Description	(AB002560) CUC2 [Arabidopsis thaliana]

Seq. No.	395251
Contig ID	58411_1.R1084
5'-most EST	g6031131
Method	BLASTX
NCBI GI	g2501499
BLAST score	131
E value	1.0e-11
Match length	111
% identity	41
NCBI Description	INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE (IAA-GLU SYNTHETASE) ((URIDINE 5'-DIPHOSPHATE-GLUCOSE:INDOL-3-YLACETYL)-BETA-D-GLUCOSYL TRANSFERASE) >gi_626043_pir__A54739 indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) - maize >gi_548195 (L34847) IAA-glu synthetase [Zea mays]

Seq. No.	395252
Contig ID	58415_1.R1084
5'-most EST	g3759149
Method	BLASTX
NCBI GI	g4406770
BLAST score	182
E value	3.0e-17
Match length	72
% identity	68
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	395253
Contig ID	58418_1.R1084
5'-most EST	g5803501
Method	BLASTN
NCBI GI	g4757662
BLAST score	35

E value	8.0e-10
Match length	67
% identity	78
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	395254
Contig ID	58426_1.R1084
5'-most EST	g4879389

Seq. No.	395255
Contig ID	58434_1.R1084
5'-most EST	g426146
Method	BLASTX
NCBI GI	g2191175
BLAST score	177
E value	3.0e-17
Match length	155
% identity	40
NCBI Description	(AF007270) A_IG002P16.24 gene product [Arabidopsis thaliana]

Seq. No.	395256
Contig ID	58460_1.R1084
5'-most EST	g426653

Seq. No.	395257
Contig ID	58473_1.R1084
5'-most EST	g2310748
Method	BLASTX
NCBI GI	g2088649
BLAST score	221
E value	7.0e-18
Match length	80
% identity	54
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	395258
Contig ID	58474_1.R1084
5'-most EST	g426185
Method	BLASTX
NCBI GI	g2827649
BLAST score	203
E value	1.0e-15
Match length	44
% identity	80
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	395259
Contig ID	58481_1.R1084
5'-most EST	g2312106

Seq. No.	395260
Contig ID	58496_1.R1084
5'-most EST	g426208

Seq. No.	395261

Contig ID	58519_1.R1084
5'-most EST	g426231
Method	BLASTX
NCBI GI	g2961284
BLAST score	186
E value	1.0e-24
Match length	115
% identity	56
NCBI Description	(Y16848) cinnamyl alcohol dehydrogenase-like protein, subunit a [Arabidopsis thaliana] >gi_4467103_emb_CAB37537_ (AL035538) cinnamyl alcohol dehydrogenase-like protein, LCADa [Arabidopsis thaliana]

Seq. No.	395262
Contig ID	58521_1.R1084
5'-most EST	g4879144

Seq. No.	395263
Contig ID	58523_1.R1084
5'-most EST	g426235
Method	BLASTX
NCBI GI	g4558484
BLAST score	351
E value	1.0e-44
Match length	108
% identity	83
NCBI Description	(AF097363) heat shock protein 101 [Triticum aestivum]

Seq. No.	395264
Contig ID	58529_1.R1084
5'-most EST	g4879988
Method	BLASTX
NCBI GI	g3641839
BLAST score	162
E value	6.0e-11
Match length	67
% identity	54
NCBI Description	(AL023094) isoflavone reductase-like protein [Arabidopsis thaliana]

Seq. No.	395265
Contig ID	58532_1.R1084
5'-most EST	g426245
Method	BLASTX
NCBI GI	g4926866
BLAST score	345
E value	9.0e-43
Match length	137
% identity	66
NCBI Description	(AC007509) putative amp-binding protein [Arabidopsis thaliana]

Seq. No.	395266
Contig ID	58540_1.R1084
5'-most EST	g426254

Seq. No.	395267

Contig ID 58544_1.R1084
5'-most EST g426258
Method BLASTX
NCBI GI g5080782
BLAST score 150
E value 8.0e-18
Match length 98
% identity 48
NCBI Description (AC007576) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 395268
Contig ID 58564_1.R1084
5'-most EST g426279

Seq. No. 395269
Contig ID 58572_1.R1084
5'-most EST g426285
Method BLASTX
NCBI GI g1839188
BLAST score 460
E value 1.0e-45
Match length 252
% identity 32
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 395270
Contig ID 58578_1.R1084
5'-most EST g426291

Seq. No. 395271
Contig ID 58579_1.R1084
5'-most EST g5004565

Seq. No. 395272
Contig ID 58581_1.R1084
5'-most EST g571918

Seq. No. 395273
Contig ID 58584_1.R1084
5'-most EST g2309694

Seq. No. 395274
Contig ID 58588_1.R1084
5'-most EST g2312293

Seq. No. 395275
Contig ID 58598_1.R1084
5'-most EST g2312225
Method BLASTN
NCBI GI g2058310
BLAST score 36
E value 1.0e-10
Match length 59
% identity 90
NCBI Description E.gunnii CCR mRNA

Seq. No. 395276

Contig ID 58612_1.R1084
5'-most EST g426325

Seq. No. 395277
Contig ID 58656_1.R1084
5'-most EST g701369

Seq. No. 395278
Contig ID 58660_1.R1084
5'-most EST g5701673
Method BLASTX
NCBI GI g1351409
BLAST score 662
E value 1.0e-107
Match length 229
% identity 81
NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_543699_pir__JQ2387 vacuolar processing enzyme precursor - castor bean >gi_471162_dbj_BAA04225_ (D17401) precursor of vacuolar processing enzyme [Ricinus communis]

Seq. No. 395279
Contig ID 58661_1.R1084
5'-most EST g426382
Method BLASTX
NCBI GI g2281115
BLAST score 707
E value 1.0e-74
Match length 178
% identity 76
NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No. 395280
Contig ID 58662_1.R1084
5'-most EST g571678
Method BLASTX
NCBI GI g1405561
BLAST score 410
E value 2.0e-39
Match length 174
% identity 36
NCBI Description (X98540) FSGTP1 [Fagus sylvatica]

Seq. No. 395281
Contig ID 58670_1.R1084
5'-most EST g426394

Seq. No. 395282
Contig ID 58686_1.R1084
5'-most EST g6012794

Seq. No. 395283
Contig ID 58694_1.R1084
5'-most EST g569325
Method BLASTX
NCBI GI g4325345

BLAST score	202
E value	8.0e-26
Match length	83
% identity	73
NCBI Description	(AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]

Seq. No.	395284
Contig ID	58709_1.R1084
5'-most EST	g5002778

Seq. No.	395285
Contig ID	58715_1.R1084
5'-most EST	g2310492

Seq. No.	395286
Contig ID	58722_1.R1084
5'-most EST	g426493
Method	BLASTX
NCBI GI	g2129771
BLAST score	201
E value	1.0e-15
Match length	62
% identity	60
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No.	395287
Contig ID	58729_1.R1084
5'-most EST	g1631737

Seq. No.	395288
Contig ID	58732_1.R1084
5'-most EST	g5443718

Seq. No.	395289
Contig ID	58733_1.R1084
5'-most EST	g2801127
Method	BLASTX
NCBI GI	g4415936
BLAST score	215
E value	9.0e-17
Match length	266
% identity	27
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana]

Seq. No.	395290
Contig ID	58738_1.R1084
5'-most EST	g426508

Seq. No.	395291
Contig ID	58758_1.R1084

5'-most EST	g2311539
Method	BLASTX
NCBI GI	g4006902
BLAST score	119
E value	2.0e-11
Match length	98
% identity	41
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	395292
Contig ID	58765_1.R1084
5'-most EST	g701421
Method	BLASTX
NCBI GI	g4895220
BLAST score	375
E value	6.0e-36
Match length	134
% identity	38
NCBI Description	(AC007660) unknown protein [Arabidopsis thaliana]

Seq. No.	395293
Contig ID	58766_1.R1084
5'-most EST	g426539

Seq. No.	395294
Contig ID	58768_1.R1084
5'-most EST	g431801
Method	BLASTX
NCBI GI	g5001734
BLAST score	349
E value	8.0e-33
Match length	100
% identity	64
NCBI Description	(AF129511) very-long-chain fatty acid condensing enzyme CUT1 [Arabidopsis thaliana]

Seq. No.	395295
Contig ID	58780_1.R1084
5'-most EST	g426552

Seq. No.	395296
Contig ID	58827_1.R1084
5'-most EST	g426596

Seq. No.	395297
Contig ID	58833_1.R1084
5'-most EST	g426607

Seq. No.	395298
Contig ID	58838_1.R1084
5'-most EST	g4880234

Seq. No.	395299
Contig ID	58842_1.R1084
5'-most EST	g426617
Method	BLASTX
NCBI GI	g3522958

BLAST score 100
E value 1.0e-12
Match length 159
% identity 38
NCBI Description (AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 395300
Contig ID 58845_1.R1084
5'-most EST g426621
Method BLASTX
NCBI GI g2739309
BLAST score 266
E value 4.0e-34
Match length 143
% identity 32
NCBI Description (Y15990) P-glycoprotein-like protein [Arabidopsis thaliana]

Seq. No. 395301
Contig ID 58853_1.R1084
5'-most EST g700308
Method BLASTX
NCBI GI g3953471
BLAST score 139
E value 8.0e-08
Match length 183
% identity 31
NCBI Description (AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No. 395302
Contig ID 58863_1.R1084
5'-most EST g426643

Seq. No. 395303
Contig ID 58870_1.R1084
5'-most EST g426650

Seq. No. 395304
Contig ID 58875_1.R1084
5'-most EST g3768279
Method BLASTX
NCBI GI g2244899
BLAST score 305
E value 1.0e-41
Match length 169
% identity 54
NCBI Description (Z97338) UFD1 like protein [Arabidopsis thaliana]

Seq. No. 395305
Contig ID 58920_1.R1084
5'-most EST g425852
Method BLASTX
NCBI GI g4581156
BLAST score 378
E value 7.0e-46
Match length 183
% identity 53
NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No. 395306
Contig ID 58983_1.R1084
5'-most EST g425918

Seq. No. 395307
Contig ID 58986_1.R1084
5'-most EST g2800447

Seq. No. 395308
Contig ID 58986_2.R1084
5'-most EST g425921

Seq. No. 395309
Contig ID 58987_1.R1084
5'-most EST g425922
Method BLASTX
NCBI GI g1052973
BLAST score 271
E value 1.0e-23
Match length 62
% identity 87
NCBI Description (U37838) fructokinase [Beta vulgaris]

Seq. No. 395310
Contig ID 59113_1.R1084
5'-most EST g702763

Seq. No. 395311
Contig ID 59125_1.R1084
5'-most EST g4968614

Seq. No. 395312
Contig ID 59129_1.R1084
5'-most EST g2311400

Seq. No. 395313
Contig ID 59130_1.R1084
5'-most EST g3760972
Method BLASTX
NCBI GI g567893
BLAST score 325
E value 7.0e-30
Match length 120
% identity 66
NCBI Description (L37382) beta-galactosidase-complementation protein [Cloning vector]

Seq. No. 395314
Contig ID 59160_1.R1084
5'-most EST g3761009
Method BLASTX
NCBI GI g3402817
BLAST score 153
E value 3.0e-15
Match length 85
% identity 49

NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]
Seq. No.	395315
Contig ID	59161_1.R1084
5'-most EST	g426731
Seq. No.	395316
Contig ID	59184_1.R1084
5'-most EST	g2311081
Method	BLASTX
NCBI GI	g1084415
BLAST score	307
E value	5.0e-28
Match length	98
% identity	59
NCBI Description	RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_ (D26182) RNA-binding glycine rich protein (RGP-2) [Nicotiana sylvestris]
Seq. No.	395317
Contig ID	59186_1.R1084
5'-most EST	g426756
Seq. No.	395318
Contig ID	59205_1.R1084
5'-most EST	g5455331
Seq. No.	395319
Contig ID	59210_1.R1084
5'-most EST	g426780
Seq. No.	395320
Contig ID	59233_1.R1084
5'-most EST	g2442334
Method	BLASTX
NCBI GI	g3142297
BLAST score	349
E value	2.0e-35
Match length	180
% identity	48
NCBI Description	(AC002411) Contains similarity to serine/threonine protein phosphatase gb_X83099 from S. cerevisiae. [Arabidopsis thaliana]
Seq. No.	395321
Contig ID	59234_1.R1084
5'-most EST	g426807
Method	BLASTN
NCBI GI	g2351071
BLAST score	34
E value	2.0e-09
Match length	74
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence
Seq. No.	395322

Contig ID 59244_1.R1084
5'-most EST g426817

Seq. No. 395323
Contig ID 59252_1.R1084
5'-most EST g2312432
Method BLASTX
NCBI GI g2982942
BLAST score 519
E value 1.0e-52
Match length 205
% identity 54
NCBI Description (AE000679) GMP synthase [Aquifex aeolicus]

Seq. No. 395324
Contig ID 59267_1.R1084
5'-most EST g2797470
Method BLASTX
NCBI GI g1946372
BLAST score 159
E value 1.0e-10
Match length 62
% identity 52
NCBI Description (U93215) yeast hypothetical protein YDB1_SCHPO isolog [Arabidopsis thaliana]

Seq. No. 395325
Contig ID 59283_1.R1084
5'-most EST g426854

Seq. No. 395326
Contig ID 59285_1.R1084
5'-most EST g426856

Seq. No. 395327
Contig ID 59306_1.R1084
5'-most EST g3763306
Method BLASTX
NCBI GI g5706504
BLAST score 254
E value 1.0e-21
Match length 58
% identity 64
NCBI Description (AL109739) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 395328
Contig ID 59323_1.R1084
5'-most EST g426899

Seq. No. 395329
Contig ID 59327_1.R1084
5'-most EST g2311176
Method BLASTX
NCBI GI g4406775
BLAST score 160
E value 9.0e-11
Match length 69

% identity 45
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 395330
Contig ID 59345_1.R1084
5'-most EST g426923

Seq. No. 395331
Contig ID 59369_1.R1084
5'-most EST g2799615
Method BLASTN
NCBI GI g1041814
BLAST score 199
E value 1.0e-108
Match length 305
% identity 96
NCBI Description Oryza sativa putative lipid transfer protein (Ltp-2) gene, complete cds

Seq. No. 395332
Contig ID 59378_1.R1084
5'-most EST g2312088
Method BLASTX
NCBI GI g2499945
BLAST score 234
E value 1.0e-19
Match length 80
% identity 57
NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) [INCLUDES: OROTATE PHOSPHORIBOSYLTRANSFERASE (OPRTASE); OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (OMPDECASE)] >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No. 395333
Contig ID 59386_1.R1084
5'-most EST g426965

Seq. No. 395334
Contig ID 59388_1.R1084
5'-most EST g702230
Method BLASTX
NCBI GI g4512651
BLAST score 472
E value 2.0e-47
Match length 174
% identity 51
NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No. 395335
Contig ID 59392_1.R1084
5'-most EST g5002782
Method BLASTX
NCBI GI g4874264

BLAST score	335
E value	3.0e-31
Match length	109
% identity	68
NCBI Description	(AC007354) Similar to gb_U54559 eIF3-p40 subunit from Homo sapiens and is a member of the PF_01398 Mov34 family. ESTs gb_N96623 and gb_N07519 come from this gene. [Arabidopsis thaliana]

Seq. No.	395336
Contig ID	59409_1.R1084
5'-most EST	g427266

Seq. No.	395337
Contig ID	59410_1.R1084
5'-most EST	g3760332
Method	BLASTX
NCBI GI	g2499945
BLAST score	491
E value	3.0e-51
Match length	178
% identity	65
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) [INCLUDES: OROTATE PHOSPHORIBOSYLTRANSFERASE (OPRTASE); OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (OMPDECASE)] >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No.	395338
Contig ID	59411_1.R1084
5'-most EST	g3758993

Seq. No.	395339
Contig ID	59415_1.R1084
5'-most EST	g569857
Method	BLASTX
NCBI GI	g4091117
BLAST score	470
E value	5.0e-47
Match length	142
% identity	64
NCBI Description	(AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No.	395340
Contig ID	59429_1.R1084
5'-most EST	g427866

Seq. No.	395341
Contig ID	59432_1.R1084
5'-most EST	g2428923
Method	BLASTX
NCBI GI	g1351365
BLAST score	178
E value	1.0e-12
Match length	56

% identity	57
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN (CR6) >gi_2130002_pir__S68969 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) - potato >gi_633683_emb_CAA57768_ (X82325) cytochrome c reductase subunit [Solanum tuberosum]

Seq. No.	395342
Contig ID	59435_1.R1084
5'-most EST	g2800605

Seq. No.	395343
Contig ID	59443_1.R1084
5'-most EST	g3766812

Seq. No.	395344
Contig ID	59447_1.R1084
5'-most EST	g427033

Seq. No.	395345
Contig ID	59454_1.R1084
5'-most EST	g427039
Method	BLASTX
NCBI GI	g3341685
BLAST score	351
E value	5.0e-33
Match length	99
% identity	69
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	395346
Contig ID	59473_1.R1084
5'-most EST	g427057
Method	BLASTX
NCBI GI	g2253442
BLAST score	170
E value	9.0e-12
Match length	48
% identity	58
NCBI Description	(AF007784) LTCOR11 [Lavatera thuringiaca]

Seq. No.	395347
Contig ID	59478_1.R1084
5'-most EST	g427084
Method	BLASTX
NCBI GI	g3088573
BLAST score	208
E value	2.0e-16
Match length	71
% identity	54
NCBI Description	(AF059530) protein arginine N-methyltransferase 3 [Rattus norvegicus]

Seq. No.	395348
Contig ID	59484_1.R1084
5'-most EST	g427068
Method	BLASTX
NCBI GI	g1946355

BLAST score	265
E value	2.0e-26
Match length	134
% identity	42
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	395349
Contig ID	59493_1.R1084
5'-most EST	g2442246
Method	BLASTX
NCBI GI	g5453930
BLAST score	247
E value	4.0e-25
Match length	111
% identity	46
NCBI Description	polymerase (RNA) II (DNA directed) polypeptide I (14.5kD) >gi_548702_sp_P36954_RPB9_HUMAN DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE (RPB9) (RPB14.5) >gi_543001_pir__S41621 DNA-directed RNA polymerase (EC 2.7.7.6) II 14.5K chain - human >gi_397150_emb_CAA80649_ (Z23102) RNA Polymerase II subunit 14.5 kD [Homo sapiens] >gi_1905901 (AD001527) HUMAN DNA-DIRECTED RNA POLYMERASE II 14.5 KD SUBUNIT [Homo sapiens]

Seq. No.	395350
Contig ID	59498_1.R1084
5'-most EST	g427082

Seq. No.	395351
Contig ID	59520_1.R1084
5'-most EST	g427103

Seq. No.	395352
Contig ID	59522_1.R1084
5'-most EST	g427105

Seq. No.	395353
Contig ID	59527_1.R1084
5'-most EST	g2312666
Method	BLASTX
NCBI GI	g3850579
BLAST score	186
E value	7.0e-14
Match length	59
% identity	58
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_H37281, gb_T44167, gb_T21813, gb_N38437, gb_Z26470, gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373, gb_Z34678 an

Seq. No.	395354
Contig ID	59529_1.R1084
5'-most EST	g2311932
Method	BLASTX

NCBI GI g4249388
BLAST score 356
E value 2.0e-54
Match length 187
% identity 58
NCBI Description (AC005966) Similar to gb_AF025438 Opa-interacting protein (OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 395355
Contig ID 59530_1.R1084
5'-most EST g2310453
Method BLASTX
NCBI GI g4490316
BLAST score 220
E value 7.0e-18
Match length 115
% identity 43
NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No. 395356
Contig ID 59545_1.R1084
5'-most EST g427307

Seq. No. 395357
Contig ID 59564_1.R1084
5'-most EST g3759048

Seq. No. 395358
Contig ID 59567_1.R1084
5'-most EST g427150

Seq. No. 395359
Contig ID 59571_1.R1084
5'-most EST g427154

Seq. No. 395360
Contig ID 59584_1.R1084
5'-most EST g568076
Method BLASTX
NCBI GI g3738230
BLAST score 259
E value 1.0e-22
Match length 67
% identity 67
NCBI Description (AB007790) DREB2A [Arabidopsis thaliana] >gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis thaliana]

Seq. No. 395361
Contig ID 59590_1.R1084
5'-most EST g427209

Seq. No. 395362
Contig ID 59611_1.R1084
5'-most EST g427194

Seq. No. 395363

Contig ID 59615_1.R1084
5'-most EST g2798140
Method BLASTX
NCBI GI g130172
BLAST score 489
E value 1.0e-67
Match length 147
% identity 79
NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH PHOSPHORYLASE L) >gi_168276 (M64362) starch phosphorylase [Ipomoea batatas]

Seq. No. 395364
Contig ID 59622_1.R1084
5'-most EST g3759842

Seq. No. 395365
Contig ID 59631_1.R1084
5'-most EST g427229

Seq. No. 395366
Contig ID 59634_1.R1084
5'-most EST g427217
Method BLASTX
NCBI GI g4883609
BLAST score 114
E value 4.0e-09
Match length 85
% identity 27
NCBI Description (AC006922) unknown protein [Arabidopsis thaliana]

Seq. No. 395367
Contig ID 59638_1.R1084
5'-most EST g2310322
Method BLASTX
NCBI GI g5834248
BLAST score 277
E value 3.0e-24
Match length 85
% identity 65
NCBI Description (AF175124) SINAH1 protein [Gossypium hirsutum]

Seq. No. 395368
Contig ID 59651_1.R1084
5'-most EST g2442461

Seq. No. 395369
Contig ID 59652_1.R1084
5'-most EST g2310597
Method BLASTX
NCBI GI g3128177
BLAST score 295
E value 1.0e-26
Match length 106
% identity 54
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	395370
Contig ID	59662_1.R1084
5'-most EST	g2311464
Method	BLASTX
NCBI GI	g2245136
BLAST score	339
E value	8.0e-32
Match length	95
% identity	66
NCBI Description	(Z97344) trehalose-6-phosphate synthase like protein [Arabidopsis thaliana]

Seq. No.	395371
Contig ID	59671_1.R1084
5'-most EST	g3759829

Seq. No.	395372
Contig ID	59673_1.R1084
5'-most EST	g2443145

Seq. No.	395373
Contig ID	59677_1.R1084
5'-most EST	g2312152

Seq. No.	395374
Contig ID	59683_1.R1084
5'-most EST	g5039043
Method	BLASTX
NCBI GI	g2864610
BLAST score	148
E value	4.0e-09
Match length	67
% identity	40
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049336_emb_CAA22561.1_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	395375
Contig ID	59696_1.R1084
5'-most EST	g2312822
Method	BLASTX
NCBI GI	g3128177
BLAST score	326
E value	6.0e-30
Match length	135
% identity	50
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	395376
Contig ID	59728_1.R1084
5'-most EST	g2428306
Method	BLASTX
NCBI GI	g5230841
BLAST score	331
E value	7.0e-31
Match length	91
% identity	71

NCBI Description (AF112538) actin [Malva pusilla]

Seq. No. 395377
Contig ID 59729_1.R1084
5'-most EST g3759089
Method BLASTX
NCBI GI g3608140
BLAST score 184
E value 4.0e-13
Match length 147
% identity 37
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 395378
Contig ID 59739_1.R1084
5'-most EST g427353

Seq. No. 395379
Contig ID 59747_1.R1084
5'-most EST g431822

Seq. No. 395380
Contig ID 59801_1.R1084
5'-most EST g427419

Seq. No. 395381
Contig ID 59811_1.R1084
5'-most EST g571555
Method BLASTN
NCBI GI g6041757
BLAST score 37
E value 4.0e-11
Match length 45
% identity 96
NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence

Seq. No. 395382
Contig ID 59821_1.R1084
5'-most EST g427440

Seq. No. 395383
Contig ID 59833_1.R1084
5'-most EST g5771050
Method BLASTX
NCBI GI g3738328
BLAST score 249
E value 6.0e-21
Match length 67
% identity 66
NCBI Description (AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 395384
Contig ID 59838_1.R1084
5'-most EST g2280545

Seq. No.	395385
Contig ID	59839_1.R1084
5'-most EST	g4968637
Method	BLASTX
NCBI GI	g2288887
BLAST score	555
E value	8.0e-57
Match length	168
% identity	65
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803.1_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	395386
Contig ID	59854_1.R1084
5'-most EST	g2310121

Seq. No.	395387
Contig ID	59891_1.R1084
5'-most EST	g5005513

Seq. No.	395388
Contig ID	59909_1.R1084
5'-most EST	g427560
Method	BLASTX
NCBI GI	g2854117
BLAST score	162
E value	4.0e-11
Match length	42
% identity	62
NCBI Description	(AF045453) protein kinase YakA [Dictyostelium discoideum]

Seq. No.	395389
Contig ID	59920_1.R1084
5'-most EST	g4879123

Seq. No.	395390
Contig ID	59922_1.R1084
5'-most EST	g3107500

Seq. No.	395391
Contig ID	59926_1.R1084
5'-most EST	g2312272
Method	BLASTX
NCBI GI	g4884932
BLAST score	246
E value	9.0e-21
Match length	61
% identity	74
NCBI Description	(AF141659) AtHVA22a [Arabidopsis thaliana] >gi_4884944_gb_AAD31885.1_AF141977_1 (AF141977) AtHVA22a [Arabidopsis thaliana]

Seq. No.	395392
Contig ID	59937_1.R1084

5'-most EST	g5900745
Seq. No.	395393
Contig ID	59953_1.R1084
5'-most EST	g427585
Seq. No.	395394
Contig ID	59956_1.R1084
5'-most EST	g427589
Seq. No.	395395
Contig ID	59964_1.R1084
5'-most EST	g427598
Seq. No.	395396
Contig ID	59965_1.R1084
5'-most EST	g427599
Method	BLASTX
NCBI GI	g2827141
BLAST score	355
E value	1.0e-33
Match length	147
% identity	53
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4914447_emb_CAB43650.1_ (AL050351) cellulose synthase catalytic subunit (Ath-A) [Arabidopsis thaliana]
Seq. No.	395397
Contig ID	59970_1.R1084
5'-most EST	g427604
Seq. No.	395398
Contig ID	59974_1.R1084
5'-most EST	g427608
Method	BLASTX
NCBI GI	g1708463
BLAST score	460
E value	1.0e-55
Match length	205
% identity	54
NCBI Description	IAA-AMINO ACID HYDROLASE >gi_887785 (U23794) ILR1 [Arabidopsis thaliana]
Seq. No.	395399
Contig ID	59995_1.R1084
5'-most EST	g427630
Seq. No.	395400
Contig ID	60003_1.R1084
5'-most EST	g427638
Seq. No.	395401
Contig ID	60009_1.R1084
5'-most EST	g427689
Seq. No.	395402

Contig ID	60010_1.R1084
5'-most EST	g427645
Method	BLASTX
NCBI GI	g2262173
BLAST score	480
E value	3.0e-48
Match length	130
% identity	73
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	395403
Contig ID	60012_1.R1084
5'-most EST	g427646
Method	BLASTX
NCBI GI	g2146740
BLAST score	230
E value	7.0e-36
Match length	135
% identity	63
NCBI Description	inner mitochondrial membrane protein - Arabidopsis thaliana >gi_603056 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]

Seq. No.	395404
Contig ID	60013_1.R1084
5'-most EST	g427647

Seq. No.	395405
Contig ID	60022_1.R1084
5'-most EST	g5771188
Method	BLASTN
NCBI GI	g5803242
BLAST score	776
E value	0.0e+00
Match length	807
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	395406
Contig ID	60028_1.R1084
5'-most EST	g427662

Seq. No.	395407
Contig ID	60029_1.R1084
5'-most EST	g427663
Method	BLASTX
NCBI GI	g5882747
BLAST score	277
E value	2.0e-42
Match length	154
% identity	57
NCBI Description	(AC008263) Similar to gb_AF049930 PGP237-11 from Petunia x hybrida and contains a PF_00097 Zinc (RING) finger domain. [Arabidopsis thaliana]

Seq. No. 395408

Contig ID 60031_1.R1084
5'-most EST g427665
Method BLASTX
NCBI GI g2335100
BLAST score 697
E value 2.0e-73
Match length 176
% identity 72
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 395409
Contig ID 60036_1.R1084
5'-most EST g3767064
Method BLASTX
NCBI GI g629846
BLAST score 223
E value 5.0e-18
Match length 54
% identity 80
NCBI Description initiator-binding protein - maize >gi_483444_emb_CAA55693_ (X79086) initiator-binding protein [Zea mays]

Seq. No. 395410
Contig ID 60039_1.R1084
5'-most EST g427674

Seq. No. 395411
Contig ID 60045_1.R1084
5'-most EST g2428961
Method BLASTX
NCBI GI g4388730
BLAST score 211
E value 1.0e-16
Match length 59
% identity 71
NCBI Description (AC006413) hypothetical protein [Arabidopsis thaliana]

Seq. No. 395412
Contig ID 60062_1.R1084
5'-most EST g2442594
Method BLASTX
NCBI GI g3036801
BLAST score 233
E value 9.0e-35
Match length 114
% identity 59
NCBI Description (AL022373) putative ascorbate peroxidase [Arabidopsis thaliana] >gi_3805863_emb_CAA21483.1_ (AL031986) putative ascorbate peroxidase [Arabidopsis thaliana]

Seq. No. 395413
Contig ID 60074_1.R1084
5'-most EST g427709
Method BLASTX
NCBI GI g2981015
BLAST score 159
E value 8.0e-15

Match length 203
% identity 13
NCBI Description (AF041456) tectonin II [Physarum polycephalum]

Seq. No. 395414
Contig ID 60081_1.R1084
5'-most EST g2443187

Seq. No. 395415
Contig ID 60087_1.R1084
5'-most EST g2428972

Seq. No. 395416
Contig ID 60095_1.R1084
5'-most EST g427731
Method BLASTX
NCBI GI g4850271
BLAST score 341
E value 1.0e-31
Match length 90
% identity 78
NCBI Description (AJ238244) putative high affinity sulfate transporter [Aegilops tauschii]

Seq. No. 395417
Contig ID 60099_1.R1084
5'-most EST g3767974

Seq. No. 395418
Contig ID 60109_1.R1084
5'-most EST g3767654

Seq. No. 395419
Contig ID 60111_1.R1084
5'-most EST g427746
Method BLASTX
NCBI GI g4262224
BLAST score 203
E value 2.0e-20
Match length 112
% identity 48
NCBI Description (AC006200) putative amino acid or GABA permease [Arabidopsis thaliana]

Seq. No. 395420
Contig ID 60121_1.R1084
5'-most EST g2275877
Method BLASTX
NCBI GI g4835770
BLAST score 264
E value 5.0e-23
Match length 91
% identity 56
NCBI Description (AC007202) EST gb_F19962 comes from this gene. [Arabidopsis thaliana]

Seq. No. 395421

Contig ID 60128_1.R1084
5'-most EST g427763
Method BLASTX
NCBI GI g3183285
BLAST score 170
E value 1.0e-11
Match length 98
% identity 41
NCBI Description HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION >gi_1742787_dbj_BAA15475_ (D90813) ORF_ID:o322#7; similar to [SwissProt Accession Number Q06373] [Escherichia coli] >gi_1787999 (AE000266) orf, hypothetical protein [Escherichia coli]

Seq. No. 395422
Contig ID 60137_1.R1084
5'-most EST g431829
Method BLASTX
NCBI GI g1143511
BLAST score 812
E value 6.0e-87
Match length 156
% identity 93
NCBI Description (Z47076) Ser/Thr protein phosphatase homologous to PPX [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein phosphatase [Malus domestica]

Seq. No. 395423
Contig ID 60152_1.R1084
5'-most EST g427798

Seq. No. 395424
Contig ID 60157_1.R1084
5'-most EST g568425

Seq. No. 395425
Contig ID 60170_1.R1084
5'-most EST g3760035

Seq. No. 395426
Contig ID 60175_1.R1084
5'-most EST g2431286
Method BLASTX
NCBI GI g3372230
BLAST score 342
E value 4.0e-32
Match length 103
% identity 59
NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6 (AC005287) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana]

Seq. No. 395427
Contig ID 60182_1.R1084
5'-most EST g427821
Method BLASTX

NCBI GI g4678747
BLAST score 176
E value 1.0e-12
Match length 116
% identity 33
NCBI Description (AL049669) hypothetical protein [Homo sapiens]

Seq. No. 395428
Contig ID 60198_1.R1084
5'-most EST g427836
Method BLASTX
NCBI GI g2827637
BLAST score 221
E value 8.0e-18
Match length 84
% identity 54
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 395429
Contig ID 60213_1.R1084
5'-most EST g3761552
Method BLASTX
NCBI GI g4567262
BLAST score 380
E value 3.0e-73
Match length 203
% identity 68
NCBI Description (AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No. 395430
Contig ID 60216_1.R1084
5'-most EST g454521

Seq. No. 395431
Contig ID 60234_1.R1084
5'-most EST g431833
Method BLASTX
NCBI GI g1592812
BLAST score 119
E value 1.0e-10
Match length 60
% identity 65
NCBI Description (X95957) 22 kDa polypeptide [Nicotiana tabacum]

Seq. No. 395432
Contig ID 60242_1.R1084
5'-most EST g5002988
Method BLASTX
NCBI GI g2191173
BLAST score 360
E value 6.0e-34
Match length 159
% identity 46
NCBI Description (AF007270) contains similarity to DNA polymerase III, alpha chain (SP:P47277) [Arabidopsis thaliana]

Seq. No. 395433

Contig ID	60252_1.R1084
5'-most EST	g431834
Method	BLASTX
NCBI GI	g4680190
BLAST score	178
E value	9.0e-13
Match length	77
% identity	47
NCBI Description	(AF111710) putative dnaJ-like protein [Oryza sativa subsp. indica]

Seq. No.	395434
Contig ID	60258_1.R1084
5'-most EST	g702806
Method	BLASTX
NCBI GI	g4584685
BLAST score	184
E value	6.0e-14
Match length	89
% identity	51
NCBI Description	(AJ237754) putative lectin [Hordeum vulgare]

Seq. No.	395435
Contig ID	60270_1.R1084
5'-most EST	g3767704

Seq. No.	395436
Contig ID	60278_1.R1084
5'-most EST	g431835
Method	BLASTX
NCBI GI	g4262162
BLAST score	481
E value	2.0e-48
Match length	120
% identity	72
NCBI Description	(AC005275) putative glycosylation enzyme [Arabidopsis thaliana]

Seq. No.	395437
Contig ID	60283_1.R1084
5'-most EST	g2311253

Seq. No.	395438
Contig ID	60284_1.R1084
5'-most EST	g427922
Method	BLASTX
NCBI GI	g1542941
BLAST score	465
E value	1.0e-46
Match length	115
% identity	75
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	395439
Contig ID	60300_1.R1084
5'-most EST	g427938

Seq. No. 395440
Contig ID 60318_1.R1084
5'-most EST g3106640

Seq. No. 395441
Contig ID 60332_1.R1084
5'-most EST g427972

Seq. No. 395442
Contig ID 60333_1.R1084
5'-most EST g3767712

Seq. No. 395443
Contig ID 60338_1.R1084
5'-most EST g427978
Method BLASTX
NCBI GI g4741195
BLAST score 518
E value 1.0e-101
Match length 236
% identity 77
NCBI Description (AL049746) ABC transporter-like protein [Arabidopsis thaliana]

Seq. No. 395444
Contig ID 60346_1.R1084
5'-most EST g427986

Seq. No. 395445
Contig ID 60358_1.R1084
5'-most EST g700289
Method BLASTX
NCBI GI g5932553
BLAST score 722
E value 2.0e-76
Match length 197
% identity 65
NCBI Description (AC009465) putative kinase [Arabidopsis thaliana]

Seq. No. 395446
Contig ID 60362_1.R1084
5'-most EST g3760455

Seq. No. 395447
Contig ID 60363_1.R1084
5'-most EST g2427977

Seq. No. 395448
Contig ID 60364_1.R1084
5'-most EST g4881129
Method BLASTX
NCBI GI g6056205
BLAST score 305
E value 7.0e-28
Match length 97
% identity 55
NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	395449
Contig ID	60367_1.R1084
5'-most EST	g428432
Method	BLASTX
NCBI GI	g4164398
BLAST score	202
E value	8.0e-16
Match length	120
% identity	38
NCBI Description	(AL035248) serine threonine-protein kinase [Schizosaccharomyces pombe]

Seq. No.	395450
Contig ID	60369_1.R1084
5'-most EST	g428011
Method	BLASTX
NCBI GI	g4325282
BLAST score	326
E value	3.0e-30
Match length	101
% identity	58
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	395451
Contig ID	60373_1.R1084
5'-most EST	g2310713

Seq. No.	395452
Contig ID	60374_1.R1084
5'-most EST	g428312

Seq. No.	395453
Contig ID	60377_1.R1084
5'-most EST	g428020

Seq. No.	395454
Contig ID	60382_1.R1084
5'-most EST	g428903
Method	BLASTX
NCBI GI	g2252840
BLAST score	341
E value	9.0e-32
Match length	119
% identity	55
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] >gi_6049882_gb_AAF02797.1_AF195115_17 (AF195115) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	395455
Contig ID	60388_1.R1084
5'-most EST	g428642
Method	BLASTX

NCBI GI g3021270
BLAST score 268
E value 1.0e-23
Match length 88
% identity 64
NCBI Description (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]

Seq. No. 395456
Contig ID 60393_1.R1084
5'-most EST g2428544

Seq. No. 395457
Contig ID 60394_1.R1084
5'-most EST g2428067

Seq. No. 395458
Contig ID 60397_1.R1084
5'-most EST g568263

Seq. No. 395459
Contig ID 60403_1.R1084
5'-most EST g2442748
Method BLASTX
NCBI GI g4432814
BLAST score 288
E value 1.0e-25
Match length 155
% identity 39
NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]

Seq. No. 395460
Contig ID 60412_1.R1084
5'-most EST g428056
Method BLASTN
NCBI GI g662352
BLAST score 39
E value 2.0e-12
Match length 51
% identity 94
NCBI Description Avena sativa thaumatin-like pathogenesis-related protein (rastl-4) mRNA, complete cds

Seq. No. 395461
Contig ID 60415_1.R1084
5'-most EST g428059
Method BLASTX
NCBI GI g4056552
BLAST score 321
E value 2.0e-30
Match length 102
% identity 62
NCBI Description (AL034583) putative nucleotide binding protein [Schizosaccharomyces pombe]

Seq. No. 395462
Contig ID 60419_1.R1084

5'-most EST	g568165
Method	BLASTX
NCBI GI	g2129636
BLAST score	236
E value	2.0e-21
Match length	156
% identity	42
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	395463
Contig ID	60422_1.R1084
5'-most EST	g568226

Seq. No.	395464
Contig ID	60443_1.R1084
5'-most EST	g428093
Method	BLASTX
NCBI GI	g3413706
BLAST score	193
E value	2.0e-28
Match length	110
% identity	59
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395465
Contig ID	60451_1.R1084
5'-most EST	g5003054

Seq. No.	395466
Contig ID	60459_1.R1084
5'-most EST	g428105
Method	BLASTX
NCBI GI	g6056372
BLAST score	250
E value	2.0e-21
Match length	120
% identity	43
NCBI Description	(AC009894) Very similar to receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	395467
Contig ID	60477_1.R1084
5'-most EST	g428123
Method	BLASTX
NCBI GI	g4760700
BLAST score	237
E value	5.0e-23
Match length	90
% identity	67
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]

Seq. No.	395468
Contig ID	60500_1.R1084
5'-most EST	g4714524

Seq. No. 395469

Contig ID	60505_1.R1084
5'-most EST	g3767753

Seq. No.	395470
Contig ID	60506_1.R1084
5'-most EST	g4881088
Method	BLASTX
NCBI GI	g1546692
BLAST score	186
E value	7.0e-14
Match length	72
% identity	46
NCBI Description	(X98805) peroxidase ATP19a [Arabidopsis thaliana]

Seq. No.	395471
Contig ID	60508_1.R1084
5'-most EST	g4281555
Method	BLASTX
NCBI GI	g4587521
BLAST score	239
E value	4.0e-20
Match length	75
% identity	61
NCBI Description	(AC007060) Identical to gb_D88748 AR411 gene from Arabidopsis thaliana. EST gb_T20672 comes from this gene

Seq. No.	395472
Contig ID	60509_1.R1084
5'-most EST	g4282836

Seq. No.	395473
Contig ID	60512_1.R1084
5'-most EST	g4281559
Method	BLASTX
NCBI GI	g675505
BLAST score	181
E value	2.0e-13
Match length	67
% identity	55
NCBI Description	(L39893) cleavage stimulation factor [Caenorhabditis elegans]

Seq. No.	395474
Contig ID	60538_1.R1084
5'-most EST	g4281885

Seq. No.	395475
Contig ID	60543_1.R1084
5'-most EST	g4281990
Method	BLASTN
NCBI GI	g2586128
BLAST score	110
E value	7.0e-55
Match length	205
% identity	93
NCBI Description	Zea mays b-keto acyl reductase (glossy8) mRNA, complete cds

Seq. No.	395476
Contig ID	60552_1.R1084
5'-most EST	g2431261
Seq. No.	395477
Contig ID	60567_1.R1084
5'-most EST	g428215
Seq. No.	395478
Contig ID	60601_1.R1084
5'-most EST	g428249
Seq. No.	395479
Contig ID	60603_1.R1084
5'-most EST	g428251
Method	BLASTX
NCBI GI	g2494162
BLAST score	276
E value	2.0e-24
Match length	103
% identity	56
NCBI Description	HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR >gi_3879803_emb_CAA87414.1_ (Z47356) similar to DNAJ [Caenorhabditis elegans]
Seq. No.	395480
Contig ID	60609_1.R1084
5'-most EST	g569262
Seq. No.	395481
Contig ID	60617_1.R1084
5'-most EST	g428317
Seq. No.	395482
Contig ID	60628_1.R1084
5'-most EST	g2427351
Method	BLASTX
NCBI GI	g137476
BLAST score	583
E value	4.0e-60
Match length	164
% identity	74
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_82334_pir__A40814 H+-transporting ATPase (EC 3.6.1.35) proteolipid chain, vacuolar - oat >gi_166549 (M73232) H+-ATPase [Avena sativa]
Seq. No.	395483
Contig ID	60632_1.R1084
5'-most EST	g4881104
Method	BLASTX
NCBI GI	g1495768
BLAST score	406
E value	1.0e-39
Match length	140
% identity	42
NCBI Description	(Z68506) chloroplast inner envelope protein, 110 kD

(IEP110) [Pisum sativum]

Seq. No.	395484
Contig ID	60633_1.R1084
5'-most EST	g428281
Method	BLASTX
NCBI GI	g4335754
BLAST score	322
E value	8.0e-30
Match length	131
% identity	51
NCBI Description	(AC006284) putative acid phophatase (contains metallo-phosphoesterase motif, prosite: QDOC50185) [Arabidopsis thaliana]

Seq. No.	395485
Contig ID	60649_1.R1084
5'-most EST	g3061026

Seq. No.	395486
Contig ID	60650_1.R1084
5'-most EST	g428298
Method	BLASTX
NCBI GI	g169459
BLAST score	145
E value	1.0e-08
Match length	93
% identity	33
NCBI Description	(M18538) pop3 peptide [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No.	395487
Contig ID	60652_1.R1084
5'-most EST	g428300
Method	BLASTX
NCBI GI	g5734634
BLAST score	152
E value	6.0e-13
Match length	78
% identity	62
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No.	395488
Contig ID	60662_1.R1084
5'-most EST	g428310
Method	BLASTX
NCBI GI	g4490737
BLAST score	144
E value	4.0e-17
Match length	116
% identity	47
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	395489
Contig ID	60673_1.R1084
5'-most EST	g5607434

Method	BLASTN
NCBI GI	g5777612
BLAST score	86
E value	3.0e-40
Match length	145
% identity	93
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	395490
Contig ID	60674_1.R1084
5'-most EST	g428897
Method	BLASTX
NCBI GI	g3395440
BLAST score	410
E value	3.0e-40
Match length	110
% identity	65
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395491
Contig ID	60677_1.R1084
5'-most EST	g2428158
Method	BLASTX
NCBI GI	g2492504
BLAST score	965
E value	1.0e-106
Match length	214
% identity	58
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_1669660_emb_CAA70565_ (Y09396) protein of AAA family [Capsicum annuum]

Seq. No.	395492
Contig ID	60688_1.R1084
5'-most EST	g2312274
Method	BLASTX
NCBI GI	g4680697
BLAST score	286
E value	2.0e-25
Match length	93
% identity	59
NCBI Description	(AF132963) CGI-29 protein [Homo sapiens]

Seq. No.	395493
Contig ID	60696_1.R1084
5'-most EST	g428481

Seq. No.	395494
Contig ID	60708_1.R1084
5'-most EST	g2310075

Seq. No.	395495
Contig ID	60715_1.R1084
5'-most EST	g454540

Seq. No.	395496
Contig ID	60716_1.R1084

5'-most EST	g428364
Method	BLASTX
NCBI GI	g2642435
BLAST score	263
E value	1.0e-32
Match length	91
% identity	85
NCBI Description	(AC002391) MYB-related protein [Arabidopsis thaliana]

Seq. No.	395497
Contig ID	60720_1.R1084
5'-most EST	g428369
Method	BLASTX
NCBI GI	g1170088
BLAST score	188
E value	3.0e-14
Match length	81
% identity	47
NCBI Description	GLUTATHIONE S-TRANSFERASE APIC (GST CLASS-PHI) >gi_676880_dbj_BAA06150_ (D29680) The expression is induced by aluminium treatment and Pi starvation. [Nicotiana tabacum] >gi_1094818_prf__2106387B Al-induced protein [Nicotiana tabacum]

Seq. No.	395498
Contig ID	60734_1.R1084
5'-most EST	g701889

Seq. No.	395499
Contig ID	60737_1.R1084
5'-most EST	g428386

Seq. No.	395500
Contig ID	60747_1.R1084
5'-most EST	g428396

Seq. No.	395501
Contig ID	60750_1.R1084
5'-most EST	g428399
Method	BLASTX
NCBI GI	g134190
BLAST score	358
E value	5.0e-34
Match length	114
% identity	61
NCBI Description	SALT-STRESS INDUCED PROTEIN (SALT PROTEIN) >gi_82509_pir__JQ0983 SalT protein precursor - rice >gi_480562_pir__S37043 salT protein - rice >gi_256638_bbs_115371 (S45168) 15 kda organ-specific salt-induced protein=salT [Oryza sativa=rice, var. Indica, cv Taichung native 1, roots, Peptide, 145 aa] [Oryza sativa] >gi_397616_emb_CAA81059_ (Z25811) salT [Oryza sativa]

Seq. No.	395502
Contig ID	60754_1.R1084
5'-most EST	g428403

Seq. No.	395503
Contig ID	60757_1.R1084
5'-most EST	g428406

Seq. No.	395504
Contig ID	60776_1.R1084
5'-most EST	g2428172
Method	BLASTX
NCBI GI	g3123270
BLAST score	314
E value	1.0e-58
Match length	130
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620) >gi_2463335_emb_CAA75242_ (Y15009) ribosomal protein S4 [Oryza sativa]

Seq. No.	395505
Contig ID	60785_1.R1084
5'-most EST	g428434
Method	BLASTX
NCBI GI	g6091756
BLAST score	132
E value	1.0e-10
Match length	57
% identity	52
NCBI Description	(AC009327) putative peroxidase [Arabidopsis thaliana]

Seq. No.	395506
Contig ID	60787_1.R1084
5'-most EST	g3061097

Seq. No.	395507
Contig ID	60790_1.R1084
5'-most EST	g428439
Method	BLASTX
NCBI GI	g5902181
BLAST score	166
E value	1.0e-12
Match length	113
% identity	46
NCBI Description	(AF005050) aspartyl aminopeptidase [Homo sapiens]

Seq. No.	395508
Contig ID	60818_1.R1084
5'-most EST	g428467

Seq. No.	395509
Contig ID	60824_1.R1084
5'-most EST	g428675
Method	BLASTX
NCBI GI	g3258569
BLAST score	423
E value	1.0e-41
Match length	117
% identity	73

NCBI Description	(U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]

Seq. No.	395510
Contig ID	60827_1.R1084
5'-most EST	g2310436
Method	BLASTX
NCBI GI	g2735841
BLAST score	529
E value	4.0e-54
Match length	128
% identity	75
NCBI Description	(AF010283) No definition line found [Sorghum bicolor]

Seq. No.	395511
Contig ID	60834_1.R1084
5'-most EST	g2310396

Seq. No.	395512
Contig ID	60839_1.R1084
5'-most EST	g428487
Method	BLASTX
NCBI GI	g2661412
BLAST score	434
E value	1.0e-42
Match length	123
% identity	66
NCBI Description	(AJ000728) MAP kinase kinase [Lycopersicon esculentum]

Seq. No.	395513
Contig ID	60845_1.R1084
5'-most EST	g428493
Method	BLASTX
NCBI GI	g4530611
BLAST score	552
E value	2.0e-94
Match length	176
% identity	97
NCBI Description	(AF134552) serine/threonine protein phosphatase PP2A-2 catalytic subunit [Oryza sativa subsp. indica]

Seq. No.	395514
Contig ID	60849_1.R1084
5'-most EST	g700611

Seq. No.	395515
Contig ID	60878_1.R1084
5'-most EST	g428526
Method	BLASTX
NCBI GI	g4204313
BLAST score	215
E value	3.0e-17
Match length	57
% identity	81
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	395516
Contig ID	60881_1.R1084
5'-most EST	g428529
Method	BLASTX
NCBI GI	g2129636
BLAST score	186
E value	2.0e-16
Match length	92
% identity	59
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	395517
Contig ID	60890_1.R1084
5'-most EST	g428539

Seq. No.	395518
Contig ID	60901_1.R1084
5'-most EST	g428551
Method	BLASTX
NCBI GI	g3046731
BLAST score	661
E value	3.0e-69
Match length	161
% identity	81
NCBI Description	(AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No.	395519
Contig ID	60901_2.R1084
5'-most EST	g4715389
Method	BLASTX
NCBI GI	g3046731
BLAST score	519
E value	1.0e-52
Match length	185
% identity	43
NCBI Description	(AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No.	395520
Contig ID	60907_1.R1084
5'-most EST	g428660
Method	BLASTX
NCBI GI	g6016736
BLAST score	299
E value	4.0e-45
Match length	118
% identity	81
NCBI Description	(AC009325) unknown protein [Arabidopsis thaliana]

Seq. No.	395521
Contig ID	60910_1.R1084
5'-most EST	g5004986
Method	BLASTX
NCBI GI	g4586249
BLAST score	252
E value	2.0e-21
Match length	81

% identity	64
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]

Seq. No.	395522
Contig ID	60910_2.R1084
5'-most EST	g428561

Seq. No.	395523
Contig ID	60926_1.R1084
5'-most EST	g428576

Seq. No.	395524
Contig ID	60938_1.R1084
5'-most EST	g428588
Method	BLASTX
NCBI GI	g2653285
BLAST score	410
E value	6.0e-40
Match length	159
% identity	79
NCBI Description	(AJ003025) enoyl-ACP reductase [Oryza sativa]

Seq. No.	395525
Contig ID	60942_1.R1084
5'-most EST	g3766690

Seq. No.	395526
Contig ID	60965_1.R1084
5'-most EST	g4881167
Method	BLASTX
NCBI GI	g5042446
BLAST score	198
E value	2.0e-26
Match length	101
% identity	60
NCBI Description	(AC007789) putative WRKY DNA binding protein [Oryza sativa]

Seq. No.	395527
Contig ID	60994_1.R1084
5'-most EST	g428645

Seq. No.	395528
Contig ID	61003_1.R1084
5'-most EST	g5004637

Seq. No.	395529
Contig ID	61007_1.R1084
5'-most EST	g5004742

Seq. No.	395530
Contig ID	61044_1.R1084
5'-most EST	g428696

Seq. No.	395531
Contig ID	61048_1.R1084
5'-most EST	g3768401

Method	BLASTX
NCBI GI	g4760700
BLAST score	193
E value	8.0e-15
Match length	59
% identity	61
NCBI Description	(AB024437) peroxidase 1 [Scutellaria baicalensis]

Seq. No.	395532
Contig ID	61099_1.R1084
5'-most EST	g428750

Seq. No.	395533
Contig ID	61106_1.R1084
5'-most EST	g428756
Method	BLASTX
NCBI GI	g266567
BLAST score	480
E value	4.0e-48
Match length	186
% identity	50
NCBI Description	MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi_421956_pir__S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato >gi_21493_emb_CAA46990_ (X66284) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	395534
Contig ID	61115_1.R1084
5'-most EST	g428766
Method	BLASTX
NCBI GI	g2351374
BLAST score	276
E value	2.0e-38
Match length	95
% identity	86
NCBI Description	(U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No.	395535
Contig ID	61117_1.R1084
5'-most EST	g428785

Seq. No.	395536
Contig ID	61124_1.R1084
5'-most EST	g428773

Seq. No.	395537
Contig ID	61139_1.R1084
5'-most EST	g428788

Seq. No.	395538
Contig ID	61140_1.R1084
5'-most EST	g428823
Method	BLASTX
NCBI GI	g1706958

BLAST score 221
E value 6.0e-18
Match length 54
% identity 78
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 395539
Contig ID 61149_1.R1084
5'-most EST g428798

Seq. No. 395540
Contig ID 61151_1.R1084
5'-most EST g428800
Method BLASTX
NCBI GI g1708462
BLAST score 370
E value 1.0e-35
Match length 115
% identity 60
NCBI Description IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi_902791 (U23796) ILL2 [Arabidopsis thaliana]

Seq. No. 395541
Contig ID 61182_1.R1084
5'-most EST g428946

Seq. No. 395542
Contig ID 61183_1.R1084
5'-most EST g568434
Method BLASTX
NCBI GI g2129651
BLAST score 241
E value 3.0e-20
Match length 137
% identity 43
NCBI Description myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis thaliana]

Seq. No. 395543
Contig ID 61190_1.R1084
5'-most EST g428843
Method BLASTX
NCBI GI g1170242
BLAST score 528
E value 4.0e-54
Match length 108
% identity 94
NCBI Description FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) >gi_474966_dbj_BAA05101_ (D26105) ferrochelatase [Hordeum vulgare]

Seq. No. 395544
Contig ID 61191_1.R1084
5'-most EST g4881169
Method BLASTX
NCBI GI g2626753

BLAST score 357
E value 7.0e-34
Match length 140
% identity 55
NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No. 395545
Contig ID 61205_1.R1084
5'-most EST g2427843
Method BLASTX
NCBI GI g3641863
BLAST score 177
E value 5.0e-13
Match length 41
% identity 78
NCBI Description (AJ005042) beta-galactosidase [Cicer arietinum]

Seq. No. 395546
Contig ID 61214_1.R1084
5'-most EST g4288668

Seq. No. 395547
Contig ID 61215_1.R1084
5'-most EST g3768043

Seq. No. 395548
Contig ID 61217_1.R1084
5'-most EST g4289880

Seq. No. 395549
Contig ID 61235_1.R1084
5'-most EST g2310302

Seq. No. 395550
Contig ID 61241_1.R1084
5'-most EST g3767357
Method BLASTX
NCBI GI g3785997
BLAST score 206
E value 7.0e-16
Match length 90
% identity 48
NCBI Description (AC005499) putative annexin [Arabidopsis thaliana]

Seq. No. 395551
Contig ID 61247_1.R1084
5'-most EST g4289001

Seq. No. 395552
Contig ID 61276_1.R1084
5'-most EST g3767983
Method BLASTX
NCBI GI g3402817
BLAST score 313
E value 3.0e-28
Match length 68
% identity 90

NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]
Seq. No.	395553
Contig ID	61286_1.R1084
5'-most EST	g4715343
Method	BLASTX
NCBI GI	g2632254
BLAST score	515
E value	5.0e-68
Match length	226
% identity	66
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]
Seq. No.	395554
Contig ID	61304_1.R1084
5'-most EST	g702472
Method	BLASTX
NCBI GI	g2498731
BLAST score	929
E value	1.0e-100
Match length	316
% identity	57
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.	395555
Contig ID	61337_1.R1084
5'-most EST	g428995
Method	BLASTX
NCBI GI	g2959358
BLAST score	418
E value	4.0e-41
Match length	96
% identity	88
NCBI Description	(X96758) clathrin coat assembly protein AP17 [Zea mays]
Seq. No.	395556
Contig ID	61339_1.R1084
5'-most EST	g428997
Method	BLASTX
NCBI GI	g4204793
BLAST score	308
E value	3.0e-28
Match length	121
% identity	24
NCBI Description	(U52079) P-glycoprotein [Solanum tuberosum]
Seq. No.	395557
Contig ID	61343_1.R1084
5'-most EST	g3760620
Seq. No.	395558
Contig ID	61355_1.R1084
5'-most EST	g3760738

Seq. No. 395559
Contig ID 61370_1.R1084
5'-most EST g3760898

Seq. No. 395560
Contig ID 61380_1.R1084
5'-most EST g5455494
Method BLASTX
NCBI GI g2132302
BLAST score 265
E value 1.0e-22
Match length 190
% identity 35
NCBI Description hypothetical protein YPR144c - yeast (Saccharomyces cerevisiae) >gi_1066493 (U40829) Weak similarity near C-terminus to RNA Polymerase beta subunit (Swiss Prot. accession number P11213) and CCAAT-binding transcription factor (PIR accession number A36368) [Saccharomyces cerevisiae]

Seq. No. 395561
Contig ID 61384_1.R1084
5'-most EST g3760977
Method BLASTX
NCBI GI g1708236
BLAST score 235
E value 2.0e-19
Match length 70
% identity 67
NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No. 395562
Contig ID 61387_1.R1084
5'-most EST g454504

Seq. No. 395563
Contig ID 61391_1.R1084
5'-most EST g3767614

Seq. No. 395564
Contig ID 61401_1.R1084
5'-most EST g454523
Method BLASTX
NCBI GI g4206197
BLAST score 324
E value 3.0e-30
Match length 87
% identity 35
NCBI Description (AF071527) putative pre-mRNA splicing factor [Arabidopsis thaliana]

Seq. No.	395565
Contig ID	61405_1.R1084
5'-most EST	g454527
Method	BLASTX
NCBI GI	g2160314
BLAST score	199
E value	3.0e-15
Match length	112
% identity	47
NCBI Description	(D25236) possible 1-3,1-4-beta-glucanase coding sequence [Oryza sativa]

Seq. No.	395566
Contig ID	61411_1.R1084
5'-most EST	g3767787
Method	BLASTX
NCBI GI	g3769673
BLAST score	117
E value	2.0e-10
Match length	69
% identity	40
NCBI Description	(AF095285) Tic20 [Pisum sativum]

Seq. No.	395567
Contig ID	61424_1.R1084
5'-most EST	g568153
Method	BLASTX
NCBI GI	g6013204
BLAST score	418
E value	6.0e-41
Match length	111
% identity	68
NCBI Description	(AF177989) alpha-soluble NSF attachment protein; alpha-SNAP [Arabidopsis thaliana]

Seq. No.	395568
Contig ID	61430_1.R1084
5'-most EST	g5004034
Method	BLASTN
NCBI GI	g14394
BLAST score	566
E value	0.0e+00
Match length	618
% identity	98
NCBI Description	T.aestivum mitochondrion fMet, 18S, 5S repeat unit DNA

Seq. No.	395569
Contig ID	61472_1.R1084
5'-most EST	g567992
Method	BLASTX
NCBI GI	g6093997
BLAST score	374
E value	6.0e-36
Match length	78
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L11 >gi_2570507 (AF022736) ribosomal

protein [Oryza sativa]

Seq. No.	395570
Contig ID	61476_1.R1084
5'-most EST	g6012834

Seq. No.	395571
Contig ID	61499_1.R1084
5'-most EST	g568026
Method	BLASTX
NCBI GI	g3980397
BLAST score	214
E value	5.0e-17
Match length	65
% identity	71
NCBI Description	(AC004561) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	395572
Contig ID	61515_1.R1084
5'-most EST	g3061232

Seq. No.	395573
Contig ID	61547_1.R1084
5'-most EST	g4968631
Method	BLASTX
NCBI GI	g2160166
BLAST score	144
E value	3.0e-09
Match length	63
% identity	48
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	395574
Contig ID	61577_1.R1084
5'-most EST	g4716788
Method	BLASTX
NCBI GI	g4126471
BLAST score	142
E value	6.0e-18
Match length	85
% identity	60
NCBI Description	(AB014722) rSALT-1(806) [Rattus norvegicus]

Seq. No.	395575
Contig ID	61605_1.R1084
5'-most EST	g5455394
Method	BLASTN
NCBI GI	g5852170
BLAST score	248
E value	1.0e-137
Match length	542
% identity	50
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No. 395576

Contig ID	61605_3.R1084
5'-most EST	g5851006
Method	BLASTN
NCBI GI	g6063530
BLAST score	215
E value	1.0e-117
Match length	343
% identity	96
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	395577
Contig ID	61612_1.R1084
5'-most EST	g568157

Seq. No.	395578
Contig ID	61640_1.R1084
5'-most EST	g568185

Seq. No.	395579
Contig ID	61642_1.R1084
5'-most EST	g4881041

Seq. No.	395580
Contig ID	61701_1.R1084
5'-most EST	g568248
Method	BLASTX
NCBI GI	g4588012
BLAST score	460
E value	5.0e-46
Match length	98
% identity	82
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	395581
Contig ID	61812_1.R1084
5'-most EST	g568454
Method	BLASTX
NCBI GI	g2541876
BLAST score	175
E value	7.0e-14
Match length	82
% identity	51
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	395582
Contig ID	61852_1.R1084
5'-most EST	g2309768

Seq. No.	395583
Contig ID	61858_1.R1084
5'-most EST	g568409
Method	BLASTN
NCBI GI	g6006355
BLAST score	267
E value	1.0e-148

Match length	285
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	395584
Contig ID	61861_1.R1084
5'-most EST	g5002990

Seq. No.	395585
Contig ID	61864_1.R1084
5'-most EST	g568416
Method	BLASTX
NCBI GI	g3702340
BLAST score	243
E value	1.0e-20
Match length	123
% identity	41
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395586
Contig ID	61890_1.R1084
5'-most EST	g568442

Seq. No.	395587
Contig ID	61906_1.R1084
5'-most EST	g568460
Method	BLASTX
NCBI GI	g4427003
BLAST score	273
E value	5.0e-24
Match length	76
% identity	70
NCBI Description	(AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No.	395588
Contig ID	61914_1.R1084
5'-most EST	g568470
Method	BLASTX
NCBI GI	g4106690
BLAST score	372
E value	2.0e-43
Match length	164
% identity	56
NCBI Description	(AL035065) putative urea active transporter [Schizosaccharomyces pombe]

Seq. No.	395589
Contig ID	61921_1.R1084
5'-most EST	g3767239
Method	BLASTX
NCBI GI	g1518540
BLAST score	465
E value	4.0e-81
Match length	183
% identity	91
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	395590
Contig ID	61926_1.R1084
5'-most EST	g2311171
Method	BLASTX
NCBI GI	g2244994
BLAST score	292
E value	1.0e-41
Match length	109
% identity	79
NCBI Description	(Z97341) isp4 like protein [Arabidopsis thaliana]

Seq. No.	395591
Contig ID	61938_1.R1084
5'-most EST	g568495
Method	BLASTX
NCBI GI	g4063821
BLAST score	208
E value	2.0e-16
Match length	51
% identity	82
NCBI Description	(AB015204) plastidic ATP sulfurylase [Oryza sativa]

Seq. No.	395592
Contig ID	61948_1.R1084
5'-most EST	g568505
Method	BLASTX
NCBI GI	g1669599
BLAST score	209
E value	1.0e-16
Match length	90
% identity	50
NCBI Description	(D88746) AR791 [Arabidopsis thaliana]

Seq. No.	395593
Contig ID	61952_1.R1084
5'-most EST	g568509
Method	BLASTX
NCBI GI	g4733981
BLAST score	300
E value	5.0e-35
Match length	100
% identity	77
NCBI Description	(AC007268) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	395594
Contig ID	61970_1.R1084
5'-most EST	g1854288

Seq. No.	395595
Contig ID	62000_1.R1084
5'-most EST	g572395
Method	BLASTX
NCBI GI	g2183249
BLAST score	558
E value	3.0e-57
Match length	176

% identity	65
NCBI Description	(AF002211) glutathione-S-transferase [Triticum aestivum] >gi_4185800 (AF109714) glutathione S-transferase [Triticum aestivum]

Seq. No.	395596
Contig ID	62012_1.R1084
5'-most EST	g568572

Seq. No.	395597
Contig ID	62018_1.R1084
5'-most EST	g568578

Seq. No.	395598
Contig ID	62019_1.R1084
5'-most EST	g568579

Seq. No.	395599
Contig ID	62031_1.R1084
5'-most EST	g568591

Seq. No.	395600
Contig ID	62033_1.R1084
5'-most EST	g4969366

Seq. No.	395601
Contig ID	62045_1.R1084
5'-most EST	g571983
Method	BLASTN
NCBI GI	g2407276
BLAST score	181
E value	4.0e-97
Match length	313
% identity	91
NCBI Description	Oryza sativa lipid transfer protein LPT IV mRNA, complete cds

Seq. No.	395602
Contig ID	62069_1.R1084
5'-most EST	g568630
Method	BLASTX
NCBI GI	g1945283
BLAST score	489
E value	2.0e-49
Match length	124
% identity	83
NCBI Description	(Y11351) myb factor [Oryza sativa]

Seq. No.	395603
Contig ID	62078_1.R1084
5'-most EST	g702367
Method	BLASTX
NCBI GI	g5031281
BLAST score	148
E value	3.0e-09
Match length	38
% identity	74

NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 395604
Contig ID 62089_1.R1084
5'-most EST g568651

Seq. No. 395605
Contig ID 62109_1.R1084
5'-most EST g568672
Method BLASTX
NCBI GI g5669871
BLAST score 438
E value 1.0e-51
Match length 134
% identity 84
NCBI Description (AF135014) dihydrolipoamide S-acetyltransferase [Zea mays]

Seq. No. 395606
Contig ID 62115_1.R1084
5'-most EST g568686
Method BLASTN
NCBI GI g6069643
BLAST score 35
E value 3.0e-10
Match length 43
% identity 95
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0514G12

Seq. No. 395607
Contig ID 62122_1.R1084
5'-most EST g569312

Seq. No. 395608
Contig ID 62124_1.R1084
5'-most EST g2428073
Method BLASTX
NCBI GI g3649758
BLAST score 339
E value 6.0e-37
Match length 176
% identity 52
NCBI Description (Z98547) predicted using hexExon; MAL3P3.6 (PFC0350c), T-complex protein eta subunit, len: 540 aa; Similarity to T-complex proteins, eta subunit. H.sapiens T-complex protein, eta subunit (SW:TCPH_HUMAN) BLAST Score: 1549, sum

Seq. No. 395609
Contig ID 62134_1.R1084
5'-most EST g568708
Method BLASTX
NCBI GI g5326544
BLAST score 291
E value 3.0e-26
Match length 112
% identity 53
NCBI Description (Y18055) calcium dependent protein kinase [Arachis hypogaea]

Seq. No. 395610
Contig ID 62172_1.R1084
5'-most EST g2311102

Seq. No. 395611
Contig ID 62172_2.R1084
5'-most EST g571688
Method BLASTX
NCBI GI g5733886
BLAST score 222
E value 1.0e-44
Match length 160
% identity 68
NCBI Description (AC007932) F11A17.20 [Arabidopsis thaliana]

Seq. No. 395612
Contig ID 62172_3.R1084
5'-most EST g1631762
Method BLASTX
NCBI GI g5733886
BLAST score 263
E value 3.0e-23
Match length 67
% identity 75
NCBI Description (AC007932) F11A17.20 [Arabidopsis thaliana]

Seq. No. 395613
Contig ID 62176_1.R1084
5'-most EST g4880871
Method BLASTX
NCBI GI g1155090
BLAST score 492
E value 1.0e-49
Match length 136
% identity 62
NCBI Description (X94986) beta glucosidase [Manihot esculenta]

Seq. No. 395614
Contig ID 62189_1.R1084
5'-most EST g568754

Seq. No. 395615
Contig ID 62196_1.R1084
5'-most EST g569022
Method BLASTX
NCBI GI g4588012
BLAST score 352
E value 3.0e-33
Match length 130
% identity 52
NCBI Description (AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No. 395616
Contig ID 62200_1.R1084
5'-most EST g4715072

Seq. No.	395617
Contig ID	62204_1.R1084
5'-most EST	g568947

Seq. No.	395618
Contig ID	62205_1.R1084
5'-most EST	g2309953
Method	BLASTX
NCBI GI	g4337025
BLAST score	372
E value	1.0e-35
Match length	125
% identity	56
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana] >gi_4972047_emb_CAB43915.1_ (AL078470) AIM1 protein [Arabidopsis thaliana]

Seq. No.	395619
Contig ID	62211_1.R1084
5'-most EST	g5003665
Method	BLASTX
NCBI GI	g2129944
BLAST score	368
E value	7.0e-35
Match length	85
% identity	84
NCBI Description	RNA-binding protein RZ-1 - wood tobacco >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1 [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861) RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No.	395620
Contig ID	62213_1.R1084
5'-most EST	g568780

Seq. No.	395621
Contig ID	62217_1.R1084
5'-most EST	g3761550
Method	BLASTX
NCBI GI	g3152559
BLAST score	257
E value	7.0e-22
Match length	87
% identity	57
NCBI Description	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No.	395622
Contig ID	62219_1.R1084
5'-most EST	g568787

Seq. No.	395623
Contig ID	62236_1.R1084
5'-most EST	g568804
Method	BLASTX

NCBI GI	g1402912
BLAST score	151
E value	7.0e-11
Match length	53
% identity	79
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	395624
Contig ID	62276_1.R1084
5'-most EST	g568927

Seq. No.	395625
Contig ID	62278_1.R1084
5'-most EST	g568848

Seq. No.	395626
Contig ID	62282_1.R1084
5'-most EST	g2280820

Seq. No.	395627
Contig ID	62284_1.R1084
5'-most EST	g569049

Seq. No.	395628
Contig ID	62289_1.R1084
5'-most EST	g2428690

Seq. No.	395629
Contig ID	62293_1.R1084
5'-most EST	g699877

Seq. No.	395630
Contig ID	62299_1.R1084
5'-most EST	g568869

Seq. No.	395631
Contig ID	62303_1.R1084
5'-most EST	g568873

Seq. No.	395632
Contig ID	62315_1.R1084
5'-most EST	g568904
Method	BLASTX
NCBI GI	g4580394
BLAST score	231
E value	2.0e-19
Match length	86
% identity	50
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	395633
Contig ID	62318_1.R1084
5'-most EST	g2427699

Seq. No.	395634
Contig ID	62323_1.R1084

5'-most EST	g568893
Method	BLASTX
NCBI GI	g2673918
BLAST score	337
E value	3.0e-31
Match length	101
% identity	65
NCBI Description	(AC002561) unknwon protein [Arabidopsis thaliana]

Seq. No.	395635
Contig ID	62345_1.R1084
5'-most EST	g568915
Method	BLASTX
NCBI GI	g4325324
BLAST score	574
E value	4.0e-59
Match length	119
% identity	89
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana] >gi_6041823_gb_AAF02138.1_AC009918_10 (AC009918) lysyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	395636
Contig ID	62349_1.R1084
5'-most EST	g568920

Seq. No.	395637
Contig ID	62356_1.R1084
5'-most EST	g568928

Seq. No.	395638
Contig ID	62361_1.R1084
5'-most EST	g569395
Method	BLASTX
NCBI GI	g1621268
BLAST score	235
E value	1.0e-19
Match length	63
% identity	68
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	395639
Contig ID	62362_1.R1084
5'-most EST	g568934

Seq. No.	395640
Contig ID	62366_1.R1084
5'-most EST	g568938
Method	BLASTX
NCBI GI	g3881978
BLAST score	336
E value	2.0e-31
Match length	148
% identity	48
NCBI Description	(Y11348) annexin-like protein [Medicago sativa]

Seq. No. 395641

Contig ID	62378_1.R1084
5'-most EST	g3762904
Method	BLASTX
NCBI GI	g3292832
BLAST score	208
E value	3.0e-16
Match length	82
% identity	60
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	395642
Contig ID	62381_1.R1084
5'-most EST	g2310145

Seq. No.	395643
Contig ID	62394_1.R1084
5'-most EST	g4878595

Seq. No.	395644
Contig ID	62402_1.R1084
5'-most EST	g5803390
Method	BLASTX
NCBI GI	g4314355
BLAST score	393
E value	4.0e-38
Match length	122
% identity	56
NCBI Description	(AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	395645
Contig ID	62412_1.R1084
5'-most EST	g569103
Method	BLASTX
NCBI GI	g4454480
BLAST score	285
E value	7.0e-26
Match length	75
% identity	67
NCBI Description	(AC006234) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]

Seq. No.	395646
Contig ID	62427_1.R1084
5'-most EST	g569458

Seq. No.	395647
Contig ID	62441_1.R1084
5'-most EST	g572263

Seq. No.	395648
Contig ID	62454_1.R1084
5'-most EST	g569041

Seq. No.	395649
Contig ID	62468_1.R1084
5'-most EST	g571619
Method	BLASTX

NCBI GI	g4836910
BLAST score	281
E value	4.0e-27
Match length	96
% identity	66
NCBI Description	(AC007153) 51396 [Arabidopsis thaliana]

Seq. No.	395650
Contig ID	62487_1.R1084
5'-most EST	g569065
Method	BLASTX
NCBI GI	g1707016
BLAST score	274
E value	1.0e-24
Match length	59
% identity	83
NCBI Description	(U78721) cadmium-induced protein isolog [Arabidopsis thaliana]

Seq. No.	395651
Contig ID	62555_1.R1084
5'-most EST	g569136
Method	BLASTX
NCBI GI	g4056552
BLAST score	349
E value	6.0e-33
Match length	96
% identity	68
NCBI Description	(AL034583) putative nucleotide binding protein [Schizosaccharomyces pombe]

Seq. No.	395652
Contig ID	62565_1.R1084
5'-most EST	g569146
Method	BLASTN
NCBI GI	g5257255
BLAST score	79
E value	2.0e-36
Match length	234
% identity	33
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	395653
Contig ID	62567_1.R1084
5'-most EST	g4715059
Method	BLASTX
NCBI GI	g4902476
BLAST score	238
E value	8.0e-20
Match length	72
% identity	60
NCBI Description	(AJ238802) MAP kinase [Arabidopsis thaliana]

Seq. No.	395654
Contig ID	62573_1.R1084
5'-most EST	g4969321
Method	BLASTX

NCBI GI	g2072553
BLAST score	264
E value	9.0e-23
Match length	78
% identity	65
NCBI Description	(AF001395) salT gene product [Oryza sativa]

Seq. No.	395655
Contig ID	62575_1.R1084
5'-most EST	g569336
Method	BLASTX
NCBI GI	g1143381
BLAST score	147
E value	2.0e-09
Match length	40
% identity	60
NCBI Description	(Z49063) polygalacturonase inhibitor [Actinidia deliciosa]

Seq. No.	395656
Contig ID	62577_1.R1084
5'-most EST	g569158

Seq. No.	395657
Contig ID	62580_1.R1084
5'-most EST	g3763631
Method	BLASTX
NCBI GI	g5091508
BLAST score	212
E value	1.0e-16
Match length	79
% identity	56
NCBI Description	(AB023482) ESTs C22458(C62866),C22459(C62866) correspond to a region of the predicted gene.; Similar to genomic sequence of Arabidopsis thaliana BAC F8A5, complete sequence.(AC002292) [Oryza sativa]

Seq. No.	395658
Contig ID	62585_1.R1084
5'-most EST	g569166

Seq. No.	395659
Contig ID	62594_1.R1084
5'-most EST	g701081
Method	BLASTX
NCBI GI	g5702190
BLAST score	174
E value	2.0e-12
Match length	47
% identity	66
NCBI Description	(AF106087) 4-coumarate:CoA ligase 3 [Arabidopsis thaliana] >gi_5702192_gb_AAD47195.1_AF106088_1 (AF106088) 4-coumarate:CoA ligase 3 [Arabidopsis thaliana]

Seq. No.	395660
Contig ID	62598_1.R1084
5'-most EST	g569179

Seq. No.	395661
Contig ID	62617_1.R1084
5'-most EST	g569571
Method	BLASTN
NCBI GI	g5777612
BLAST score	74
E value	3.0e-33
Match length	148
% identity	34
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	395662
Contig ID	62629_1.R1084
5'-most EST	g569210

Seq. No.	395663
Contig ID	62650_1.R1084
5'-most EST	g569244

Seq. No.	395664
Contig ID	62655_1.R1084
5'-most EST	g569253
Method	BLASTX
NCBI GI	g4678342
BLAST score	179
E value	6.0e-13
Match length	114
% identity	39
NCBI Description	(AL049659) lipase-like protein [Arabidopsis thaliana]

Seq. No.	395665
Contig ID	62664_1.R1084
5'-most EST	g569264
Method	BLASTX
NCBI GI	g2736186
BLAST score	302
E value	4.0e-27
Match length	133
% identity	36
NCBI Description	(AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No.	395666
Contig ID	62669_1.R1084
5'-most EST	g569269

Seq. No.	395667
Contig ID	62674_1.R1084
5'-most EST	g2310561

Seq. No.	395668
Contig ID	62679_1.R1084
5'-most EST	g700770
Method	BLASTX
NCBI GI	g2982783
BLAST score	181
E value	9.0e-16
Match length	135

% identity	37
NCBI Description	(AE000670) 3-hydroxyisobutyrate dehydrogenase [Aquifex aeolicus]

Seq. No.	395669
Contig ID	62692_1.R1084
5'-most EST	g569292

Seq. No.	395670
Contig ID	62693_1.R1084
5'-most EST	g569293

Seq. No.	395671
Contig ID	62696_1.R1084
5'-most EST	g569296
Method	BLASTX
NCBI GI	g3540194
BLAST score	320
E value	1.0e-46
Match length	128
% identity	77
NCBI Description	(AC004260) AtVPS45p [Arabidopsis thaliana]

Seq. No.	395672
Contig ID	62716_1.R1084
5'-most EST	g569316

Seq. No.	395673
Contig ID	62726_1.R1084
5'-most EST	g2428626
Method	BLASTX
NCBI GI	g3482929
BLAST score	215
E value	4.0e-17
Match length	63
% identity	65
NCBI Description	(AC003970) Putative transcription factor [Arabidopsis thaliana]

Seq. No.	395674
Contig ID	62728_1.R1084
5'-most EST	g5667610
Method	BLASTX
NCBI GI	g5441889
BLAST score	291
E value	3.0e-51
Match length	164
% identity	61
NCBI Description	(AP000367) Similar to SEC7 protein, Saccharomyces cerevisiae, PIR2:S49764; Contains Immunoglobulins and major histocompatibility complex proteins signature. (AL022604) [Oryza sativa]

Seq. No.	395675
Contig ID	62731_1.R1084
5'-most EST	g4878638
Method	BLASTX

NCBI GI g2224915
BLAST score 383
E value 8.0e-37
Match length 112
% identity 61
NCBI Description (U95968) beta-expansin [Oryza sativa]

Seq. No. 395676
Contig ID 62738_1.R1084
5'-most EST g569338
Method BLASTX
NCBI GI g2132930
BLAST score 294
E value 1.0e-26
Match length 86
% identity 58
NCBI Description probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae) >gi_1420591_emb_CAA99484_ (Z75170) ORF YOR262w [Saccharomyces cerevisiae]

Seq. No. 395677
Contig ID 62742_1.R1084
5'-most EST g569342

Seq. No. 395678
Contig ID 62753_1.R1084
5'-most EST g3061106

Seq. No. 395679
Contig ID 62765_1.R1084
5'-most EST g569370

Seq. No. 395680
Contig ID 62769_1.R1084
5'-most EST g569561
Method BLASTX
NCBI GI g4006905
BLAST score 649
E value 4.0e-68
Match length 140
% identity 89
NCBI Description (Z99708) ATPase-like protein [Arabidopsis thaliana]

Seq. No. 395681
Contig ID 62780_1.R1084
5'-most EST g569387

Seq. No. 395682
Contig ID 62810_1.R1084
5'-most EST g569417
Method BLASTX
NCBI GI g1076748
BLAST score 171
E value 5.0e-12
Match length 91
% identity 46
NCBI Description major intrinsic protein - rice >gi_440869_dbj_BAA04257_

(D17443) major intrinsic protein [Oryza sativa]

Seq. No.	395683
Contig ID	62815_1.R1084
5'-most EST	g571632

Seq. No.	395684
Contig ID	62830_1.R1084
5'-most EST	g569460

Seq. No.	395685
Contig ID	62835_1.R1084
5'-most EST	g569444
Method	BLASTX
NCBI GI	g4262142
BLAST score	173
E value	1.0e-12
Match length	55
% identity	60
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	395686
Contig ID	62836_1.R1084
5'-most EST	g702036

Seq. No.	395687
Contig ID	62844_1.R1084
5'-most EST	g569453
Method	BLASTX
NCBI GI	g5733866
BLAST score	217
E value	1.0e-26
Match length	84
% identity	70
NCBI Description	(AC007932) Contains similarity to gb_M73488 1-aminocyclopropane-1-carboxylate deaminase from Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from this gene. [Arabidopsis thaliana]

Seq. No.	395688
Contig ID	62845_1.R1084
5'-most EST	g2312554
Method	BLASTX
NCBI GI	g2281115
BLAST score	351
E value	1.0e-39
Match length	121
% identity	73
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	395689
Contig ID	62864_1.R1084
5'-most EST	g569965

Seq. No.	395690

Contig ID	62868_1.R1084
5'-most EST	g569490
Method	BLASTX
NCBI GI	g3927832
BLAST score	194
E value	8.0e-15
Match length	71
% identity	54
NCBI Description	(AC005727) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	395691
Contig ID	62882_1.R1084
5'-most EST	g569504
Method	BLASTX
NCBI GI	g1272347
BLAST score	223
E value	4.0e-18
Match length	91
% identity	48
NCBI Description	(U51739) secreted glycoprotein 2 [Ipomoea trifida]

Seq. No.	395692
Contig ID	62886_1.R1084
5'-most EST	g2280574
Method	BLASTX
NCBI GI	g1084462
BLAST score	186
E value	6.0e-14
Match length	69
% identity	57
NCBI Description	RCg2 protein - rice >gi_786130 (L27209) RCc2 [Oryza sativa] >gi_786134 (L27210) root-specific protein [Oryza sativa]

Seq. No.	395693
Contig ID	62901_1.R1084
5'-most EST	g569524

Seq. No.	395694
Contig ID	62933_1.R1084
5'-most EST	g569556
Method	BLASTX
NCBI GI	g3025189
BLAST score	169
E value	5.0e-12
Match length	107
% identity	34
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]

Seq. No.	395695
Contig ID	62975_1.R1084
5'-most EST	g569599
Method	BLASTX
NCBI GI	g2655098
BLAST score	314
E value	1.0e-28

Match length 74
% identity 76
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 395696
Contig ID 63009_1.R1084
5'-most EST g702678

Seq. No. 395697
Contig ID 63024_1.R1084
5'-most EST g5667640

Seq. No. 395698
Contig ID 63027_1.R1084
5'-most EST g571756

Seq. No. 395699
Contig ID 63035_1.R1084
5'-most EST g571950

Seq. No. 395700
Contig ID 63039_1.R1084
5'-most EST g569667

Seq. No. 395701
Contig ID 63044_1.R1084
5'-most EST g571654
Method BLASTX
NCBI GI g3894187
BLAST score 228
E value 1.0e-36
Match length 104
% identity 77
NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No. 395702
Contig ID 63046_1.R1084
5'-most EST g569891

Seq. No. 395703
Contig ID 63054_1.R1084
5'-most EST g569715

Seq. No. 395704
Contig ID 63060_1.R1084
5'-most EST g4969192

Seq. No. 395705
Contig ID 63065_1.R1084
5'-most EST g569693

Seq. No. 395706
Contig ID 63083_1.R1084
5'-most EST g571838

Seq. No. 395707
Contig ID 63109_1.R1084

5'-most EST	g569738
Seq. No.	395708
Contig ID	63118_1.R1084
5'-most EST	g569747
Seq. No.	395709
Contig ID	63140_1.R1084
5'-most EST	g571745
Method	BLASTX
NCBI GI	g729775
BLAST score	156
E value	3.0e-10
Match length	134
% identity	37
NCBI Description	HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR) >gi_100264_pir__S25481 heat shock transcription factor 8 - Peruvian tomato >gi_19492_emb_CAA47869_ (X67600) heat shock transcription factor 8 [Lycopersicon peruvianum]
Seq. No.	395710
Contig ID	63142_1.R1084
5'-most EST	g569772
Seq. No.	395711
Contig ID	63145_1.R1084
5'-most EST	g571695
Method	BLASTX
NCBI GI	g4938497
BLAST score	356
E value	4.0e-48
Match length	129
% identity	71
NCBI Description	(AL078465) isp4 like protein [Arabidopsis thaliana]
Seq. No.	395712
Contig ID	63152_1.R1084
5'-most EST	g569782
Method	BLASTX
NCBI GI	g5263330
BLAST score	239
E value	4.0e-20
Match length	79
% identity	57
NCBI Description	(AC007727) Contains similarity to gb_AJ000644 SPOP (speckle-type POZ protein) from Homo sapiens and contains a PF_00651 BTB/POZ domain. ESTs gb_T75841, gb_R89974, gb_R30221, gb_N96386, gb_T76457, gb_AI100013 and gb
Seq. No.	395713
Contig ID	63173_1.R1084
5'-most EST	g569803
Seq. No.	395714
Contig ID	63174_1.R1084
5'-most EST	g569889

Seq. No.	395715
Contig ID	63183_1.R1084
5'-most EST	g569813
Seq. No.	395716
Contig ID	63201_1.R1084
5'-most EST	g571927
Method	BLASTX
NCBI GI	g2129826
BLAST score	407
E value	1.0e-39
Match length	127
% identity	64
NCBI Description	dynamin-like protein phragmoplastin 5 - soybean >gi_1218004 (U36430) SDL5A [Glycine max]
Seq. No.	395717
Contig ID	63209_1.R1084
5'-most EST	g571758
Method	BLASTX
NCBI GI	g3341679
BLAST score	396
E value	6.0e-44
Match length	137
% identity	66
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]
Seq. No.	395718
Contig ID	63213_1.R1084
5'-most EST	g569843
Seq. No.	395719
Contig ID	63217_1.R1084
5'-most EST	g572082
Method	BLASTX
NCBI GI	g3068705
BLAST score	197
E value	8.0e-15
Match length	95
% identity	48
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]
Seq. No.	395720
Contig ID	63220_1.R1084
5'-most EST	g569900
Seq. No.	395721
Contig ID	63221_1.R1084
5'-most EST	g569852
Seq. No.	395722
Contig ID	63236_1.R1084
5'-most EST	g2431517
Seq. No.	395723

Contig ID	63240_1.R1084
5'-most EST	g569892
Seq. No.	395724
Contig ID	63241_1.R1084
5'-most EST	g3768047
Method	BLASTX
NCBI GI	g3080427
BLAST score	384
E value	5.0e-65
Match length	189
% identity	67
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]
Seq. No.	395725
Contig ID	63251_1.R1084
5'-most EST	g569881
Seq. No.	395726
Contig ID	63289_1.R1084
5'-most EST	g2428119
Method	BLASTX
NCBI GI	g1765899
BLAST score	928
E value	1.0e-112
Match length	217
% identity	80
NCBI Description	(Y07917) Spot 3 protein [Arabidopsis thaliana] >gi_1839244 (U86700) EGF receptor like protein [Arabidopsis thaliana]
Seq. No.	395727
Contig ID	63298_1.R1084
5'-most EST	g3762650
Seq. No.	395728
Contig ID	63352_1.R1084
5'-most EST	g4969195
Method	BLASTX
NCBI GI	g4886273
BLAST score	160
E value	6.0e-11
Match length	64
% identity	50
NCBI Description	(AL050300) hypothetical protein [Arabidopsis thaliana]
Seq. No.	395729
Contig ID	63359_1.R1084
5'-most EST	g571641
Seq. No.	395730
Contig ID	63361_1.R1084
5'-most EST	g4714840
Seq. No.	395731
Contig ID	63371_1.R1084
5'-most EST	g701743

Seq. No.	395732
Contig ID	63382_1.R1084
5'-most EST	g2280976
Method	BLASTN
NCBI GI	g2804255
BLAST score	40
E value	5.0e-13
Match length	47
% identity	96
NCBI Description	Oryctolagus cuniculus mRNA for interferon gamma, complete cds

Seq. No.	395733
Contig ID	63383_1.R1084
5'-most EST	g2311575
Method	BLASTX
NCBI GI	g3320122
BLAST score	189
E value	6.0e-14
Match length	143
% identity	34
NCBI Description	(U46007) espin [Rattus norvegicus]

Seq. No.	395734
Contig ID	63395_1.R1084
5'-most EST	g4878255
Method	BLASTX
NCBI GI	g3643611
BLAST score	290
E value	5.0e-26
Match length	103
% identity	58
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	395735
Contig ID	63400_1.R1084
5'-most EST	g570034

Seq. No.	395736
Contig ID	63401_1.R1084
5'-most EST	g570035

Seq. No.	395737
Contig ID	63402_1.R1084
5'-most EST	g572162

Seq. No.	395738
Contig ID	63412_1.R1084
5'-most EST	g571948

Seq. No.	395739
Contig ID	63418_1.R1084
5'-most EST	g570052

Seq. No.	395740
Contig ID	63420_1.R1084
5'-most EST	g571728

Seq. No.	395741
Contig ID	63435_1.R1084
5'-most EST	g570070
Method	BLASTX
NCBI GI	g5882732
BLAST score	607
E value	5.0e-63
Match length	139
% identity	83
NCBI Description	(AC008263) Similar to gb_AF135422 GDP-mannose pyrophosphorylase A (GMPPA) from Homo sapiens. ESTs gb_AA712990, gb_N65247, gb_N38149, gb_T04179, gb_Z38092, gb_T76473, gb_N96403, gb_AA394551 and gb_AA728527 come from

Seq. No.	395742
Contig ID	63461_1.R1084
5'-most EST	g570099

Seq. No.	395743
Contig ID	63465_1.R1084
5'-most EST	g572064
Method	BLASTX
NCBI GI	g4584539
BLAST score	197
E value	2.0e-15
Match length	50
% identity	66
NCBI Description	(AL049608) extensin-like protein [Arabidopsis thaliana]

Seq. No.	395744
Contig ID	63466_1.R1084
5'-most EST	g571792

Seq. No.	395745
Contig ID	63494_1.R1084
5'-most EST	g570132
Method	BLASTX
NCBI GI	g4558659
BLAST score	343
E value	3.0e-32
Match length	121
% identity	56
NCBI Description	(AC007063) unknown protein [Arabidopsis thaliana]

Seq. No.	395746
Contig ID	63507_1.R1084
5'-most EST	g571959

Seq. No.	395747
Contig ID	63514_1.R1084
5'-most EST	g571868

Seq. No.	395748
Contig ID	63534_1.R1084
5'-most EST	g5003590

Seq. No.	395749
Contig ID	63539_1.R1084
5'-most EST	g570178
Seq. No.	395750
Contig ID	63565_1.R1084
5'-most EST	g571708
Method	BLASTX
NCBI GI	g4490338
BLAST score	126
E value	9.0e-13
Match length	74
% identity	61
NCBI Description	(AL035656) putative auxin-induced protein [Arabidopsis thaliana]
Seq. No.	395751
Contig ID	63580_1.R1084
5'-most EST	g572185
Method	BLASTX
NCBI GI	g4586112
BLAST score	388
E value	2.0e-37
Match length	132
% identity	57
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]
Seq. No.	395752
Contig ID	63595_1.R1084
5'-most EST	g572103
Method	BLASTX
NCBI GI	g1169782
BLAST score	401
E value	3.0e-41
Match length	141
% identity	63
NCBI Description	FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]
Seq. No.	395753
Contig ID	63596_1.R1084
5'-most EST	g571583
Seq. No.	395754
Contig ID	63604_1.R1084
5'-most EST	g571603
Seq. No.	395755
Contig ID	63609_1.R1084
5'-most EST	g571597
Seq. No.	395756
Contig ID	63612_1.R1084
5'-most EST	g571939
Method	BLASTX
NCBI GI	g2586127
BLAST score	219

E value	5.0e-18
Match length	61
% identity	70
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.	395757
Contig ID	63630_1.R1084
5'-most EST	g571618
Method	BLASTX
NCBI GI	g3924612
BLAST score	291
E value	4.0e-26
Match length	63
% identity	90
NCBI Description	(AF069442) mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	395758
Contig ID	63647_1.R1084
5'-most EST	g572105

Seq. No.	395759
Contig ID	63662_1.R1084
5'-most EST	g572164
Method	BLASTX
NCBI GI	g4914423
BLAST score	231
E value	5.0e-19
Match length	138
% identity	38
NCBI Description	(AL050351) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	395760
Contig ID	63746_1.R1084
5'-most EST	g572022

Seq. No.	395761
Contig ID	63836_1.R1084
5'-most EST	g571835
Method	BLASTX
NCBI GI	g4580391
BLAST score	154
E value	7.0e-10
Match length	119
% identity	38
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	395762
Contig ID	63838_1.R1084
5'-most EST	g571837

Seq. No.	395763
Contig ID	63850_1.R1084
5'-most EST	g571941
Method	BLASTX

NCBI GI	g2832629
BLAST score	122
E value	5.0e-15
Match length	96
% identity	49
NCBI Description	(AL021711) 4-coumarate-CoA ligase-like [Arabidopsis thaliana]

Seq. No.	395764
Contig ID	63917_1.R1084
5'-most EST	g572048

Seq. No.	395765
Contig ID	63943_1.R1084
5'-most EST	g3769048

Seq. No.	395766
Contig ID	63969_1.R1084
5'-most EST	g4969196

Seq. No.	395767
Contig ID	64040_1.R1084
5'-most EST	g572049
Method	BLASTX
NCBI GI	g4191784
BLAST score	342
E value	4.0e-32
Match length	113
% identity	57
NCBI Description	(AC005917) putative WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	395768
Contig ID	64089_1.R1084
5'-most EST	g701270
Method	BLASTX
NCBI GI	g4850398
BLAST score	441
E value	5.0e-45
Match length	156
% identity	50
NCBI Description	(AC007357) Strong similarity to gi_3313615 F21J9.9 from Arabidopsis thaliana and is a member of the PF_00067 Cytochrome P450 family

Seq. No.	395769
Contig ID	64092_1.R1084
5'-most EST	g5005474
Method	BLASTX
NCBI GI	g1848225
BLAST score	193
E value	2.0e-14
Match length	61
% identity	52
NCBI Description	(U88090) nonspecific lipid transfer protein [Hordeum vulgare]

Seq. No. 395770
Contig ID 64107_1.R1084
5'-most EST g700394

Seq. No. 395771
Contig ID 64108_1.R1084
5'-most EST g3769127
Method BLASTX
NCBI GI g3668086
BLAST score 181
E value 3.0e-13
Match length 50
% identity 72
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 395772
Contig ID 64137_1.R1084
5'-most EST g572153

Seq. No. 395773
Contig ID 64147_1.R1084
5'-most EST g2442325
Method BLASTX
NCBI GI g4240033
BLAST score 343
E value 6.0e-32
Match length 84
% identity 73
NCBI Description (AB018587) ZmGR1a [Zea mays]

Seq. No. 395774
Contig ID 64165_1.R1084
5'-most EST g572178

Seq. No. 395775
Contig ID 64205_1.R1084
5'-most EST g572215

Seq. No. 395776
Contig ID 64260_1.R1084
5'-most EST g701662

Seq. No. 395777
Contig ID 64285_1.R1084
5'-most EST g4714258
Method BLASTX
NCBI GI g2695861
BLAST score 572
E value 6.0e-59
Match length 128
% identity 84
NCBI Description (Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273) 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum]

Seq. No. 395778

Contig ID	64312_1.R1084
5'-most EST	g572350
Method	BLASTX
NCBI GI	g2911073
BLAST score	295
E value	2.0e-26
Match length	80
% identity	71
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	395779
Contig ID	64326_1.R1084
5'-most EST	g572366

Seq. No.	395780
Contig ID	64333_1.R1084
5'-most EST	g572374
Method	BLASTX
NCBI GI	g4522012
BLAST score	638
E value	2.0e-66
Match length	231
% identity	55
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395781
Contig ID	64352_2.R1084
5'-most EST	g2801042

Seq. No.	395782
Contig ID	64353_1.R1084
5'-most EST	g572400

Seq. No.	395783
Contig ID	64391_1.R1084
5'-most EST	g572443
Method	BLASTX
NCBI GI	g3176687
BLAST score	513
E value	4.0e-52
Match length	142
% identity	67
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	395784
Contig ID	64392_1.R1084
5'-most EST	g3061019
Method	BLASTX
NCBI GI	g3033397
BLAST score	296
E value	7.0e-28
Match length	142
% identity	54
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 395785
Contig ID 64403_1.R1084
5'-most EST g2275822
Method BLASTX
NCBI GI g4218120
BLAST score 162
E value 2.0e-11
Match length 39
% identity 77
NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 395786
Contig ID 64418_1.R1084
5'-most EST g572473

Seq. No. 395787
Contig ID 64479_1.R1084
5'-most EST g2443090

Seq. No. 395788
Contig ID 64487_1.R1084
5'-most EST g5667558

Seq. No. 395789
Contig ID 64494_1.R1084
5'-most EST g699696

Seq. No. 395790
Contig ID 64497_1.R1084
5'-most EST g1036894

Seq. No. 395791
Contig ID 64542_1.R1084
5'-most EST g699867

Seq. No. 395792
Contig ID 64552_1.R1084
5'-most EST g699846

Seq. No. 395793
Contig ID 64560_1.R1084
5'-most EST g699767
Method BLASTX
NCBI GI g3540184
BLAST score 360
E value 5.0e-40
Match length 135
% identity 27
NCBI Description (AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No. 395794
Contig ID 64574_1.R1084
5'-most EST g699783
Method BLASTX
NCBI GI g2792295

BLAST score 166
E value 8.0e-24
Match length 130
% identity 50
NCBI Description (AF039182) unknown [Fragaria x ananassa]

Seq. No. 395795
Contig ID 64582_1.R1084
5'-most EST g699791

Seq. No. 395796
Contig ID 64591_1.R1084
5'-most EST g699800
Method BLASTX
NCBI GI g5103807
BLAST score 684
E value 9.0e-72
Match length 203
% identity 62
NCBI Description (AC007591) Contains similarity to gb_AF014403 type-2 phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo sapiens. ESTs gb_T88254 and gb_AA394650 come from this gene. [Arabidopsis thaliana]

Seq. No. 395797
Contig ID 64595_1.R1084
5'-most EST g5455603
Method BLASTN
NCBI GI g6041757
BLAST score 40
E value 6.0e-13
Match length 153
% identity 88
NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence

Seq. No. 395798
Contig ID 64619_1.R1084
5'-most EST g5004332
Method BLASTX
NCBI GI g3096935
BLAST score 392
E value 7.0e-38
Match length 154
% identity 58
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 395799
Contig ID 64649_1.R1084
5'-most EST g4880941
Method BLASTX
NCBI GI g6041851
BLAST score 205
E value 1.0e-15
Match length 122
% identity 61
NCBI Description (AC009853) unknown protein [Arabidopsis thaliana]

Seq. No. 395800
Contig ID 64656_1.R1084
5'-most EST g702521

Seq. No. 395801
Contig ID 64664_1.R1084
5'-most EST g699893

Seq. No. 395802
Contig ID 64690_1.R1084
5'-most EST g700163

Seq. No. 395803
Contig ID 64718_1.R1084
5'-most EST g701257

Seq. No. 395804
Contig ID 64728_1.R1084
5'-most EST g699988
Method BLASTX
NCBI GI g4490702
BLAST score 261
E value 1.0e-22
Match length 124
% identity 51
NCBI Description (AL035680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 395805
Contig ID 64779_1.R1084
5'-most EST g700009
Method BLASTX
NCBI GI g167012
BLAST score 301
E value 2.0e-27
Match length 104
% identity 56
NCBI Description (J03897) carboxypeptidase I precursor [Hordeum vulgare]

Seq. No. 395806
Contig ID 64782_1.R1084
5'-most EST g700558
Method BLASTX
NCBI GI g3738297
BLAST score 312
E value 1.0e-28
Match length 131
% identity 25
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 395807
Contig ID 64785_1.R1084
5'-most EST g700015
Method BLASTX
NCBI GI g1170871
BLAST score 774
E value 2.0e-82

Match length	212
% identity	73
NCBI Description	MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_1076749_pir__S46499 NADP-dependent malic enzyme - rice >gi_415315_dbj_BAA03949_ (D16499) NADP-dependent malic enzyme [Oryza sativa]

Seq. No.	395808
Contig ID	64797_1.R1084
5'-most EST	g700027

Seq. No.	395809
Contig ID	64806_1.R1084
5'-most EST	g700037

Seq. No.	395810
Contig ID	64829_1.R1084
5'-most EST	g700060
Method	BLASTX
NCBI GI	g5262190
BLAST score	349
E value	3.0e-37
Match length	136
% identity	62
NCBI Description	(AL080252) inositol 1, 3, 4-trisphosphate 5/6-kinase-like protein [Arabidopsis thaliana]

Seq. No.	395811
Contig ID	64831_1.R1084
5'-most EST	g700062

Seq. No.	395812
Contig ID	64841_1.R1084
5'-most EST	g700074
Method	BLASTX
NCBI GI	g3047109
BLAST score	191
E value	2.0e-15
Match length	117
% identity	44
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	395813
Contig ID	64853_1.R1084
5'-most EST	g700269
Method	BLASTX
NCBI GI	g2388578
BLAST score	403
E value	3.0e-39
Match length	121
% identity	65
NCBI Description	(AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs gb_T75785,gb_R30580,gb_T04698 come from this gene. [Arabidopsis thaliana]

Seq. No.	395814

Contig ID	64861_1.R1084
5'-most EST	g5455594
Method	BLASTN
NCBI GI	g5091496
BLAST score	37
E value	2.0e-11
Match length	85
% identity	43
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	395815
Contig ID	64863_1.R1084
5'-most EST	g700096

Seq. No.	395816
Contig ID	64866_1.R1084
5'-most EST	g700157
Method	BLASTX
NCBI GI	g475784
BLAST score	181
E value	2.0e-13
Match length	130
% identity	12
NCBI Description	(M99575) 85 kDa protein [Babesia bovis]

Seq. No.	395817
Contig ID	64868_1.R1084
5'-most EST	g3768595

Seq. No.	395818
Contig ID	64884_1.R1084
5'-most EST	g5667369

Seq. No.	395819
Contig ID	64887_1.R1084
5'-most EST	g700177
Method	BLASTX
NCBI GI	g4309969
BLAST score	112
E value	6.0e-09
Match length	72
% identity	47
NCBI Description	(AC002983) putative phosphoglyceride transfer protein [Arabidopsis thaliana]

Seq. No.	395820
Contig ID	64907_1.R1084
5'-most EST	g700141
Method	BLASTX
NCBI GI	g2429288
BLAST score	346
E value	1.0e-32
Match length	88
% identity	76
NCBI Description	(AF014468) peroxidase [Oryza sativa]

Seq. No.	395821
Contig ID	64940_1.R1084
5'-most EST	g700181
Method	BLASTX
NCBI GI	g4417283
BLAST score	154
E value	2.0e-15
Match length	97
% identity	41
NCBI Description	(AC007019) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	395822
Contig ID	64966_1.R1084
5'-most EST	g2442322

Seq. No.	395823
Contig ID	64972_1.R1084
5'-most EST	g4715074
Method	BLASTX
NCBI GI	g586797
BLAST score	159
E value	3.0e-11
Match length	88
% identity	43
NCBI Description	HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III

Seq. No.	395824
Contig ID	64973_1.R1084
5'-most EST	g700210
Method	BLASTX
NCBI GI	g3695059
BLAST score	450
E value	1.0e-44
Match length	111
% identity	85
NCBI Description	(AF064787) rac GTPase activating protein 1 [Lotus japonicus]

Seq. No.	395825
Contig ID	64986_1.R1084
5'-most EST	g702111

Seq. No.	395826
Contig ID	64987_1.R1084
5'-most EST	g700224

Seq. No.	395827
Contig ID	64990_1.R1084
5'-most EST	g700510
Method	BLASTX
NCBI GI	g1769901
BLAST score	189
E value	2.0e-14
Match length	73
% identity	52
NCBI Description	(X95737) proline transporter 1 [Arabidopsis thaliana] >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis

thaliana]

Seq. No.	395828
Contig ID	64993_1.R1084
5'-most EST	g5803548

Seq. No.	395829
Contig ID	64997_1.R1084
5'-most EST	g3768833
Method	BLASTN
NCBI GI	g415261
BLAST score	74
E value	4.0e-33
Match length	78
% identity	99
NCBI Description	Schizosaccharomyces pombe (clone pJK210) DNA sequence

Seq. No.	395830
Contig ID	64997_3.R1084
5'-most EST	g4714254

Seq. No.	395831
Contig ID	65017_1.R1084
5'-most EST	g700255

Seq. No.	395832
Contig ID	65052_1.R1084
5'-most EST	g2442667
Method	BLASTX
NCBI GI	g3687240
BLAST score	177
E value	1.0e-12
Match length	172
% identity	36
NCBI Description	(AC005169) extensin-like protein [Arabidopsis thaliana]

Seq. No.	395833
Contig ID	65079_1.R1084
5'-most EST	g700319

Seq. No.	395834
Contig ID	65082_1.R1084
5'-most EST	g701014

Seq. No.	395835
Contig ID	65090_1.R1084
5'-most EST	g700330

Seq. No.	395836
Contig ID	65096_1.R1084
5'-most EST	g2309933
Method	BLASTX
NCBI GI	g3193324
BLAST score	171
E value	5.0e-12
Match length	91
% identity	42

NCBI Description	(AF069299) contains similarity to WD domains, G-beta repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84) [Arabidopsis thaliana]

Seq. No.	395837
Contig ID	65097_1.R1084
5'-most EST	g700337

Seq. No.	395838
Contig ID	65116_1.R1084
5'-most EST	g701535

Seq. No.	395839
Contig ID	65125_1.R1084
5'-most EST	g4714273
Method	BLASTX
NCBI GI	g2781362
BLAST score	173
E value	5.0e-12
Match length	95
% identity	42
NCBI Description	(AC003113) F24O1.18 [Arabidopsis thaliana] >gi_5454187_gb_AAD43602.1_AC005698_1 (AC005698) T3P18.1 [Arabidopsis thaliana]

Seq. No.	395840
Contig ID	65156_1.R1084
5'-most EST	g4716121
Method	BLASTX
NCBI GI	g6006869
BLAST score	294
E value	1.0e-29
Match length	156
% identity	49
NCBI Description	(AC009540) putative cationic amino acid transporter [Arabidopsis thaliana]

Seq. No.	395841
Contig ID	65159_1.R1084
5'-most EST	g700403
Method	BLASTX
NCBI GI	g3059131
BLAST score	205
E value	1.0e-17
Match length	99
% identity	47
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No.	395842
Contig ID	65168_1.R1084
5'-most EST	g700412

Seq. No.	395843
Contig ID	65204_1.R1084
5'-most EST	g700448
Method	BLASTX
NCBI GI	g2244830

BLAST score	151
E value	1.0e-09
Match length	56
% identity	57
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395844
Contig ID	65211_1.R1084
5'-most EST	g700482
Method	BLASTX
NCBI GI	g112785
BLAST score	121
E value	6.0e-11
Match length	88
% identity	42
NCBI Description	DNA-3-METHYLADENINE GLYCOSYLASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) (DNA-3-METHYLADENINE GLYCOSIDASE I) >gi_67508_pir__DGECM1 3-methyladenine DNA glycosylase (EC 3.2.2.-) I - Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa 1-187) [Escherichia coli] >gi_147920 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_466687 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432) 3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]

Seq. No.	395845
Contig ID	65213_1.R1084
5'-most EST	g700458

Seq. No.	395846
Contig ID	65230_1.R1084
5'-most EST	g700486
Method	BLASTX
NCBI GI	g3063469
BLAST score	144
E value	6.0e-09
Match length	58
% identity	52
NCBI Description	(AC003981) F22O13.31 [Arabidopsis thaliana]

Seq. No.	395847
Contig ID	65275_2.R1084
5'-most EST	g700547
Method	BLASTX
NCBI GI	g3288564
BLAST score	166
E value	1.0e-14
Match length	44
% identity	95
NCBI Description	(X97066) 1-aminocyclopropane-1-carboxylic acid synthase [Oryza sativa]

Seq. No.	395848
Contig ID	65347_1.R1084
5'-most EST	g700598
Method	BLASTX

NCBI GI	g5006473
BLAST score	194
E value	7.0e-15
Match length	52
% identity	37
NCBI Description	(AF139098) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	395849
Contig ID	65380_1.R1084
5'-most EST	g2310449

Seq. No.	395850
Contig ID	65389_1.R1084
5'-most EST	g700762
Method	BLASTX
NCBI GI	g2119045
BLAST score	181
E value	2.0e-13
Match length	82
% identity	52
NCBI Description	small nuclear ribonucleoprotein U1A - potato >gi_1050840_emb_CAA90282_ (Z49990) U1snRNP-specific protein, U1A [Solanum tuberosum]

Seq. No.	395851
Contig ID	65403_1.R1084
5'-most EST	g701189

Seq. No.	395852
Contig ID	65404_1.R1084
5'-most EST	g700808

Seq. No.	395853
Contig ID	65408_1.R1084
5'-most EST	g700661
Method	BLASTX
NCBI GI	g217995
BLAST score	296
E value	1.0e-35
Match length	140
% identity	55
NCBI Description	(D13683) peroxidase [Populus kitakamiensis]

Seq. No.	395854
Contig ID	65422_1.R1084
5'-most EST	g4715152
Method	BLASTX
NCBI GI	g4097948
BLAST score	792
E value	1.0e-102
Match length	217
% identity	87
NCBI Description	(U72255) beta-1,3-glucanase precursor [Oryza sativa]

Seq. No.	395855
Contig ID	65428_1.R1084

5'-most EST	g700725
Method	BLASTX
NCBI GI	g5668773
BLAST score	151
E value	8.0e-16
Match length	65
% identity	60
NCBI Description	(AC005916) Contains similarity to gb_AF113001 silencing mediator of retinoic acid and thyroid hormone receptor alpha and gb_AF109179 cyclin T1 from Mus musculus. ESTs gb_N95317, gb_Z29139 and gb_Z30853 come from th

Seq. No.	395856
Contig ID	65472_1.R1084
5'-most EST	g2427945

Seq. No.	395857
Contig ID	65508_1.R1084
5'-most EST	g700799

Seq. No.	395858
Contig ID	65518_1.R1084
5'-most EST	g700848
Method	BLASTX
NCBI GI	g3559805
BLAST score	242
E value	1.0e-23
Match length	108
% identity	61
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	395859
Contig ID	65527_1.R1084
5'-most EST	g700849

Seq. No.	395860
Contig ID	65534_1.R1084
5'-most EST	g700792
Method	BLASTX
NCBI GI	g1653665
BLAST score	189
E value	4.0e-26
Match length	101
% identity	62
NCBI Description	(D90915) peptide chain release factor [Synechocystis sp.]

Seq. No.	395861
Contig ID	65544_1.R1084
5'-most EST	g4878930
Method	BLASTX
NCBI GI	g1709203
BLAST score	573
E value	4.0e-59
Match length	132
% identity	81
NCBI Description	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (IMP 1) (INOSITOL

MONOPHOSPHATASE 1) >gi_1098977 (U39444) myo-inositol monophosphatase 1 [Lycopersicon esculentum]

Seq. No.	395862
Contig ID	65553_1.R1084
5'-most EST	g700811
Method	BLASTX
NCBI GI	g1814405
BLAST score	610
E value	3.0e-63
Match length	163
% identity	80
NCBI Description	(U84890) putative phosphate permease [Mesembryanthemum crystallinum]

Seq. No.	395863
Contig ID	65566_1.R1084
5'-most EST	g700847
Method	BLASTX
NCBI GI	g2911067
BLAST score	474
E value	1.0e-47
Match length	109
% identity	83
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No.	395864
Contig ID	65568_1.R1084
5'-most EST	g5005188
Method	BLASTX
NCBI GI	g6063549
BLAST score	544
E value	5.0e-60
Match length	118
% identity	97
NCBI Description	(AP000615) EST AU070346(S12172) corresponds to a region of the predicted gene.; similar to AMP-binding protein. (X94625) [Oryza sativa]

Seq. No.	395865
Contig ID	65600_1.R1084
5'-most EST	g700860
Method	BLASTX
NCBI GI	g3935168
BLAST score	362
E value	2.0e-34
Match length	102
% identity	66
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	395866
Contig ID	65604_1.R1084
5'-most EST	g2427941

Seq. No.	395867
Contig ID	65606_1.R1084

5'-most EST	g701719
Method	BLASTX
NCBI GI	g3341443
BLAST score	307
E value	6.0e-28
Match length	124
% identity	52
NCBI Description	(AJ223074) acid phosphatase [Glycine max]

Seq. No.	395868
Contig ID	65610_1.R1084
5'-most EST	g700870

Seq. No.	395869
Contig ID	65611_1.R1084
5'-most EST	g4879869
Method	BLASTX
NCBI GI	g3738285
BLAST score	243
E value	2.0e-20
Match length	100
% identity	54
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	395870
Contig ID	65614_1.R1084
5'-most EST	g2310434
Method	BLASTX
NCBI GI	g3548818
BLAST score	401
E value	1.0e-38
Match length	144
% identity	58
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	395871
Contig ID	65622_1.R1084
5'-most EST	g700882

Seq. No.	395872
Contig ID	65628_1.R1084
5'-most EST	g701567
Method	BLASTX
NCBI GI	g3024764
BLAST score	439
E value	1.0e-45
Match length	143
% identity	65
NCBI Description	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (UBIQUITIN THIOLESTERASE T) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T) (DEUBIQUITINATING ENZYME T) (ISOPEPTIDASE T) >gi_3287373 (AC002397) ISOT [Mus musculus]

Seq. No.	395873
Contig ID	65640_1.R1084
5'-most EST	g4879463
Method	BLASTX

NCBI GI	g1619602
BLAST score	252
E value	2.0e-21
Match length	70
% identity	64
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	395874
Contig ID	65668_1.R1084
5'-most EST	g700934
Method	BLASTX
NCBI GI	g3482914
BLAST score	259
E value	2.0e-22
Match length	121
% identity	48
NCBI Description	(AC003970) Similar to nodulins and lipase [Arabidopsis thaliana]

Seq. No.	395875
Contig ID	65670_1.R1084
5'-most EST	g701417

Seq. No.	395876
Contig ID	65678_1.R1084
5'-most EST	g2428849
Method	BLASTX
NCBI GI	g4586246
BLAST score	439
E value	2.0e-43
Match length	161
% identity	50
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	395877
Contig ID	65686_1.R1084
5'-most EST	g701024
Method	BLASTX
NCBI GI	g2570511
BLAST score	289
E value	2.0e-26
Match length	61
% identity	90
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	395878
Contig ID	65692_1.R1084
5'-most EST	g701371
Method	BLASTX
NCBI GI	g3790102
BLAST score	505
E value	3.0e-51
Match length	150
% identity	63
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	395879
Contig ID	65697_1.R1084
5'-most EST	g702108
Method	BLASTX
NCBI GI	g4662634
BLAST score	160
E value	3.0e-15
Match length	64
% identity	73
NCBI Description	(AC007267) unknown protein [Arabidopsis thaliana]

Seq. No.	395880
Contig ID	65698_1.R1084
5'-most EST	g700964
Method	BLASTX
NCBI GI	g421980
BLAST score	242
E value	4.0e-43
Match length	109
% identity	79
NCBI Description	transforming protein (myb3) - barley >gi_19059_emb_CAA50223_ (X70878) MybHv33 [Hordeum vulgare]

Seq. No.	395881
Contig ID	65707_1.R1084
5'-most EST	g701316
Method	BLASTX
NCBI GI	g4903006
BLAST score	354
E value	2.0e-33
Match length	152
% identity	46
NCBI Description	(AB027458) ACE [Arabidopsis thaliana] >gi_5903086_gb_AAD55644.1_AC008017_17 (AC008017) ACE [Arabidopsis thaliana]

Seq. No.	395882
Contig ID	65727_1.R1084
5'-most EST	g700994

Seq. No.	395883
Contig ID	65743_1.R1084
5'-most EST	g5004781
Method	BLASTX
NCBI GI	g4914331
BLAST score	238
E value	2.0e-19
Match length	66
% identity	71
NCBI Description	(AC005489) F14N23.17 [Arabidopsis thaliana]

Seq. No.	395884
Contig ID	65747_1.R1084
5'-most EST	g701483

Seq. No.	395885
Contig ID	65752_1.R1084

5'-most EST	g701387
Method	BLASTX
NCBI GI	g1086111
BLAST score	205
E value	4.0e-16
Match length	79
% identity	51
NCBI Description	peroxidase (EC 1.11.1.7) - Spirodela polyrrhiza >gi_438245_emb_CAA80502_ (Z22920) peroxidase [Spirodela polyrrhiza]

Seq. No.	395886
Contig ID	65753_1.R1084
5'-most EST	g701365

Seq. No.	395887
Contig ID	65763_1.R1084
5'-most EST	g701105
Method	BLASTN
NCBI GI	g22592
BLAST score	74
E value	3.0e-33
Match length	125
% identity	90
NCBI Description	S.vulgare PEPC gene for phosphoenolpyruvate carboxylase

Seq. No.	395888
Contig ID	65765_2.R1084
5'-most EST	g701034
Method	BLASTX
NCBI GI	g4914419
BLAST score	171
E value	1.0e-16
Match length	88
% identity	46
NCBI Description	(AL050352) putative protein [Arabidopsis thaliana]

Seq. No.	395889
Contig ID	65791_1.R1084
5'-most EST	g701061

Seq. No.	395890
Contig ID	65802_1.R1084
5'-most EST	g4880949

Seq. No.	395891
Contig ID	65815_1.R1084
5'-most EST	g3768615

Seq. No.	395892
Contig ID	65819_1.R1084
5'-most EST	g701435

Seq. No.	395893
Contig ID	65828_1.R1084
5'-most EST	g3768644

Seq. No.	395894
Contig ID	65840_1.R1084
5'-most EST	g701115
Seq. No.	395895
Contig ID	65862_1.R1084
5'-most EST	g701137
Seq. No.	395896
Contig ID	65904_1.R1084
5'-most EST	g4878340
Seq. No.	395897
Contig ID	65954_1.R1084
5'-most EST	g1944241
Seq. No.	395898
Contig ID	65962_1.R1084
5'-most EST	g701242
Seq. No.	395899
Contig ID	65969_1.R1084
5'-most EST	g701298
Seq. No.	395900
Contig ID	65987_1.R1084
5'-most EST	g701267
Seq. No.	395901
Contig ID	66029_1.R1084
5'-most EST	g701309
Method	BLASTX
NCBI GI	g4204313
BLAST score	330
E value	1.0e-30
Match length	93
% identity	70
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	395902
Contig ID	66077_1.R1084
5'-most EST	g4879876
Method	BLASTX
NCBI GI	g4929767
BLAST score	190
E value	2.0e-20
Match length	106
% identity	53
NCBI Description	(AF151907) CGI-149 protein [Homo sapiens]
Seq. No.	395903
Contig ID	66098_1.R1084
5'-most EST	g5771177
Seq. No.	395904
Contig ID	66134_1.R1084

5'-most EST	g701492
Method	BLASTX
NCBI GI	g3549671
BLAST score	136
E value	4.0e-09
Match length	66
% identity	58
NCBI Description	(AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395905
Contig ID	66144_1.R1084
5'-most EST	g701427
Method	BLASTX
NCBI GI	g1661160
BLAST score	406
E value	9.0e-42
Match length	101
% identity	92
NCBI Description	(U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	395906
Contig ID	66197_1.R1084
5'-most EST	g5039060
Method	BLASTX
NCBI GI	g4539656
BLAST score	182
E value	2.0e-23
Match length	67
% identity	83
NCBI Description	(AF061282) patatin-like protein [Sorghum bicolor]

Seq. No.	395907
Contig ID	66234_1.R1084
5'-most EST	g5005221
Method	BLASTX
NCBI GI	g3643090
BLAST score	249
E value	4.0e-21
Match length	70
% identity	67
NCBI Description	(AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	395908
Contig ID	66291_1.R1084
5'-most EST	g701642

Seq. No.	395909
Contig ID	66294_1.R1084
5'-most EST	g701757

Seq. No.	395910
Contig ID	66299_1.R1084
5'-most EST	g5005224
Method	BLASTX
NCBI GI	g4406759
BLAST score	213

E value	5.0e-17
Match length	73
% identity	55
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395911
Contig ID	66306_1.R1084
5'-most EST	g701657
Method	BLASTX
NCBI GI	g2739383
BLAST score	288
E value	2.0e-25
Match length	145
% identity	49
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	395912
Contig ID	66328_1.R1084
5'-most EST	g701681

Seq. No.	395913
Contig ID	66330_1.R1084
5'-most EST	g4968932
Method	BLASTX
NCBI GI	g3193234
BLAST score	279
E value	1.0e-24
Match length	97
% identity	57
NCBI Description	(AF068690) peroxisomal targeting signal-1 receptor [Citrullus lanatus]

Seq. No.	395914
Contig ID	66333_1.R1084
5'-most EST	g2427930
Method	BLASTX
NCBI GI	g1352186
BLAST score	167
E value	2.0e-14
Match length	82
% identity	56
NCBI Description	ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74A) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No.	395915
Contig ID	66346_1.R1084
5'-most EST	g701699

Seq. No.	395916
Contig ID	66351_1.R1084
5'-most EST	g701704

Seq. No.	395917
Contig ID	66382_1.R1084
5'-most EST	g701766
Method	BLASTX

NCBI GI	g3337361
BLAST score	524
E value	2.0e-53
Match length	131
% identity	71
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	395918
Contig ID	66394_1.R1084
5'-most EST	g701750

Seq. No.	395919
Contig ID	66420_1.R1084
5'-most EST	g701776
Method	BLASTX
NCBI GI	g2497539
BLAST score	515
E value	3.0e-52
Match length	122
% identity	81
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	395920
Contig ID	66438_1.R1084
5'-most EST	g4878215
Method	BLASTX
NCBI GI	g3426043
BLAST score	179
E value	7.0e-13
Match length	79
% identity	47
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	395921
Contig ID	66469_1.R1084
5'-most EST	g3767002

Seq. No.	395922
Contig ID	66475_1.R1084
5'-most EST	g3768771

Seq. No.	395923
Contig ID	66487_1.R1084
5'-most EST	g702436
Method	BLASTX
NCBI GI	g2129759
BLAST score	247
E value	4.0e-21
Match length	80
% identity	59
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	395924
Contig ID	66488_1.R1084

5'-most EST	g5003786
Method	BLASTX
NCBI GI	g1781299
BLAST score	315
E value	1.0e-28
Match length	95
% identity	64
NCBI Description	(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]

Seq. No.	395925
Contig ID	66492_1.R1084
5'-most EST	g701850
Method	BLASTN
NCBI GI	g4973430
BLAST score	83
E value	1.0e-38
Match length	239
% identity	85
NCBI Description	Oryza sativa subsp. indica putative aldehyde dehydrogenase OS-ALDH mRNA, complete cds

Seq. No.	395926
Contig ID	66537_1.R1084
5'-most EST	g701896
Method	BLASTX
NCBI GI	g2501555
BLAST score	422
E value	3.0e-41
Match length	116
% identity	69
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	395927
Contig ID	66555_1.R1084
5'-most EST	g5038710
Method	BLASTX
NCBI GI	g4585708
BLAST score	308
E value	4.0e-28
Match length	109
% identity	56
NCBI Description	(AJ238117) putative phospholipase A2 [Oryza sativa]

Seq. No.	395928
Contig ID	66558_1.R1084
5'-most EST	g702815
Method	BLASTX
NCBI GI	g2651310
BLAST score	211
E value	8.0e-17
Match length	93
% identity	45
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	395929
Contig ID	66581_1.R1084
5'-most EST	g701940
Method	BLASTX
NCBI GI	g2702269
BLAST score	192
E value	2.0e-14
Match length	76
% identity	71
NCBI Description	(AC003033) hypothetical protein [Arabidopsis thaliana]

Seq. No.	395930
Contig ID	66583_1.R1084
5'-most EST	g2798580

Seq. No.	395931
Contig ID	66597_1.R1084
5'-most EST	g2310267

Seq. No.	395932
Contig ID	66600_1.R1084
5'-most EST	g2442819
Method	BLASTX
NCBI GI	g6002459
BLAST score	385
E value	6.0e-56
Match length	137
% identity	80
NCBI Description	(AB032797) phytoene synthase [Daucus carota]

Seq. No.	395933
Contig ID	66607_1.R1084
5'-most EST	g701967
Method	BLASTX
NCBI GI	g1657859
BLAST score	193
E value	4.0e-25
Match length	67
% identity	88
NCBI Description	(U73218) chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]

Seq. No.	395934
Contig ID	66629_1.R1084
5'-most EST	g5667537
Method	BLASTX
NCBI GI	g2702268
BLAST score	359
E value	3.0e-58
Match length	219
% identity	56
NCBI Description	(AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No.	395935
Contig ID	66645_1.R1084
5'-most EST	g702007

Seq. No.	395936
Contig ID	66648_1.R1084
5'-most EST	g702010

Seq. No.	395937
Contig ID	66651_1.R1084
5'-most EST	g702013
Method	BLASTX
NCBI GI	g2252866
BLAST score	232
E value	3.0e-19
Match length	50
% identity	92
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	395938
Contig ID	66657_1.R1084
5'-most EST	g702021

Seq. No.	395939
Contig ID	66662_1.R1084
5'-most EST	g3090678
Method	BLASTX
NCBI GI	g2653558
BLAST score	298
E value	3.0e-36
Match length	160
% identity	51
NCBI Description	(D50679) ferredoxin-sulfite reductase precursor [Zea mays]

Seq. No.	395940
Contig ID	66679_1.R1084
5'-most EST	g4878235

Seq. No.	395941
Contig ID	66680_1.R1084
5'-most EST	g702044

Seq. No.	395942
Contig ID	66681_1.R1084
5'-most EST	g3768788

Seq. No.	395943
Contig ID	66707_1.R1084
5'-most EST	g4879059

Seq. No.	395944
Contig ID	66726_1.R1084
5'-most EST	g702401
Method	BLASTX
NCBI GI	g3047079
BLAST score	183
E value	1.0e-15
Match length	47
% identity	83
NCBI Description	(AF058914) Arabidopsis thaliana transcription factor ATMYB4

(GB:X95297) [Arabidopsis thaliana]

Seq. No.	395945
Contig ID	66754_1.R1084
5'-most EST	g702120
Method	BLASTX
NCBI GI	g5734638
BLAST score	437
E value	4.0e-43
Match length	110
% identity	82
NCBI Description	(AP000391) EST AU077859(S14590) corresponds to a region of the predicted gene.; Similar to Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence; unknown protein (AC003680) [Oryza sativa]

Seq. No.	395946
Contig ID	66769_1.R1084
5'-most EST	g702135
Method	BLASTX
NCBI GI	g1661160
BLAST score	383
E value	1.0e-42
Match length	113
% identity	88
NCBI Description	(U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	395947
Contig ID	66797_1.R1084
5'-most EST	g702165

Seq. No.	395948
Contig ID	66808_1.R1084
5'-most EST	g4878410

Seq. No.	395949
Contig ID	66818_1.R1084
5'-most EST	g2798475
Method	BLASTX
NCBI GI	g5702015
BLAST score	436
E value	4.0e-43
Match length	136
% identity	60
NCBI Description	(AJ012215) GAL83 protein [Solanum tuberosum]

Seq. No.	395950
Contig ID	66819_1.R1084
5'-most EST	g702187
Method	BLASTX
NCBI GI	g5734639
BLAST score	372
E value	2.0e-57
Match length	216
% identity	54
NCBI Description	(AP000391) ESTs AU056036(S20239),C72753(E2173), AU056035(S20239) correspond to a region of the predicted

gene.; Similar to putative cytochrome P-450 (AC003680) [Oryza sativa]

Seq. No.	395951
Contig ID	66825_1.R1084
5'-most EST	g3760019

Seq. No.	395952
Contig ID	66846_1.R1084
5'-most EST	g702216

Seq. No.	395953
Contig ID	66853_1.R1084
5'-most EST	g2442685
Method	BLASTX
NCBI GI	g3355471
BLAST score	181
E value	2.0e-20
Match length	89
% identity	49
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	395954
Contig ID	66869_1.R1084
5'-most EST	g702239

Seq. No.	395955
Contig ID	66875_1.R1084
5'-most EST	g702245
Method	BLASTX
NCBI GI	g5777366
BLAST score	324
E value	8.0e-30
Match length	105
% identity	58
NCBI Description	(AJ009782) phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]

Seq. No.	395956
Contig ID	66927_1.R1084
5'-most EST	g4969105

Seq. No.	395957
Contig ID	66948_1.R1084
5'-most EST	g5005197
Method	BLASTX
NCBI GI	g4539340
BLAST score	167
E value	2.0e-11
Match length	46
% identity	57
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	395958
Contig ID	66957_1.R1084
5'-most EST	g2800500

Seq. No.	395959
Contig ID	67033_1.R1084
5'-most EST	g702406
Method	BLASTX
NCBI GI	g6002459
BLAST score	450
E value	1.0e-44
Match length	116
% identity	77
NCBI Description	(AB032797) phytoene synthase [Daucus carota]

Seq. No.	395960
Contig ID	67061_1.R1084
5'-most EST	g702435

Seq. No.	395961
Contig ID	67085_1.R1084
5'-most EST	g3763313
Method	BLASTX
NCBI GI	g1620451
BLAST score	173
E value	5.0e-12
Match length	89
% identity	40
NCBI Description	(X94978) multifunctional protein 2 [Rattus norvegicus]

Seq. No.	395962
Contig ID	67103_1.R1084
5'-most EST	g702481

Seq. No.	395963
Contig ID	67159_1.R1084
5'-most EST	g4968913
Method	BLASTX
NCBI GI	g115787
BLAST score	234
E value	2.0e-26
Match length	94
% identity	79
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	395964
Contig ID	67168_1.R1084
5'-most EST	g5003824

Seq. No.	395965
Contig ID	67170_1.R1084
5'-most EST	g2799533

Seq. No.	395966
Contig ID	67182_1.R1084
5'-most EST	g702561

Method	BLASTX
NCBI GI	g4204300
BLAST score	271
E value	1.0e-23
Match length	104
% identity	51
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	395967
Contig ID	67184_1.R1084
5'-most EST	g702563

Seq. No.	395968
Contig ID	67188_1.R1084
5'-most EST	g702567
Method	BLASTX
NCBI GI	g4335763
BLAST score	263
E value	8.0e-23
Match length	101
% identity	55
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	395969
Contig ID	67191_1.R1084
5'-most EST	g5038583
Method	BLASTX
NCBI GI	g729103
BLAST score	461
E value	6.0e-46
Match length	121
% identity	79
NCBI Description	CHALCONE--FLAVONONE ISOMERASE (CHALCONE ISOMERASE) >gi_542181_pir__S41570 chalcone isomerase (EC 5.5.1.6) - maize >gi_396149_emb_CAA80441_ (Z22760) chalcone flavonone isomerase [Zea mays]

Seq. No.	395970
Contig ID	67199_1.R1084
5'-most EST	g702578

Seq. No.	395971
Contig ID	67223_1.R1084
5'-most EST	g702608

Seq. No.	395972
Contig ID	67239_1.R1084
5'-most EST	g702628
Method	BLASTX
NCBI GI	g4097547
BLAST score	173
E value	3.0e-12
Match length	45
% identity	34
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	395973

Contig ID	67280_1.R1084
5'-most EST	g4879782
Method	BLASTX
NCBI GI	g4164473
BLAST score	181
E value	3.0e-13
Match length	64
% identity	59
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No.	395974
Contig ID	67288_1.R1084
5'-most EST	g702679
Method	BLASTX
NCBI GI	g3915477
BLAST score	145
E value	5.0e-09
Match length	73
% identity	41
NCBI Description	HYPOTHETICAL 20.9 KD PROTEIN T06G6.9 IN CHROMOSOME I >gi_3879580_emb_CAB04707_ (Z81587) Similarity to Human VHL binding protein-1 (TR:Q15765); cDNA EST EMBL:C13429 comes from this gene; cDNA EST EMBL:C10456 comes from this gene; cDNA EST yk486h8.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	395975
Contig ID	67313_1.R1084
5'-most EST	g702760
Method	BLASTX
NCBI GI	g4572671
BLAST score	215
E value	3.0e-17
Match length	112
% identity	44
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	395976
Contig ID	67315_1.R1084
5'-most EST	g702706

Seq. No.	395977
Contig ID	67319_1.R1084
5'-most EST	g702722
Method	BLASTX
NCBI GI	g2244835
BLAST score	574
E value	3.0e-59
Match length	118
% identity	90
NCBI Description	(Z97337) kinase like protein [Arabidopsis thaliana]

Seq. No.	395978
Contig ID	67339_1.R1084
5'-most EST	g702730

Seq. No.	395979
Contig ID	67347_2.R1084
5'-most EST	g6062520
Method	BLASTX
NCBI GI	g1171429
BLAST score	229
E value	2.0e-32
Match length	273
% identity	43
NCBI Description	(U44028) CKC [Arabidopsis thaliana]

Seq. No.	395980
Contig ID	67365_1.R1084
5'-most EST	g702768

Seq. No.	395981
Contig ID	67369_1.R1084
5'-most EST	g702761

Seq. No.	395982
Contig ID	67381_1.R1084
5'-most EST	g5003440
Method	BLASTX
NCBI GI	g1171579
BLAST score	201
E value	1.0e-15
Match length	64
% identity	62
NCBI Description	(X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No.	395983
Contig ID	67407_1.R1084
5'-most EST	g702800

Seq. No.	395984
Contig ID	67422_1.R1084
5'-most EST	g702816

Seq. No.	395985
Contig ID	67444_1.R1084
5'-most EST	g702838
Method	BLASTX
NCBI GI	g4164473
BLAST score	174
E value	4.0e-12
Match length	64
% identity	62
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No.	395986
Contig ID	67450_1.R1084
5'-most EST	g702844

Seq. No.	395987
Contig ID	67452_1.R1084

5'-most EST	g2280716
Method	BLASTX
NCBI GI	g3152558
BLAST score	477
E value	7.0e-48
Match length	129
% identity	67
NCBI Description	(AC002986) Similar to M. tuberculosis gene gb_Z96072 and M. leprae gene gb_400019. [Arabidopsis thaliana]

Seq. No.	395988
Contig ID	67475_1.R1084
5'-most EST	g4716193
Method	BLASTX
NCBI GI	g2129774
BLAST score	351
E value	1.0e-33
Match length	123
% identity	63
NCBI Description	xyloglucan endotransglycosylase-related protein XTR4 - Arabidopsis thaliana (fragment) >gi_1244754 (U43486) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	395989
Contig ID	67484_1.R1084
5'-most EST	g703018
Method	BLASTX
NCBI GI	g3860258
BLAST score	419
E value	8.0e-41
Match length	124
% identity	60
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	395990
Contig ID	67501_1.R1084
5'-most EST	g2431401
Method	BLASTX
NCBI GI	g4335719
BLAST score	260
E value	5.0e-22
Match length	124
% identity	41
NCBI Description	(AC006248) putative RING-H2 finger protein RHG1a [Arabidopsis thaliana]

Seq. No.	395991
Contig ID	67543_1.R1084
5'-most EST	g3768896
Method	BLASTX
NCBI GI	g729103
BLAST score	127
E value	4.0e-11
Match length	75
% identity	64
NCBI Description	CHALCONE--FLAVONONE ISOMERASE (CHALCONE ISOMERASE)

>gi_542181_pir__S41570 chalcone isomerase (EC 5.5.1.6) - maize >gi_396149_emb_CAA80441_ (Z22760) chalcone flavonone isomerase [Zea mays]

Seq. No.	395992
Contig ID	67551_1.R1084
5'-most EST	g2800296

Seq. No.	395993
Contig ID	67553_1.R1084
5'-most EST	g702949

Seq. No.	395994
Contig ID	67554_1.R1084
5'-most EST	g702955

Seq. No.	395995
Contig ID	67563_1.R1084
5'-most EST	g2310662
Method	BLASTX
NCBI GI	g4510381
BLAST score	192
E value	3.0e-14
Match length	95
% identity	46
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	395996
Contig ID	67576_1.R1084
5'-most EST	g2275826
Method	BLASTX
NCBI GI	g4510386
BLAST score	160
E value	2.0e-10
Match length	102
% identity	29
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	395997
Contig ID	67578_1.R1084
5'-most EST	g4968999

Seq. No.	395998
Contig ID	67631_2.R1084
5'-most EST	g703029

Seq. No.	395999
Contig ID	67635_1.R1084
5'-most EST	g703033

Seq. No.	396000
Contig ID	67687_1.R1084
5'-most EST	g969006

Seq. No.	396001
Contig ID	67690_1.R1084
5'-most EST	g3767703

Method	BLASTX
NCBI GI	g4850282
BLAST score	173
E value	2.0e-14
Match length	58
% identity	76
NCBI Description	(AL049876) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	396002
Contig ID	67716_1.R1084
5'-most EST	g1036859

Seq. No.	396003
Contig ID	67717_1.R1084
5'-most EST	g2275881
Method	BLASTX
NCBI GI	g5262197
BLAST score	136
E value	5.0e-09
Match length	86
% identity	48
NCBI Description	(AL080252) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396004
Contig ID	67720_1.R1084
5'-most EST	g2800662
Method	BLASTX
NCBI GI	g3687243
BLAST score	177
E value	2.0e-12
Match length	61
% identity	61
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	396005
Contig ID	67732_1.R1084
5'-most EST	g1036906

Seq. No.	396006
Contig ID	67752_1.R1084
5'-most EST	g1036897

Seq. No.	396007
Contig ID	67754_1.R1084
5'-most EST	g4969191

Seq. No.	396008
Contig ID	67768_1.R1084
5'-most EST	g3763421

Seq. No.	396009
Contig ID	67783_1.R1084
5'-most EST	g1036928

Seq. No.	396010

Contig ID	67789_1.R1084
5'-most EST	g3767895
Method	BLASTN
NCBI GI	g5295936
BLAST score	658
E value	0.0e+00
Match length	719
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	396011
Contig ID	67792_1.R1084
5'-most EST	g1036938

Seq. No.	396012
Contig ID	67814_1.R1084
5'-most EST	g5455404
Method	BLASTX
NCBI GI	g3641868
BLAST score	152
E value	1.0e-09
Match length	102
% identity	45
NCBI Description	(AJ011012) hypothetical protein [Cicer arietinum]

Seq. No.	396013
Contig ID	67847_1.R1084
5'-most EST	g4715201

Seq. No.	396014
Contig ID	67869_1.R1084
5'-most EST	g2801088

Seq. No.	396015
Contig ID	67884_1.R1084
5'-most EST	g1632046
Method	BLASTX
NCBI GI	g3540201
BLAST score	176
E value	1.0e-12
Match length	54
% identity	65
NCBI Description	(AC004260) Putative nuclear protein [Arabidopsis thaliana]

Seq. No.	396016
Contig ID	67922_1.R1084
5'-most EST	g5607488
Method	BLASTX
NCBI GI	g1350736
BLAST score	252
E value	2.0e-21
Match length	55
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L37 >gi_629673_pir__S44313 ribosomal protein L37 - tomato >gi_483586_emb_CAA55674_ (X79074) ribosomal protein L37 [Lycopersicon esculentum]

Seq. No.	396017
Contig ID	67923_1.R1084
5'-most EST	g3761870

Seq. No.	396018
Contig ID	67944_1.R1084
5'-most EST	g6024960

Seq. No.	396019
Contig ID	67948_1.R1084
5'-most EST	g3766590

Seq. No.	396020
Contig ID	67981_1.R1084
5'-most EST	g1631418

Seq. No.	396021
Contig ID	67996_1.R1084
5'-most EST	g1631434
Method	BLASTN
NCBI GI	g5441876
BLAST score	57
E value	4.0e-23
Match length	94
% identity	89
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	396022
Contig ID	68005_1.R1084
5'-most EST	g1631445

Seq. No.	396023
Contig ID	68014_1.R1084
5'-most EST	g2428187
Method	BLASTX
NCBI GI	g3492806
BLAST score	176
E value	9.0e-13
Match length	59
% identity	54
NCBI Description	(AJ225045) adventitious rooting related oxygenase [Malus domestica]

Seq. No.	396024
Contig ID	68015_1.R1084
5'-most EST	g4714614
Method	BLASTX
NCBI GI	g3386596
BLAST score	386
E value	4.0e-37
Match length	126
% identity	58
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana] >gi_3702346 (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	396025
Contig ID	68106_1.R1084
5'-most EST	g1631553
Seq. No.	396026
Contig ID	68137_1.R1084
5'-most EST	g1632382
Seq. No.	396027
Contig ID	68139_1.R1084
5'-most EST	g5003072
Method	BLASTX
NCBI GI	g4337174
BLAST score	174
E value	2.0e-12
Match length	68
% identity	57
NCBI Description	(AC006416) Similar to gi_1573829 HI0816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gb_U32764. [Arabidopsis thaliana]
Seq. No.	396028
Contig ID	68147_1.R1084
5'-most EST	g2309974
Method	BLASTX
NCBI GI	g4337025
BLAST score	254
E value	2.0e-22
Match length	95
% identity	68
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana] >gi_4972047_emb_CAB43915.1_ (AL078470) AIM1 protein [Arabidopsis thaliana]
Seq. No.	396029
Contig ID	68149_1.R1084
5'-most EST	g4714495
Method	BLASTX
NCBI GI	g2117624
BLAST score	281
E value	7.0e-25
Match length	104
% identity	62
NCBI Description	peroxidase (EC 1.11.1.7) 2 - alfalfa >gi_971564_emb_CAA62228_ (X90695) peroxidase2 [Medicago sativa]
Seq. No.	396030
Contig ID	68173_1.R1084
5'-most EST	g1631625
Seq. No.	396031
Contig ID	68193_1.R1084
5'-most EST	g1631647
Seq. No.	396032

Contig ID	68204_1.R1084
5'-most EST	g3762085
Seq. No.	396033
Contig ID	68224_1.R1084
5'-most EST	g1631678
Seq. No.	396034
Contig ID	68253_1.R1084
5'-most EST	g4880256
Method	BLASTN
NCBI GI	g5042437
BLAST score	38
E value	9.0e-12
Match length	62
% identity	64
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.	396035
Contig ID	68260_1.R1084
5'-most EST	g3768262
Method	BLASTX
NCBI GI	g5915834
BLAST score	173
E value	2.0e-21
Match length	211
% identity	35
NCBI Description	CYTOCHROME P450 76C4 >gi_2979547 (AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]
Seq. No.	396036
Contig ID	68269_1.R1084
5'-most EST	g2799758
Method	BLASTN
NCBI GI	g4097101
BLAST score	64
E value	3.0e-27
Match length	130
% identity	86
NCBI Description	Oryza sativa globulin-like protein mRNA, clone Ose710, partial cds
Seq. No.	396037
Contig ID	68276_1.R1084
5'-most EST	g1631732
Method	BLASTX
NCBI GI	g2655029
BLAST score	537
E value	5.0e-84
Match length	187
% identity	81
NCBI Description	(AF019296) starch synthase isoform zSTSII-1 [Zea mays]
Seq. No.	396038
Contig ID	68276_2.R1084
5'-most EST	g2431134
Method	BLASTX

NCBI GI	g2655029
BLAST score	546
E value	1.0e-90
Match length	187
% identity	83
NCBI Description	(AF019296) starch synthase isoform zSTSII-1 [Zea mays]

Seq. No.	396039
Contig ID	68283_1.R1084
5'-most EST	g5004834
Method	BLASTX
NCBI GI	g2130109
BLAST score	411
E value	7.0e-43
Match length	112
% identity	80
NCBI Description	porin VDAC3 - wheat >gi_558652_emb_CAA57646_ (X82148) Voltage dependent anion channel (VDAC) [Triticum aestivum]

Seq. No.	396040
Contig ID	68292_1.R1084
5'-most EST	g4715975
Method	BLASTX
NCBI GI	g303742
BLAST score	941
E value	1.0e-102
Match length	201
% identity	91
NCBI Description	(D12544) GTP-binding protein [Pisum sativum] >gi_738936_prf__2001457D GTP-binding protein [Pisum sativum]

Seq. No.	396041
Contig ID	68338_1.R1084
5'-most EST	g2442680

Seq. No.	396042
Contig ID	68351_1.R1084
5'-most EST	g1631816
Method	BLASTX
NCBI GI	g4929739
BLAST score	147
E value	8.0e-09
Match length	106
% identity	33
NCBI Description	(AF151893) CGI-135 protein [Homo sapiens]

Seq. No.	396043
Contig ID	68356_1.R1084
5'-most EST	g1632620

Seq. No.	396044
Contig ID	68365_1.R1084
5'-most EST	g1631832
Method	BLASTX
NCBI GI	g4895187
BLAST score	391

E value	1.0e-37
Match length	116
% identity	63
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No.	396045
Contig ID	68377_1.R1084
5'-most EST	g1631846
Method	BLASTN
NCBI GI	g4206193
BLAST score	42
E value	5.0e-14
Match length	42
% identity	100
NCBI Description	Reporter vector pSRF-Luc, complete sequence

Seq. No.	396046
Contig ID	68413_1.R1084
5'-most EST	g1631886

Seq. No.	396047
Contig ID	68425_1.R1084
5'-most EST	g1631899

Seq. No.	396048
Contig ID	68428_1.R1084
5'-most EST	g4968643
Method	BLASTX
NCBI GI	g5262788
BLAST score	334
E value	4.0e-47
Match length	126
% identity	80
NCBI Description	(AL080282) translation initiation factor eIF3-like protein [Arabidopsis thaliana]

Seq. No.	396049
Contig ID	68435_1.R1084
5'-most EST	g1632078

Seq. No.	396050
Contig ID	68464_1.R1084
5'-most EST	g2431218
Method	BLASTX
NCBI GI	g732003
BLAST score	130
E value	1.0e-15
Match length	129
% identity	43
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2125977_pir__I84534 outer membrane lipoprotein - Escherichia coli >gi_536993 (U14003) ORF_f177 [Escherichia coli] >gi_717134 (U21726) lipocalin precursor [Escherichia coli] >gi_1790592 (AE000487) outer membrane lipoprotein (lipocalin) [Escherichia coli]

Seq. No.	396051

Contig ID	68488_1.R1084
5'-most EST	g2798343
Method	BLASTX
NCBI GI	g1279640
BLAST score	417
E value	1.0e-40
Match length	129
% identity	61
NCBI Description	(X92204) NAM [Petunia x hybrida] >gi_6066595_emb_CAA63102.2_ (X92205) NAM [Petunia x hybrida]

Seq. No.	396052
Contig ID	68561_1.R1084
5'-most EST	g4879022

Seq. No.	396053
Contig ID	68583_1.R1084
5'-most EST	g2799824
Method	BLASTX
NCBI GI	g1177320
BLAST score	171
E value	6.0e-12
Match length	65
% identity	51
NCBI Description	(X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza sativa]

Seq. No.	396054
Contig ID	68586_1.R1084
5'-most EST	g1632070
Method	BLASTX
NCBI GI	g3080400
BLAST score	286
E value	2.0e-25
Match length	84
% identity	65
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	396055
Contig ID	68587_1.R1084
5'-most EST	g2800587

Seq. No.	396056
Contig ID	68653_1.R1084
5'-most EST	g5667298

Seq. No.	396057
Contig ID	68662_1.R1084
5'-most EST	g2797373

Seq. No.	396058
Contig ID	68664_1.R1084
5'-most EST	g1632154
Method	BLASTX

NCBI GI	g3080442
BLAST score	119
E value	1.0e-14
Match length	64
% identity	61
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	396059
Contig ID	68670_1.R1084
5'-most EST	g1632305
Method	BLASTN
NCBI GI	g3986093
BLAST score	71
E value	2.0e-31
Match length	151
% identity	88
NCBI Description	Chalinochromis brichardi DNA, microsatellite region

Seq. No.	396060
Contig ID	68678_1.R1084
5'-most EST	g1632168

Seq. No.	396061
Contig ID	68703_1.R1084
5'-most EST	g4969369

Seq. No.	396062
Contig ID	68728_1.R1084
5'-most EST	g2310987
Method	BLASTX
NCBI GI	g4204277
BLAST score	169
E value	6.0e-12
Match length	65
% identity	56
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	396063
Contig ID	68753_1.R1084
5'-most EST	g1632247
Method	BLASTX
NCBI GI	g3377843
BLAST score	303
E value	2.0e-27
Match length	84
% identity	70
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]

Seq. No.	396064
Contig ID	68764_1.R1084
5'-most EST	g3759975
Method	BLASTX
NCBI GI	g5823571
BLAST score	346
E value	1.0e-38
Match length	124

% identity	81
NCBI Description	(AL049730) Ribosomal protein L7Ae-like [Arabidopsis thaliana]

Seq. No.	396065
Contig ID	68780_1.R1084
5'-most EST	g1632276

Seq. No.	396066
Contig ID	68789_1.R1084
5'-most EST	g1632285
Method	BLASTX
NCBI GI	g2605714
BLAST score	403
E value	3.0e-46
Match length	131
% identity	64
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	396067
Contig ID	68789_2.R1084
5'-most EST	g2799139
Method	BLASTX
NCBI GI	g1109612
BLAST score	146
E value	3.0e-13
Match length	96
% identity	43
NCBI Description	(D45077) MP23 precursor [Cucurbita sp.]

Seq. No.	396068
Contig ID	68851_1.R1084
5'-most EST	g1632531

Seq. No.	396069
Contig ID	68878_1.R1084
5'-most EST	g1632377
Method	BLASTX
NCBI GI	g4587546
BLAST score	154
E value	3.0e-10
Match length	46
% identity	61
NCBI Description	(AC006577) Belongs to the PF_00011 Hsp20/alpha crystallin family. EST gb_W4312 comes from this gene. [Arabidopsis thaliana]

Seq. No.	396070
Contig ID	68888_1.R1084
5'-most EST	g1632388

Seq. No.	396071
Contig ID	68908_1.R1084
5'-most EST	g1632569
Method	BLASTX
NCBI GI	g4519539

BLAST score	131
E value	8.0e-18
Match length	69
% identity	67
NCBI Description	(AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No.	396072
Contig ID	68945_1.R1084
5'-most EST	g2431159
Method	BLASTX
NCBI GI	g1169521
BLAST score	204
E value	1.0e-30
Match length	73
% identity	100
NCBI Description	EMBRYONIC ABUNDANT PROTEIN 1 >gi_82464_pir__S22483 embryonic abundant protein emp1 - rice >gi_20200_emb_CAA44836_ (X63126) Emp1 [Oryza sativa] >gi_733119 (U22102) similar to embryonic abundant protein emp1, PIR Accession Number S22483; similar to the product encoded by the wheat Em gene, Swiss-Prot Accession Number P22701 [Oryza sativa]

Seq. No.	396073
Contig ID	68953_1.R1084
5'-most EST	g4969313

Seq. No.	396074
Contig ID	68965_1.R1084
5'-most EST	g5900675

Seq. No.	396075
Contig ID	69003_1.R1084
5'-most EST	g1632513

Seq. No.	396076
Contig ID	69014_1.R1084
5'-most EST	g1632525

Seq. No.	396077
Contig ID	69022_1.R1084
5'-most EST	g5039113
Method	BLASTN
NCBI GI	g5828965
BLAST score	33
E value	8.0e-09
Match length	57
% identity	89
NCBI Description	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

Seq. No.	396078
Contig ID	69036_1.R1084
5'-most EST	g1632547

Seq. No. 396079

Contig ID 69118_1.R1084
5'-most EST g3763081

Seq. No. 396080
Contig ID 69125_1.R1084
5'-most EST g1632640

Seq. No. 396081
Contig ID 69141_1.R1084
5'-most EST g1632656

Seq. No. 396082
Contig ID 69145_1.R1084
5'-most EST g3762176

Seq. No. 396083
Contig ID 69148_1.R1084
5'-most EST g2442679
Method BLASTX
NCBI GI g3128176
BLAST score 207
E value 2.0e-23
Match length 118
% identity 52
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 396084
Contig ID 69208_1.R1084
5'-most EST g4715718

Seq. No. 396085
Contig ID 69214_1.R1084
5'-most EST g3090643

Seq. No. 396086
Contig ID 69232_1.R1084
5'-most EST g2310527
Method BLASTX
NCBI GI g4218535
BLAST score 313
E value 6.0e-29
Match length 78
% identity 73
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 396087
Contig ID 69234_1.R1084
5'-most EST g4714561
Method BLASTN
NCBI GI g732975
BLAST score 35
E value 4.0e-10
Match length 79
% identity 86
NCBI Description T.aestivum pox4 gene

Seq. No. 396088

Contig ID	69247_1.R1084
5'-most EST	g1854118
Seq. No.	396089
Contig ID	69249_1.R1084
5'-most EST	g2798528
Seq. No.	396090
Contig ID	69268_1.R1084
5'-most EST	g2317352
Method	BLASTX
NCBI GI	g6041804
BLAST score	548
E value	6.0e-56
Match length	115
% identity	89
NCBI Description	(AC009755) putative protein kinase [Arabidopsis thaliana]
Seq. No.	396091
Contig ID	69284_1.R1084
5'-most EST	g3767440
Seq. No.	396092
Contig ID	69285_1.R1084
5'-most EST	g2798664
Seq. No.	396093
Contig ID	69303_1.R1084
5'-most EST	g1854175
Method	BLASTX
NCBI GI	g1778149
BLAST score	752
E value	5.0e-80
Match length	167
% identity	87
NCBI Description	(U66404) phosphate/phosphoenolpyruvate translocator precursor [Zea mays]
Seq. No.	396094
Contig ID	69310_1.R1084
5'-most EST	g1854182
Method	BLASTX
NCBI GI	g2245394
BLAST score	310
E value	4.0e-28
Match length	86
% identity	67
NCBI Description	(U89771) ARF1-binding protein [Arabidopsis thaliana]
Seq. No.	396095
Contig ID	69321_1.R1084
5'-most EST	g2312842
Method	BLASTX
NCBI GI	g3482974
BLAST score	490
E value	1.0e-49
Match length	121

% identity	77
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	396096
Contig ID	69335_1.R1084
5'-most EST	g4715620

Seq. No.	396097
Contig ID	69345_1.R1084
5'-most EST	g2276013

Seq. No.	396098
Contig ID	69366_1.R1084
5'-most EST	g3762095
Method	BLASTX
NCBI GI	g1362151
BLAST score	576
E value	1.0e-77
Match length	155
% identity	92
NCBI Description	mitogen-activated protein kinase 1 homolog (clone Aspk9) - oat >gi_871984_emb_CAA56314_ (X79993) MAP KINASE [Avena sativa]

Seq. No.	396099
Contig ID	69380_1.R1084
5'-most EST	g3768023

Seq. No.	396100
Contig ID	69391_1.R1084
5'-most EST	g5003850
Method	BLASTX
NCBI GI	g3128205
BLAST score	250
E value	3.0e-21
Match length	73
% identity	70
NCBI Description	(AC004077) putative pyruvate dehydrogenase complex E1 beta subunit [Arabidopsis thaliana] >gi_5702375_gb_AAD47282.1_AF167983_1 (AF167983) putative pyruvate dehydrogenase beta subunit [Arabidopsis thaliana]

Seq. No.	396101
Contig ID	69408_1.R1084
5'-most EST	g3768667

Seq. No.	396102
Contig ID	69414_1.R1084
5'-most EST	g3762174
Method	BLASTX
NCBI GI	g3928091
BLAST score	298
E value	7.0e-27
Match length	77
% identity	69
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	396103
Contig ID	69420_1.R1084
5'-most EST	g1944293
Seq. No.	396104
Contig ID	69423_1.R1084
5'-most EST	g4715664
Seq. No.	396105
Contig ID	69436_1.R1084
5'-most EST	g2317288
Seq. No.	396106
Contig ID	69477_1.R1084
5'-most EST	g3761953
Method	BLASTN
NCBI GI	g5295936
BLAST score	336
E value	0.0e+00
Match length	864
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence
Seq. No.	396107
Contig ID	69545_1.R1084
5'-most EST	g5455604
Method	BLASTX
NCBI GI	g4115379
BLAST score	190
E value	4.0e-14
Match length	182
% identity	41
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]
Seq. No.	396108
Contig ID	69556_1.R1084
5'-most EST	g2275914
Seq. No.	396109
Contig ID	69574_1.R1084
5'-most EST	g2275932
Method	BLASTX
NCBI GI	g4220480
BLAST score	266
E value	8.0e-23
Match length	127
% identity	47
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.	396110
Contig ID	69580_1.R1084
5'-most EST	g2275938
Seq. No.	396111

Contig ID	69580_2.R1084
5'-most EST	g3759846

Seq. No.	396112
Contig ID	69595_1.R1084
5'-most EST	g2275954
Method	BLASTX
NCBI GI	g1532167
BLAST score	184
E value	1.0e-13
Match length	65
% identity	48
NCBI Description	(U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis thaliana]

Seq. No.	396113
Contig ID	69601_1.R1084
5'-most EST	g5038778
Method	BLASTX
NCBI GI	g4314401
BLAST score	198
E value	2.0e-15
Match length	52
% identity	71
NCBI Description	(AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	396114
Contig ID	69647_1.R1084
5'-most EST	g2280870
Method	BLASTX
NCBI GI	g4883603
BLAST score	218
E value	1.0e-18
Match length	91
% identity	58
NCBI Description	(AC006922) putative xyloglucan endo-transglycosylase [Arabidopsis thaliana]

Seq. No.	396115
Contig ID	69667_1.R1084
5'-most EST	g5003060
Method	BLASTX
NCBI GI	g4263783
BLAST score	383
E value	1.0e-36
Match length	125
% identity	58
NCBI Description	(AC006068) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	396116
Contig ID	69678_1.R1084
5'-most EST	g2276043
Method	BLASTX

NCBI GI	g3033392
BLAST score	295
E value	6.0e-39
Match length	157
% identity	55
NCBI Description	(AC004238) putative translation initiation factor EIF-2B-epsilon subunit [Arabidopsis thaliana]

Seq. No.	396117
Contig ID	69692_1.R1084
5'-most EST	g2280540

Seq. No.	396118
Contig ID	69759_1.R1084
5'-most EST	g2280607

Seq. No.	396119
Contig ID	69761_1.R1084
5'-most EST	g2280609

Seq. No.	396120
Contig ID	69763_1.R1084
5'-most EST	g3762833

Seq. No.	396121
Contig ID	69773_1.R1084
5'-most EST	g4714184
Method	BLASTX
NCBI GI	g3309543
BLAST score	174
E value	1.0e-12
Match length	60
% identity	48
NCBI Description	(AF036382) MLL [Fugu rubripes]

Seq. No.	396122
Contig ID	69781_1.R1084
5'-most EST	g3763348
Method	BLASTX
NCBI GI	g773414
BLAST score	157
E value	3.0e-10
Match length	41
% identity	76
NCBI Description	(U23751) beta galactosidase [Cloning vector pBBR1MCS-2] >gi_833819 (U25059) LacZ alpha peptide [Cloning vector pBBR1MCS-3] >gi_833823 (U25060) LacZ alpha peptide [Cloning vector pBBR1MCS-4] >gi_833827 (U25061) LacZ alpha peptide [Cloning vector pBBR1MCS-5]

Seq. No.	396123
Contig ID	69797_1.R1084
5'-most EST	g2280660
Method	BLASTX
NCBI GI	g2281103
BLAST score	185
E value	2.0e-13

Match length	57
% identity	51
NCBI Description	(AC002333) Glucan endo-1,3-beta glucosidase isolog [Arabidopsis thaliana]

Seq. No.	396124
Contig ID	69816_1.R1084
5'-most EST	g3759753
Method	BLASTN
NCBI GI	g5441876
BLAST score	44
E value	3.0e-15
Match length	81
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	396125
Contig ID	69879_1.R1084
5'-most EST	g2280839

Seq. No.	396126
Contig ID	69892_1.R1084
5'-most EST	g3766578
Method	BLASTX
NCBI GI	g4887012
BLAST score	197
E value	1.0e-25
Match length	79
% identity	77
NCBI Description	(AF123504) Nt-iaa2.3 deduced protein [Nicotiana tabacum]

Seq. No.	396127
Contig ID	69911_1.R1084
5'-most EST	g2280775
Method	BLASTX
NCBI GI	g4454470
BLAST score	337
E value	6.0e-37
Match length	131
% identity	61
NCBI Description	(AC006234) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	396128
Contig ID	69923_1.R1084
5'-most EST	g2280787
Method	BLASTX
NCBI GI	g1145408
BLAST score	150
E value	2.0e-09
Match length	108
% identity	38
NCBI Description	(U38783) brefeldin A resistance protein [Schizosaccharomyces pombe] >gi_5051486_emb_CAB44765.1_ (AL078627) brefeldin a resistance protein. [Schizosaccharomyces pombe] >gi_1589567_prf__2211346A

brefeldin A resistance protein [Schizosaccharomyces pombe]

Seq. No.	396129
Contig ID	69949_1.R1084
5'-most EST	g2280814
Method	BLASTX
NCBI GI	g1208496
BLAST score	211
E value	7.0e-17
Match length	47
% identity	83
NCBI Description	(D38124) EREBP-3 [Nicotiana tabacum]

Seq. No.	396130
Contig ID	69953_1.R1084
5'-most EST	g4969268
Method	BLASTN
NCBI GI	g5295936
BLAST score	75
E value	7.0e-34
Match length	87
% identity	21
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	396131
Contig ID	69954_1.R1084
5'-most EST	g2280819

Seq. No.	396132
Contig ID	69959_1.R1084
5'-most EST	g2280824
Method	BLASTX
NCBI GI	g4191788
BLAST score	181
E value	3.0e-13
Match length	66
% identity	53
NCBI Description	(AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No.	396133
Contig ID	69968_1.R1084
5'-most EST	g2280833

Seq. No.	396134
Contig ID	69970_1.R1084
5'-most EST	g2798809
Method	BLASTN
NCBI GI	g2894791
BLAST score	41
E value	2.0e-13
Match length	83
% identity	96
NCBI Description	Cryptosporidium parvum heat shock protein 70 (Hsp 70) mRNA, complete cds

Seq. No.	396135
Contig ID	69978_1.R1084
5'-most EST	g2280843
Method	BLASTX
NCBI GI	g100226
BLAST score	141
E value	8.0e-09
Match length	40
% identity	62
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	396136
Contig ID	70004_1.R1084
5'-most EST	g2442547

Seq. No.	396137
Contig ID	70034_1.R1084
5'-most EST	g4969318

Seq. No.	396138
Contig ID	70041_1.R1084
5'-most EST	g2280906

Seq. No.	396139
Contig ID	70078_1.R1084
5'-most EST	g4969238
Method	BLASTX
NCBI GI	g5051775
BLAST score	400
E value	7.0e-39
Match length	149
% identity	52
NCBI Description	(AL078637) putative protein [Arabidopsis thaliana]

Seq. No.	396140
Contig ID	70099_1.R1084
5'-most EST	g2442401
Method	BLASTX
NCBI GI	g3269297
BLAST score	204
E value	6.0e-16
Match length	82
% identity	49
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	396141
Contig ID	70101_1.R1084
5'-most EST	g2280967
Method	BLASTX
NCBI GI	g4680192
BLAST score	149
E value	2.0e-09
Match length	74
% identity	41

NCBI Description	(AF111710) hypothetical protein [Oryza sativa subsp. indica]

Seq. No.	396142
Contig ID	70162_1.R1084
5'-most EST	g3762096
Method	BLASTX
NCBI GI	g3396052
BLAST score	626
E value	3.0e-65
Match length	132
% identity	86
NCBI Description	(AF079318) MAP kinase homolog [Triticum aestivum]

Seq. No.	396143
Contig ID	70165_1.R1084
5'-most EST	g3106557
Method	BLASTX
NCBI GI	g5734727
BLAST score	282
E value	5.0e-25
Match length	132
% identity	47
NCBI Description	(AC007259) Very similar to receptor-like protein kinases [Arabidopsis thaliana]

Seq. No.	396144
Contig ID	70186_1.R1084
5'-most EST	g2317334
Method	BLASTX
NCBI GI	g5882721
BLAST score	229
E value	9.0e-19
Match length	75
% identity	61
NCBI Description	(AC008263) Strong similarity to gb_D21805 calcium-dependent protein kinase (CDPK) from Arabidopsis thaliana and contains a PF_00069 Eukaryotic protein kinase and 4 PF_00036 EF hand domains

Seq. No.	396145
Contig ID	70192_1.R1084
5'-most EST	g3766951
Method	BLASTX
NCBI GI	g3643610
BLAST score	582
E value	6.0e-60
Match length	126
% identity	85
NCBI Description	(AC005395) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	396146
Contig ID	70197_1.R1084
5'-most EST	g2800326

Seq. No.	396147

Contig ID	70222_1.R1084
5'-most EST	g5004087
Method	BLASTX
NCBI GI	g629858
BLAST score	391
E value	1.0e-37
Match length	88
% identity	75
NCBI Description	protein kinase C inhibitor - maize

Seq. No.	396148
Contig ID	70230_1.R1084
5'-most EST	g2317381
Method	BLASTX
NCBI GI	g3219151
BLAST score	331
E value	9.0e-31
Match length	114
% identity	61
NCBI Description	(AB015181) cdc2 related [Mesembryanthemum crystallinum]

Seq. No.	396149
Contig ID	70234_1.R1084
5'-most EST	g2317387
Method	BLASTX
NCBI GI	g3056588
BLAST score	154
E value	8.0e-22
Match length	127
% identity	54
NCBI Description	(AC004255) T1F9.9 [Arabidopsis thaliana]

Seq. No.	396150
Contig ID	70235_1.R1084
5'-most EST	g2317388

Seq. No.	396151
Contig ID	70248_1.R1084
5'-most EST	g3760526
Method	BLASTX
NCBI GI	g320622
BLAST score	306
E value	7.0e-28
Match length	65
% identity	91
NCBI Description	probable protein kinase - maize (fragment) >gi_168618 (M62985) protein kinase [Zea mays]

Seq. No.	396152
Contig ID	70252_1.R1084
5'-most EST	g2317405
Method	BLASTN
NCBI GI	g5091496
BLAST score	407
E value	0.0e+00
Match length	460
% identity	97

NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	396153
Contig ID	70263_1.R1084
5'-most EST	g2317424

Seq. No.	396154
Contig ID	70268_1.R1084
5'-most EST	g2317421
Method	BLASTX
NCBI GI	g3445397
BLAST score	261
E value	2.0e-29
Match length	109
% identity	59
NCBI Description	(AJ010166) S-domain receptor-like protein kinase [Zea mays]

Seq. No.	396155
Contig ID	70271_1.R1084
5'-most EST	g2796461
Method	BLASTX
NCBI GI	g1362051
BLAST score	387
E value	4.0e-37
Match length	138
% identity	57
NCBI Description	protein kinase 3 - soybean >gi_310582 (L19361) protein kinase 3 [Glycine max]

Seq. No.	396156
Contig ID	70275_1.R1084
5'-most EST	g2317432

Seq. No.	396157
Contig ID	70277_1.R1084
5'-most EST	g2317434
Method	BLASTX
NCBI GI	g3367520
BLAST score	211
E value	4.0e-31
Match length	134
% identity	60
NCBI Description	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb_D12522 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	396158
Contig ID	70280_1.R1084
5'-most EST	g2317520
Method	BLASTX
NCBI GI	g4115383
BLAST score	133
E value	7.0e-31
Match length	214
% identity	43
NCBI Description	(AC005967) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No.	396159
Contig ID	70286_1.R1084
5'-most EST	g5803442
Method	BLASTX
NCBI GI	g4008006
BLAST score	512
E value	8.0e-52
Match length	163
% identity	63
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	396160
Contig ID	70287_1.R1084
5'-most EST	g2317445

Seq. No.	396161
Contig ID	70292_1.R1084
5'-most EST	g2317452
Method	BLASTX
NCBI GI	g5430769
BLAST score	258
E value	5.0e-29
Match length	151
% identity	54
NCBI Description	(AC007504) Similar to somatic embryogenesis receptor-like kinase [Arabidopsis thaliana]

Seq. No.	396162
Contig ID	70294_1.R1084
5'-most EST	g2317496
Method	BLASTX
NCBI GI	g3360289
BLAST score	929
E value	1.0e-101
Match length	213
% identity	88
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	396163
Contig ID	70304_1.R1084
5'-most EST	g2317514
Method	BLASTX
NCBI GI	g2315153
BLAST score	145
E value	2.0e-19
Match length	150
% identity	42
NCBI Description	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]

Seq. No.	396164
Contig ID	70315_1.R1084
5'-most EST	g2317482
Method	BLASTX

NCBI GI	g5091508
BLAST score	326
E value	2.0e-55
Match length	153
% identity	69
NCBI Description	(AB023482) ESTs C22458(C62866),C22459(C62866) correspond to a region of the predicted gene.; Similar to genomic sequence of Arabidopsis thaliana BAC F8A5, complete sequence.(AC002292) [Oryza sativa]

Seq. No.	396165
Contig ID	70329_1.R1084
5'-most EST	g2317491

Seq. No.	396166
Contig ID	70360_1.R1084
5'-most EST	g2317525
Method	BLASTX
NCBI GI	g4455259
BLAST score	139
E value	1.0e-15
Match length	71
% identity	66
NCBI Description	(AL035523) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	396167
Contig ID	70367_1.R1084
5'-most EST	g2317542
Method	BLASTX
NCBI GI	g4530126
BLAST score	183
E value	2.0e-13
Match length	96
% identity	40
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	396168
Contig ID	70370_1.R1084
5'-most EST	g3768264

Seq. No.	396169
Contig ID	70383_1.R1084
5'-most EST	g3762207
Method	BLASTX
NCBI GI	g2947063
BLAST score	144
E value	8.0e-09
Match length	37
% identity	65
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	396170
Contig ID	70385_1.R1084
5'-most EST	g3766793

Seq. No.	396171
Contig ID	70387_1.R1084
5'-most EST	g4715344
Method	BLASTX
NCBI GI	g2632252
BLAST score	555
E value	8.0e-57
Match length	167
% identity	63
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	396172
Contig ID	70388_1.R1084
5'-most EST	g5456484

Seq. No.	396173
Contig ID	70400_1.R1084
5'-most EST	g2317570
Method	BLASTX
NCBI GI	g4559329
BLAST score	183
E value	2.0e-13
Match length	47
% identity	68
NCBI Description	(AC007087) putative protein kinase MAP3K [Arabidopsis thaliana]

Seq. No.	396174
Contig ID	70408_1.R1084
5'-most EST	g3763589
Method	BLASTX
NCBI GI	g3445397
BLAST score	233
E value	4.0e-19
Match length	117
% identity	48
NCBI Description	(AJ010166) S-domain receptor-like protein kinase [Zea mays]

Seq. No.	396175
Contig ID	70421_1.R1084
5'-most EST	g2317595
Method	BLASTX
NCBI GI	g6016708
BLAST score	208
E value	2.0e-16
Match length	50
% identity	68
NCBI Description	(AC009325) putative protein kinase [Arabidopsis thaliana]

Seq. No.	396176
Contig ID	70439_1.R1084
5'-most EST	g2317612
Method	BLASTX
NCBI GI	g6056374
BLAST score	254
E value	9.0e-22

Match length	114
% identity	42
NCBI Description	(AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	396177
Contig ID	70442_1.R1084
5'-most EST	g3760337
Method	BLASTX
NCBI GI	g3236253
BLAST score	164
E value	3.0e-13
Match length	114
% identity	46
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	396178
Contig ID	70480_1.R1084
5'-most EST	g2310264

Seq. No.	396179
Contig ID	70510_1.R1084
5'-most EST	g2309674

Seq. No.	396180
Contig ID	70511_1.R1084
5'-most EST	g2310262
Method	BLASTX
NCBI GI	g1857447
BLAST score	198
E value	3.0e-15
Match length	91
% identity	48
NCBI Description	(U82367) UDP-glucose glucosyltransferase [Solanum tuberosum]

Seq. No.	396181
Contig ID	70515_1.R1084
5'-most EST	g2309680

Seq. No.	396182
Contig ID	70518_1.R1084
5'-most EST	g2309683
Method	BLASTX
NCBI GI	g1498168
BLAST score	143
E value	2.0e-14
Match length	88
% identity	55
NCBI Description	(D86730) endoxyloglucan transferase related protein [Nicotiana tabacum]

Seq. No.	396183
Contig ID	70520_1.R1084
5'-most EST	g2309685
Method	BLASTX

NCBI GI g2245378
BLAST score 525
E value 2.0e-53
Match length 159
% identity 64
NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana] >gi_5080809_gb_AAD39318.1_AC007258_7 (AC007258) auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 396184
Contig ID 70544_1.R1084
5'-most EST g3760140
Method BLASTX
NCBI GI g3914555
BLAST score 479
E value 6.0e-48
Match length 127
% identity 81
NCBI Description PUTATIVE RIBOSOME-BINDING FACTOR A, CHLOROPLAST PRECURSOR >gi_3096942_emb_CAA18852.1_ (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 396185
Contig ID 70576_1.R1084
5'-most EST g2309741

Seq. No. 396186
Contig ID 70579_1.R1084
5'-most EST g4879029

Seq. No. 396187
Contig ID 70618_1.R1084
5'-most EST g2443143

Seq. No. 396188
Contig ID 70620_1.R1084
5'-most EST g2309785
Method BLASTX
NCBI GI g2501499
BLAST score 141
E value 1.0e-08
Match length 57
% identity 53
NCBI Description INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE (IAA-GLU SYNTHETASE) ((URIDINE 5'-DIPHOSPHATE-GLUCOSE:INDOL-3-YLACETYL)-BETA-D-GLUCOSYL TRANSFERASE) >gi_626043_pir__A54739 indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) - maize >gi_548195 (L34847) IAA-glu synthetase [Zea mays]

Seq. No. 396189
Contig ID 70647_1.R1084
5'-most EST g2309812
Method BLASTX
NCBI GI g2494165
BLAST score 215
E value 3.0e-17

Match length	124
% identity	37
NCBI Description	DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP]) >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis thaliana]

Seq. No.	396190
Contig ID	70664_1.R1084
5'-most EST	g2309829

Seq. No.	396191
Contig ID	70701_1.R1084
5'-most EST	g2309866

Seq. No.	396192
Contig ID	70716_1.R1084
5'-most EST	g5038905
Method	BLASTX
NCBI GI	g4874267
BLAST score	266
E value	1.0e-30
Match length	157
% identity	59
NCBI Description	(AC007354) Strong similarity to gb_X56267 auxin-induced protein (pCNT115) from Nicotiana tabacum and is a member of the PF_00248 Aldo/keto reductase family. [Arabidopsis thaliana]

Seq. No.	396193
Contig ID	70739_1.R1084
5'-most EST	g2309904
Method	BLASTX
NCBI GI	g3367576
BLAST score	263
E value	2.0e-22
Match length	178
% identity	39
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	396194
Contig ID	70749_1.R1084
5'-most EST	g3107494

Seq. No.	396195
Contig ID	70772_1.R1084
5'-most EST	g2309938

Seq. No.	396196
Contig ID	70789_1.R1084
5'-most EST	g2310361
Method	BLASTX
NCBI GI	g6016736
BLAST score	449
E value	2.0e-44
Match length	168
% identity	56

NCBI Description (AC009325) unknown protein [Arabidopsis thaliana]

Seq. No. 396197
Contig ID 70804_1.R1084
5'-most EST g2310601

Seq. No. 396198
Contig ID 70813_1.R1084
5'-most EST g5002970

Seq. No. 396199
Contig ID 70818_1.R1084
5'-most EST g3766716
Method BLASTX
NCBI GI g464806
BLAST score 138
E value 5.0e-17
Match length 150
% identity 35
NCBI Description SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72) >gi_423182_pir__A40692 signal recognition particle 72K chain - dog >gi_297768_emb_CAA48014_ (X67813) signal recognition particle,72 kDa subunit [Canis familiaris]

Seq. No. 396200
Contig ID 70825_1.R1084
5'-most EST g2428705
Method BLASTX
NCBI GI g1362193
BLAST score 345
E value 2.0e-32
Match length 77
% identity 83
NCBI Description heat shock factor - maize >gi_2130134_pir__S61448 heat shock factor (clone hsfb) - maize >gi_886742_emb_CAA58117_ (X82943) heat shock factor [Zea mays]

Seq. No. 396201
Contig ID 70826_1.R1084
5'-most EST g2309992

Seq. No. 396202
Contig ID 70833_1.R1084
5'-most EST g2309999
Method BLASTX
NCBI GI g6006718
BLAST score 183
E value 4.0e-26
Match length 195
% identity 41
NCBI Description (AF109376) tRNA isopentenyl transferase [Arabidopsis thaliana]

Seq. No. 396203
Contig ID 70874_1.R1084
5'-most EST g2310040
Method BLASTX

NCBI GI g1129145
BLAST score 195
E value 4.0e-26
Match length 98
% identity 77
NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No. 396204
Contig ID 70879_1.R1084
5'-most EST g2310045
Method BLASTX
NCBI GI g5091610
BLAST score 277
E value 2.0e-24
Match length 74
% identity 74
NCBI Description (AC007858) 10A19I.15 [Oryza sativa]

Seq. No. 396205
Contig ID 70919_1.R1084
5'-most EST g2310312
Method BLASTX
NCBI GI g695411
BLAST score 437
E value 3.0e-43
Match length 129
% identity 73
NCBI Description (D49475) glutamate dehydrogenase [Zea mays]

Seq. No. 396206
Contig ID 70935_1.R1084
5'-most EST g4880936
Method BLASTX
NCBI GI g4539404
BLAST score 822
E value 4.0e-88
Match length 229
% identity 65
NCBI Description (AL049524) putative protein [Arabidopsis thaliana]

Seq. No. 396207
Contig ID 70939_1.R1084
5'-most EST g2310105

Seq. No. 396208
Contig ID 70946_1.R1084
5'-most EST g4878276
Method BLASTX
NCBI GI g4056568
BLAST score 370
E value 3.0e-43
Match length 123
% identity 26
NCBI Description (U90944) PDI-like protein [Zea mays]

Seq. No. 396209
Contig ID 70948_1.R1084

5'-most EST	g2427250
Method	BLASTN
NCBI GI	g1841356
BLAST score	263
E value	1.0e-146
Match length	386
% identity	94
NCBI Description	Oryza sativa DNA for mitochondrial ribosomal protein S11 (nuclear encoded), complete cds

Seq. No.	396210
Contig ID	70950_1.R1084
5'-most EST	g2310116
Method	BLASTX
NCBI GI	g2864616
BLAST score	280
E value	1.0e-24
Match length	71
% identity	72
NCBI Description	(AL021811) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396211
Contig ID	70981_1.R1084
5'-most EST	g2428601

Seq. No.	396212
Contig ID	71017_1.R1084
5'-most EST	g2310183
Method	BLASTX
NCBI GI	g5803275
BLAST score	602
E value	3.0e-62
Match length	138
% identity	83
NCBI Description	(AP000399) EST AU056133(S20320) corresponds to a region of the predicted gene; similar to Caenorhabditis elegans cosmid D1054; hypothetical protein (Z74030) [Oryza sativa]

Seq. No.	396213
Contig ID	71020_1.R1084
5'-most EST	g2310186

Seq. No.	396214
Contig ID	71043_1.R1084
5'-most EST	g2310209
Method	BLASTX
NCBI GI	g4769012
BLAST score	305
E value	1.0e-27
Match length	147
% identity	50
NCBI Description	(AF143746) CER1 [Oryza sativa]

Seq. No.	396215
Contig ID	71056_1.R1084
5'-most EST	g4715281

Seq. No. 396216
Contig ID 71100_1.R1084
5'-most EST g3760495

Seq. No. 396217
Contig ID 71143_1.R1084
5'-most EST g2800970
Method BLASTX
NCBI GI g4982519
BLAST score 314
E value 3.0e-33
Match length 101
% identity 64
NCBI Description (AC000107) F17F8.25 [Arabidopsis thaliana]

Seq. No. 396218
Contig ID 71154_1.R1084
5'-most EST g2310321

Seq. No. 396219
Contig ID 71165_1.R1084
5'-most EST g2442627

Seq. No. 396220
Contig ID 71172_1.R1084
5'-most EST g4715190

Seq. No. 396221
Contig ID 71175_1.R1084
5'-most EST g5607467

Seq. No. 396222
Contig ID 71181_1.R1084
5'-most EST g2312153
Method BLASTX
NCBI GI g2501599
BLAST score 271
E value 7.0e-24
Match length 85
% identity 60
NCBI Description HYPOTHETICAL 29.1 KD PROTEIN W06E11.4 IN CHROMOSOME III >gi_669022 (U20862) W06E11.4 gene product [Caenorhabditis elegans]

Seq. No. 396223
Contig ID 71186_1.R1084
5'-most EST g2427553

Seq. No. 396224
Contig ID 71192_1.R1084
5'-most EST g2310360

Seq. No. 396225
Contig ID 71195_1.R1084
5'-most EST g3759099

Seq. No. 396226

Contig ID	71195_2.R1084
5'-most EST	g2310363
Seq. No.	396227
Contig ID	71198_1.R1084
5'-most EST	g5003501
Method	BLASTX
NCBI GI	g3152606
BLAST score	420
E value	6.0e-41
Match length	99
% identity	75
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]
Seq. No.	396228
Contig ID	71234_1.R1084
5'-most EST	g4878162
Method	BLASTX
NCBI GI	g3319355
BLAST score	554
E value	3.0e-68
Match length	163
% identity	82
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]
Seq. No.	396229
Contig ID	71246_1.R1084
5'-most EST	g2310415
Method	BLASTX
NCBI GI	g4803944
BLAST score	345
E value	5.0e-53
Match length	271
% identity	39
NCBI Description	(AC006264) putative C2-domain protein (prosite: PD0C00380) [Arabidopsis thaliana]
Seq. No.	396230
Contig ID	71335_1.R1084
5'-most EST	g2310637
Method	BLASTX
NCBI GI	g4914451
BLAST score	123
E value	9.0e-11
Match length	53
% identity	64
NCBI Description	(AL050398) dimethylaniline monooxygenase-like protein [Arabidopsis thaliana]
Seq. No.	396231
Contig ID	71342_1.R1084
5'-most EST	g2310511
Seq. No.	396232
Contig ID	71359_1.R1084

5'-most EST	g2310528
Method	BLASTX
NCBI GI	g3881722
BLAST score	150
E value	2.0e-09
Match length	57
% identity	29
NCBI Description	(Z69385) Similarity to Human XE169 protein (SW:XE169_HUMAN); cDNA EST EMBL:D27033 comes from this gene; cDNA EST EMBL:D27035 comes from this gene; cDNA EST EMBL:D27034 comes from this gene; cDNA EST EMBL:D27037 comes from thi

Seq. No.	396233
Contig ID	71365_1.R1084
5'-most EST	g2310534
Method	BLASTX
NCBI GI	g2498732
BLAST score	262
E value	3.0e-24
Match length	148
% identity	47
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 >gi_1362014_pir__S57612 zeta-crystallin homolog - Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	396234
Contig ID	71383_1.R1084
5'-most EST	g2310552
Method	BLASTX
NCBI GI	g4220524
BLAST score	144
E value	5.0e-09
Match length	44
% identity	61
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	396235
Contig ID	71407_1.R1084
5'-most EST	g5003168

Seq. No.	396236
Contig ID	71426_1.R1084
5'-most EST	g2310596
Method	BLASTX
NCBI GI	g1915960
BLAST score	562
E value	9.0e-58
Match length	181
% identity	28
NCBI Description	(Y07636) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	396237
Contig ID	71434_1.R1084
5'-most EST	g5003792
Method	BLASTX

NCBI GI g2497543
BLAST score 339
E value 3.0e-36
Match length 141
% identity 64
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 396238
Contig ID 71441_1.R1084
5'-most EST g2310611

Seq. No. 396239
Contig ID 71451_1.R1084
5'-most EST g2310621

Seq. No. 396240
Contig ID 71481_1.R1084
5'-most EST g2799171
Method BLASTN
NCBI GI g3660464
BLAST score 53
E value 1.0e-20
Match length 53
% identity 100
NCBI Description Arabidopsis thaliana mRNA for Inositol 1,3,4-Trisphosphate 5/6 Kinase

Seq. No. 396241
Contig ID 71486_1.R1084
5'-most EST g3106801
Method BLASTN
NCBI GI g5803242
BLAST score 351
E value 0.0e+00
Match length 594
% identity 96
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No. 396242
Contig ID 71505_1.R1084
5'-most EST g3767437

Seq. No. 396243
Contig ID 71511_1.R1084
5'-most EST g3768241
Method BLASTX
NCBI GI g4567262
BLAST score 252
E value 1.0e-21
Match length 53
% identity 85
NCBI Description (AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No. 396244
Contig ID 71515_1.R1084

5'-most EST	g2310689
Method	BLASTX
NCBI GI	g5103847
BLAST score	174
E value	6.0e-12
Match length	150
% identity	31
NCBI Description	(AC007591) Contains PF_00561 alpha/beta hydrolase fold. [Arabidopsis thaliana]

Seq. No.	396245
Contig ID	71518_1.R1084
5'-most EST	g2443106
Method	BLASTX
NCBI GI	g4567247
BLAST score	261
E value	2.0e-22
Match length	133
% identity	43
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	396246
Contig ID	71551_1.R1084
5'-most EST	g2310725

Seq. No.	396247
Contig ID	71570_1.R1084
5'-most EST	g4969034
Method	BLASTX
NCBI GI	g4262143
BLAST score	197
E value	4.0e-19
Match length	104
% identity	56
NCBI Description	(AC005275) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396248
Contig ID	71587_1.R1084
5'-most EST	g2310762

Seq. No.	396249
Contig ID	71591_1.R1084
5'-most EST	g5803520

Seq. No.	396250
Contig ID	71600_1.R1084
5'-most EST	g2310777
Method	BLASTX
NCBI GI	g4678924
BLAST score	251
E value	1.0e-21
Match length	64
% identity	72
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	396251
Contig ID	71605_1.R1084

5'-most EST	g2310782
Method	BLASTX
NCBI GI	g4680339
BLAST score	163
E value	6.0e-16
Match length	171
% identity	40
NCBI Description	(AF128457) hypothetical protein [Oryza sativa subsp. indica]

Seq. No.	396252
Contig ID	71619_1.R1084
5'-most EST	g2310796

Seq. No.	396253
Contig ID	71627_1.R1084
5'-most EST	g2442498

Seq. No.	396254
Contig ID	71660_1.R1084
5'-most EST	g2310837

Seq. No.	396255
Contig ID	71675_1.R1084
5'-most EST	g4715750
Method	BLASTX
NCBI GI	g4586255
BLAST score	314
E value	2.0e-28
Match length	121
% identity	55
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	396256
Contig ID	71684_1.R1084
5'-most EST	g5003544
Method	BLASTX
NCBI GI	g1352461
BLAST score	171
E value	3.0e-23
Match length	103
% identity	63
NCBI Description	IN2-2 PROTEIN

Seq. No.	396257
Contig ID	71691_1.R1084
5'-most EST	g2428063
Method	BLASTX
NCBI GI	g4929711
BLAST score	177
E value	2.0e-12
Match length	162
% identity	31
NCBI Description	(AF151879) CGI-121 protein [Homo sapiens]

Seq. No.	396258
Contig ID	71698_1.R1084

5'-most EST	g5003087
Seq. No.	396259
Contig ID	71705_1.R1084
5'-most EST	g2310923
Method	BLASTX
NCBI GI	g3426064
BLAST score	199
E value	1.0e-18
Match length	109
% identity	47
NCBI Description	(AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
Seq. No.	396260
Contig ID	71711_1.R1084
5'-most EST	g5004896
Method	BLASTX
NCBI GI	g5123546
BLAST score	296
E value	1.0e-26
Match length	102
% identity	59
NCBI Description	(AL079344) putative protein [Arabidopsis thaliana]
Seq. No.	396261
Contig ID	71729_1.R1084
5'-most EST	g2313010
Seq. No.	396262
Contig ID	71730_1.R1084
5'-most EST	g2310908
Seq. No.	396263
Contig ID	71733_1.R1084
5'-most EST	g5002987
Seq. No.	396264
Contig ID	71735_1.R1084
5'-most EST	g3061230
Method	BLASTN
NCBI GI	g5019261
BLAST score	35
E value	6.0e-10
Match length	95
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T4O12 from chromosome I, complete sequence
Seq. No.	396265
Contig ID	71751_1.R1084
5'-most EST	g2310929
Seq. No.	396266
Contig ID	71812_1.R1084
5'-most EST	g2310990

Method	BLASTN
NCBI GI	g1244715
BLAST score	34
E value	2.0e-09
Match length	54
% identity	91
NCBI Description	Triticum aestivum ACC synthase (TA-ACS2) gene, complete cds

Seq. No.	396267
Contig ID	71813_1.R1084
5'-most EST	g4878253
Method	BLASTX
NCBI GI	g2129771
BLAST score	206
E value	6.0e-16
Match length	134
% identity	30
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No.	396268
Contig ID	71855_1.R1084
5'-most EST	g3759841
Method	BLASTX
NCBI GI	g4468794
BLAST score	366
E value	9.0e-43
Match length	126
% identity	75
NCBI Description	(AJ010296) Glutathione transferase III(b) [Zea mays]

Seq. No.	396269
Contig ID	71859_1.R1084
5'-most EST	g2311037

Seq. No.	396270
Contig ID	71900_1.R1084
5'-most EST	g2311080
Method	BLASTX
NCBI GI	g4218537
BLAST score	411
E value	1.0e-50
Match length	145
% identity	72
NCBI Description	(AJ010830) GRAB2 protein [Triticum sp.]

Seq. No.	396271
Contig ID	71907_1.R1084
5'-most EST	g2443108
Method	BLASTX
NCBI GI	g5802225
BLAST score	272
E value	8.0e-24
Match length	92

% identity	62
NCBI Description	(AF166262) HAL3A protein [Arabidopsis thaliana]

Seq. No.	396272
Contig ID	71926_1.R1084
5'-most EST	g2311162

Seq. No.	396273
Contig ID	71934_1.R1084
5'-most EST	g2311114
Method	BLASTX
NCBI GI	g4510349
BLAST score	198
E value	2.0e-15
Match length	77
% identity	57
NCBI Description	(AC006921) putative bZIP transcription factor [Arabidopsis thaliana]

Seq. No.	396274
Contig ID	71940_1.R1084
5'-most EST	g5056058
Method	BLASTX
NCBI GI	g4512664
BLAST score	342
E value	4.0e-32
Match length	80
% identity	81
NCBI Description	(AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi_4902472_emb_CAB43553.1_ (AJ012407) phosphoribosyl diphosphate synthase [Arabidopsis thaliana]

Seq. No.	396275
Contig ID	71977_1.R1084
5'-most EST	g4881032
Method	BLASTX
NCBI GI	g3687239
BLAST score	521
E value	8.0e-53
Match length	110
% identity	87
NCBI Description	(AC005169) putative clathrin coat assembly protein [Arabidopsis thaliana]

Seq. No.	396276
Contig ID	71984_1.R1084
5'-most EST	g4714804
Method	BLASTX
NCBI GI	g2655098
BLAST score	756
E value	1.0e-96
Match length	318
% identity	55
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	396277
Contig ID	72016_1.R1084
5'-most EST	g3766904

Seq. No.	396278
Contig ID	72020_1.R1084
5'-most EST	g2311203
Method	BLASTX
NCBI GI	g629807
BLAST score	336
E value	2.0e-31
Match length	137
% identity	47
NCBI Description	VP1 protein - rice

Seq. No.	396279
Contig ID	72036_1.R1084
5'-most EST	g2311219
Method	BLASTX
NCBI GI	g4262236
BLAST score	202
E value	8.0e-16
Match length	70
% identity	56
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	396280
Contig ID	72052_2.R1084
5'-most EST	g4878617
Method	BLASTX
NCBI GI	g1703446
BLAST score	204
E value	2.0e-37
Match length	160
% identity	59
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	396281
Contig ID	72053_1.R1084
5'-most EST	g2311236
Method	BLASTX
NCBI GI	g4371279
BLAST score	310
E value	2.0e-28
Match length	119
% identity	54
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396282
Contig ID	72092_1.R1084
5'-most EST	g2311275
Method	BLASTX

NCBI GI g2792155
BLAST score 331
E value 1.0e-30
Match length 129
% identity 47
NCBI Description (AJ223291) chalcone reductase [Sesbania rostrata]

Seq. No. 396283
Contig ID 72108_1.R1084
5'-most EST g2443156

Seq. No. 396284
Contig ID 72127_1.R1084
5'-most EST g2312939

Seq. No. 396285
Contig ID 72140_1.R1084
5'-most EST g2311323

Seq. No. 396286
Contig ID 72142_1.R1084
5'-most EST g5771074
Method BLASTX
NCBI GI g128186
BLAST score 225
E value 3.0e-34
Match length 78
% identity 94
NCBI Description NITRATE REDUCTASE 1 (NR1) >gi_82490_pir__S07554 nitrate reductase (NADH) (EC 1.6.6.1) - rice

Seq. No. 396287
Contig ID 72153_1.R1084
5'-most EST g2311349

Seq. No. 396288
Contig ID 72170_1.R1084
5'-most EST g5667231

Seq. No. 396289
Contig ID 72222_1.R1084
5'-most EST g2311407

Seq. No. 396290
Contig ID 72247_1.R1084
5'-most EST g2311432

Seq. No. 396291
Contig ID 72252_1.R1084
5'-most EST g2311437

Seq. No. 396292
Contig ID 72266_1.R1084
5'-most EST g4968934

Seq. No. 396293
Contig ID 72299_1.R1084

5'-most EST	g5816492
Method	BLASTN
NCBI GI	g5257255
BLAST score	71
E value	2.0e-31
Match length	197
% identity	78
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	396294
Contig ID	72318_1.R1084
5'-most EST	g2311503
Method	BLASTX
NCBI GI	g4914424
BLAST score	413
E value	1.0e-57
Match length	163
% identity	62
NCBI Description	(AL050351) Inositol monophosphatase-like protein [Arabidopsis thaliana]

Seq. No.	396295
Contig ID	72324_1.R1084
5'-most EST	g2311511

Seq. No.	396296
Contig ID	72333_1.R1084
5'-most EST	g2797423

Seq. No.	396297
Contig ID	72356_1.R1084
5'-most EST	g2311553
Method	BLASTX
NCBI GI	g2529662
BLAST score	500
E value	2.0e-50
Match length	102
% identity	94
NCBI Description	(AC002535) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] >gi_3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana]

Seq. No.	396298
Contig ID	72374_1.R1084
5'-most EST	g5003475
Method	BLASTX
NCBI GI	g2252866
BLAST score	182
E value	7.0e-13
Match length	134
% identity	41
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	396299
Contig ID	72410_1.R1084

5'-most EST	g3759862
Method	BLASTX
NCBI GI	g3717987
BLAST score	160
E value	1.0e-10
Match length	49
% identity	67
NCBI Description	(AJ005899) G subunit of Vacuolar-type H+-ATPase [Nicotiana tabacum]

Seq. No.	396300
Contig ID	72424_1.R1084
5'-most EST	g3762586

Seq. No.	396301
Contig ID	72428_1.R1084
5'-most EST	g2311626
Method	BLASTX
NCBI GI	g4454048
BLAST score	138
E value	5.0e-11
Match length	83
% identity	48
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	396302
Contig ID	72459_1.R1084
5'-most EST	g2311658

Seq. No.	396303
Contig ID	72462_1.R1084
5'-most EST	g2311660
Method	BLASTX
NCBI GI	g5042168
BLAST score	376
E value	5.0e-82
Match length	186
% identity	81
NCBI Description	(AL078620) GTP-binding-like protein [Arabidopsis thaliana]

Seq. No.	396304
Contig ID	72467_1.R1084
5'-most EST	g5004495

Seq. No.	396305
Contig ID	72477_1.R1084
5'-most EST	g2311676
Method	BLASTX
NCBI GI	g4204695
BLAST score	359
E value	2.0e-38
Match length	144
% identity	58
NCBI Description	(AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]

Seq. No. 396306

Contig ID	72492_1.R1084
5'-most EST	g2311691
Seq. No.	396307
Contig ID	72509_1.R1084
5'-most EST	g4878443
Method	BLASTX
NCBI GI	g2494610
BLAST score	473
E value	9.0e-72
Match length	169
% identity	86
NCBI Description	CELL DIVISION PROTEIN FTSZ CHLOROPLAST HOMOLOG PRECURSOR >gi_1079732 (U39877) cpFtsZ [Arabidopsis thaliana]
Seq. No.	396308
Contig ID	72524_1.R1084
5'-most EST	g2311723
Method	BLASTN
NCBI GI	g5091496
BLAST score	160
E value	3.0e-84
Match length	247
% identity	46
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence
Seq. No.	396309
Contig ID	72560_1.R1084
5'-most EST	g2311759
Method	BLASTX
NCBI GI	g3953471
BLAST score	470
E value	1.0e-46
Match length	140
% identity	60
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]
Seq. No.	396310
Contig ID	72562_1.R1084
5'-most EST	g2312980
Seq. No.	396311
Contig ID	72563_1.R1084
5'-most EST	g2311762
Seq. No.	396312
Contig ID	72570_1.R1084
5'-most EST	g4879021
Seq. No.	396313
Contig ID	72571_1.R1084
5'-most EST	g3758994
Method	BLASTX
NCBI GI	g3785998
BLAST score	136
E value	5.0e-13

Match length 122
% identity 37
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 396314
Contig ID 72580_1.R1084
5'-most EST g4878735
Method BLASTX
NCBI GI g3334441
BLAST score 312
E value 2.0e-28
Match length 151
% identity 28
NCBI Description HYPOTHETICAL 47.9 KD PROTEIN T5I7.9 IN CHROMOSOME II >gi_2642161 (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 396315
Contig ID 72595_1.R1084
5'-most EST g2311794

Seq. No. 396316
Contig ID 72604_1.R1084
5'-most EST g2311803

Seq. No. 396317
Contig ID 72701_1.R1084
5'-most EST g2311900

Seq. No. 396318
Contig ID 72736_1.R1084
5'-most EST g2311936

Seq. No. 396319
Contig ID 72738_1.R1084
5'-most EST g3769247

Seq. No. 396320
Contig ID 72758_1.R1084
5'-most EST g2311958

Seq. No. 396321
Contig ID 72767_1.R1084
5'-most EST g2311967
Method BLASTX
NCBI GI g2695925
BLAST score 319
E value 3.0e-33
Match length 83
% identity 93
NCBI Description (AJ222776) hypothetical protein [Hordeum vulgare]

Seq. No. 396322
Contig ID 72789_1.R1084
5'-most EST g3760184

Seq. No. 396323

Contig ID	72793_1.R1084
5'-most EST	g2311997
Method	BLASTN
NCBI GI	g6041757
BLAST score	64
E value	2.0e-27
Match length	100
% identity	91
NCBI Description	Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence

Seq. No.	396324
Contig ID	72794_1.R1084
5'-most EST	g2311998
Method	BLASTX
NCBI GI	g4929803
BLAST score	182
E value	1.0e-13
Match length	48
% identity	73
NCBI Description	(AF152555) putative zinc finger protein SHI [Arabidopsis thaliana]

Seq. No.	396325
Contig ID	72799_1.R1084
5'-most EST	g3061101
Method	BLASTX
NCBI GI	g3242071
BLAST score	478
E value	4.0e-48
Match length	91
% identity	89
NCBI Description	(AJ007289) myb-like protein [Arabidopsis thaliana]

Seq. No.	396326
Contig ID	72807_1.R1084
5'-most EST	g2312011
Method	BLASTN
NCBI GI	g5042437
BLAST score	55
E value	6.0e-22
Match length	99
% identity	89
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	396327
Contig ID	72814_1.R1084
5'-most EST	g2312018

Seq. No.	396328
Contig ID	72815_1.R1084
5'-most EST	g3762939
Method	BLASTX
NCBI GI	g1915960
BLAST score	287
E value	1.0e-25
Match length	74

% identity	76
NCBI Description	(Y07636) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	396329
Contig ID	72825_1.R1084
5'-most EST	g2312029

Seq. No.	396330
Contig ID	72829_1.R1084
5'-most EST	g2312033
Method	BLASTX
NCBI GI	g3157951
BLAST score	374
E value	3.0e-35
Match length	144
% identity	71
NCBI Description	(AC002131) Contains similarity to vesicle trafficking protein gb_U91538 from Mus musculus. ESTs gb_F15494 and gb_F14097 come from this gene. [Arabidopsis thaliana]

Seq. No.	396331
Contig ID	72856_1.R1084
5'-most EST	g2312636
Method	BLASTX
NCBI GI	g300264
BLAST score	310
E value	3.0e-28
Match length	128
% identity	37
NCBI Description	(S59747) HSP68=68 kda heat-stress DnaK homolog [Solanum tuberosum=potatoes, Peptide Mitochondrial, 682 aa] [Solanum tuberosum]

Seq. No.	396332
Contig ID	72881_1.R1084
5'-most EST	g2312117

Seq. No.	396333
Contig ID	72882_1.R1084
5'-most EST	g2312087

Seq. No.	396334
Contig ID	72887_1.R1084
5'-most EST	g2312865

Seq. No.	396335
Contig ID	72906_1.R1084
5'-most EST	g2312294

Seq. No.	396336
Contig ID	72910_1.R1084
5'-most EST	g2312116
Method	BLASTN
NCBI GI	g5295936
BLAST score	349
E value	0.0e+00
Match length	478

% identity	71
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	396337
Contig ID	72918_1.R1084
5'-most EST	g4715728

Seq. No.	396338
Contig ID	72925_1.R1084
5'-most EST	g2312131
Method	BLASTX
NCBI GI	g1706884
BLAST score	224
E value	2.0e-22
Match length	120
% identity	52
NCBI Description	FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS)

Seq. No.	396339
Contig ID	72934_1.R1084
5'-most EST	g2312168

Seq. No.	396340
Contig ID	72936_1.R1084
5'-most EST	g2312142

Seq. No.	396341
Contig ID	72942_1.R1084
5'-most EST	g2312148
Method	BLASTX
NCBI GI	g5902395
BLAST score	257
E value	1.0e-39
Match length	142
% identity	55
NCBI Description	(AC008148) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	396342
Contig ID	72956_1.R1084
5'-most EST	g3760373

Seq. No.	396343
Contig ID	72978_1.R1084
5'-most EST	g3768036
Method	BLASTX
NCBI GI	g4646218
BLAST score	314
E value	6.0e-49
Match length	131
% identity	79
NCBI Description	(AC007290) putative GTP-binding protein [Arabidopsis thaliana]

Seq. No.	396344
Contig ID	72990_1.R1084

5'-most EST	g5004318
Method	BLASTX
NCBI GI	g4263048
BLAST score	283
E value	4.0e-25
Match length	71
% identity	73
NCBI Description	(AC005142) putative hydrolase [Arabidopsis thaliana]

Seq. No.	396345
Contig ID	72996_1.R1084
5'-most EST	g2312203

Seq. No.	396346
Contig ID	72997_1.R1084
5'-most EST	g2312204
Method	BLASTX
NCBI GI	g4584548
BLAST score	557
E value	2.0e-57
Match length	138
% identity	78
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	396347
Contig ID	73053_1.R1084
5'-most EST	g3061124

Seq. No.	396348
Contig ID	73072_1.R1084
5'-most EST	g2312279

Seq. No.	396349
Contig ID	73092_1.R1084
5'-most EST	g2312315

Seq. No.	396350
Contig ID	73134_1.R1084
5'-most EST	g2312341

Seq. No.	396351
Contig ID	73143_1.R1084
5'-most EST	g2312350
Method	BLASTX
NCBI GI	g4775576
BLAST score	401
E value	5.0e-39
Match length	87
% identity	87
NCBI Description	(AJ238785) MUS1 protein [Zea mays]

Seq. No.	396352
Contig ID	73146_1.R1084
5'-most EST	g2312353
Method	BLASTX
NCBI GI	g2952433
BLAST score	189

E value	2.0e-21
Match length	107
% identity	59
NCBI Description	(AF051135) putative ubiquitin activating enzyme E1 [Arabidopsis thaliana]

Seq. No.	396353
Contig ID	73153_1.R1084
5'-most EST	g2312360
Method	BLASTX
NCBI GI	g3540181
BLAST score	276
E value	2.0e-31
Match length	137
% identity	64
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	396354
Contig ID	73179_1.R1084
5'-most EST	g5667157

Seq. No.	396355
Contig ID	73211_1.R1084
5'-most EST	g2312419
Method	BLASTX
NCBI GI	g6017114
BLAST score	189
E value	2.0e-21
Match length	125
% identity	56
NCBI Description	(AC009895) unknown protein [Arabidopsis thaliana]

Seq. No.	396356
Contig ID	73225_1.R1084
5'-most EST	g2312433
Method	BLASTX
NCBI GI	g118719
BLAST score	389
E value	2.0e-37
Match length	212
% identity	40
NCBI Description	DNAJ PROTEIN >gi_72228_pir__HHECDJ heat shock protein dnaJ - Escherichia coli >gi_145769 (M12565) heat shock protein dnaJ [Escherichia coli] >gi_216441_dbj_BAA01292_ (D10483) DnaJ [Escherichia coli] >gi_1786197 (AE000112) chaperone with DnaK; heat shock protein [Escherichia coli]

Seq. No.	396357
Contig ID	73236_1.R1084
5'-most EST	g2312444
Method	BLASTX
NCBI GI	g113595
BLAST score	464
E value	1.0e-46
Match length	103
% identity	89
NCBI Description	ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE)

>gi_100562_pir__S15024 aldose reductase-related protein - barley >gi_18891_emb_CAA40747_ (X57526) aldose reductase-related protein [Hordeum vulgare]

Seq. No.	396358
Contig ID	73244_1.R1084
5'-most EST	g4878164

Seq. No.	396359
Contig ID	73267_1.R1084
5'-most EST	g2312475

Seq. No.	396360
Contig ID	73288_1.R1084
5'-most EST	g2312496
Method	BLASTX
NCBI GI	g2842493
BLAST score	183
E value	2.0e-13
Match length	60
% identity	58
NCBI Description	(AL021749) predicted protein [Arabidopsis thaliana]

Seq. No.	396361
Contig ID	73290_1.R1084
5'-most EST	g4879091

Seq. No.	396362
Contig ID	73301_1.R1084
5'-most EST	g4715722
Method	BLASTX
NCBI GI	g2465525
BLAST score	182
E value	1.0e-34
Match length	220
% identity	42
NCBI Description	(U97124) ClpB/HSP100 [Synechococcus PCC7942]

Seq. No.	396363
Contig ID	73302_1.R1084
5'-most EST	g2428046

Seq. No.	396364
Contig ID	73313_1.R1084
5'-most EST	g3760402

Seq. No.	396365
Contig ID	73337_1.R1084
5'-most EST	g2312547
Method	BLASTX
NCBI GI	g3831443
BLAST score	156
E value	5.0e-10
Match length	42
% identity	69
NCBI Description	(AC005819) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No. 396366
Contig ID 73375_1.R1084
5'-most EST g5004339

Seq. No. 396367
Contig ID 73385_1.R1084
5'-most EST g3768789

Seq. No. 396368
Contig ID 73393_1.R1084
5'-most EST g2312603
Method BLASTX
NCBI GI g2443329
BLAST score 151
E value 1.0e-09
Match length 31
% identity 84
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 396369
Contig ID 73399_1.R1084
5'-most EST g4879093
Method BLASTX
NCBI GI g4220445
BLAST score 216
E value 3.0e-17
Match length 142
% identity 4
NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible protein homolog from Arabidopsis thaliana BAC gb_AC003673. [Arabidopsis thaliana]

Seq. No. 396370
Contig ID 73404_1.R1084
5'-most EST g2312614

Seq. No. 396371
Contig ID 73413_1.R1084
5'-most EST g2312761
Method BLASTX
NCBI GI g4972045
BLAST score 157
E value 2.0e-10
Match length 66
% identity 52
NCBI Description (AL078470) putative protein [Arabidopsis thaliana]

Seq. No. 396372
Contig ID 73416_1.R1084
5'-most EST g2442711
Method BLASTX
NCBI GI g3548803
BLAST score 398
E value 1.0e-38
Match length 141
% identity 59

NCBI Description	(AC005313) putative DNA-binding protein [Arabidopsis thaliana] >gi_4335770_gb_AAD17447_ (AC006284) putative SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]
Seq. No.	396373
Contig ID	73419_1.R1084
5'-most EST	g2312629
Seq. No.	396374
Contig ID	73436_1.R1084
5'-most EST	g2312648
Seq. No.	396375
Contig ID	73514_1.R1084
5'-most EST	g5003834
Method	BLASTX
NCBI GI	g4959710
BLAST score	170
E value	5.0e-12
Match length	88
% identity	45
NCBI Description	(AF135596) Skp1 [Medicago sativa]
Seq. No.	396376
Contig ID	73528_1.R1084
5'-most EST	g2312743
Seq. No.	396377
Contig ID	73531_1.R1084
5'-most EST	g3763475
Method	BLASTX
NCBI GI	g3318615
BLAST score	253
E value	1.0e-24
Match length	118
% identity	39
NCBI Description	(AB016065) mitochondrial phosphate transporter [Oryza sativa]
Seq. No.	396378
Contig ID	73533_1.R1084
5'-most EST	g4716186
Method	BLASTX
NCBI GI	g688423
BLAST score	208
E value	5.0e-17
Match length	82
% identity	54
NCBI Description	(D26453) tumor-related protein [Nicotiana glauca X Nicotiana langsdorffii]
Seq. No.	396379
Contig ID	73561_1.R1084
5'-most EST	g4879039
Seq. No.	396380
Contig ID	73566_1.R1084

5'-most EST	g2312781
Method	BLASTX
NCBI GI	g2459417
BLAST score	191
E value	2.0e-14
Match length	48
% identity	77
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	396381
Contig ID	73577_1.R1084
5'-most EST	g2312792

Seq. No.	396382
Contig ID	73599_1.R1084
5'-most EST	g2312815
Method	BLASTN
NCBI GI	g1066160
BLAST score	43
E value	1.0e-14
Match length	96
% identity	94
NCBI Description	Wheat gene for protein H2B153, complete cds

Seq. No.	396383
Contig ID	73609_1.R1084
5'-most EST	g3762083
Method	BLASTX
NCBI GI	g5262788
BLAST score	393
E value	9.0e-38
Match length	105
% identity	62
NCBI Description	(AL080282) translation initiation factor eIF3-like protein [Arabidopsis thaliana]

Seq. No.	396384
Contig ID	73612_1.R1084
5'-most EST	g2312829

Seq. No.	396385
Contig ID	73639_1.R1084
5'-most EST	g2801145

Seq. No.	396386
Contig ID	73656_1.R1084
5'-most EST	g5851012
Method	BLASTN
NCBI GI	g6063530
BLAST score	283
E value	1.0e-158
Match length	452
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	396387

Contig ID	73664_1.R1084
5'-most EST	g6024987

Seq. No.	396388
Contig ID	73671_1.R1084
5'-most EST	g2312889

Seq. No.	396389
Contig ID	73693_1.R1084
5'-most EST	g2312912
Method	BLASTX
NCBI GI	g2494140
BLAST score	354
E value	3.0e-33
Match length	135
% identity	51
NCBI Description	(AC003002) R29515_1 [Homo sapiens] >gi_3068727 (AF058918) unknown [Homo sapiens] >gi_5734091_gb_AAD49845.1_AF157065_1 (AF157065) sedlin [Homo sapiens]

Seq. No.	396390
Contig ID	73703_1.R1084
5'-most EST	g2797368
Method	BLASTX
NCBI GI	g3080390
BLAST score	587
E value	2.0e-60
Match length	164
% identity	67
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	396391
Contig ID	73761_1.R1084
5'-most EST	g2312981
Method	BLASTX
NCBI GI	g549732
BLAST score	227
E value	2.0e-18
Match length	90
% identity	43
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION >gi_481110_pir__S37791 hypothetical protein YKL160w - yeast (Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_ (Z26877) unknown [Saccharomyces cerevisiae] >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w [Saccharomyces cerevisiae] >gi_1582545_prf__2118404F ORF [Saccharomyces cerevisiae]

Seq. No.	396392
Contig ID	73766_1.R1084
5'-most EST	g2312986
Method	BLASTX
NCBI GI	g3269289
BLAST score	262
E value	1.0e-22
Match length	87
% identity	64

NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]
Seq. No.	396393
Contig ID	73769_1.R1084
5'-most EST	g5005276
Method	BLASTX
NCBI GI	g3080400
BLAST score	147
E value	3.0e-09
Match length	38
% identity	71
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]
Seq. No.	396394
Contig ID	73779_1.R1084
5'-most EST	g3760232
Method	BLASTX
NCBI GI	g5669654
BLAST score	149
E value	5.0e-09
Match length	54
% identity	50
NCBI Description	(AF096262) ER6 protein [Lycopersicon esculentum]
Seq. No.	396395
Contig ID	73801_1.R1084
5'-most EST	g3763675
Seq. No.	396396
Contig ID	73832_1.R1084
5'-most EST	g2427217
Seq. No.	396397
Contig ID	73837_1.R1084
5'-most EST	g3761190
Seq. No.	396398
Contig ID	73910_1.R1084
5'-most EST	g2428625
Seq. No.	396399
Contig ID	73914_1.R1084
5'-most EST	g3768269
Seq. No.	396400
Contig ID	73918_1.R1084
5'-most EST	g3761235
Method	BLASTN
NCBI GI	g2280503
BLAST score	63
E value	2.0e-26
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana tRNA-Asp gene

Seq. No.	396401
Contig ID	73928_1.R1084
5'-most EST	g5038624
Method	BLASTX
NCBI GI	g4580523
BLAST score	162
E value	1.0e-24
Match length	122
% identity	56
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	396402
Contig ID	73943_1.R1084
5'-most EST	g2427332

Seq. No.	396403
Contig ID	73956_1.R1084
5'-most EST	g2427348

Seq. No.	396404
Contig ID	73983_1.R1084
5'-most EST	g2428910

Seq. No.	396405
Contig ID	74030_1.R1084
5'-most EST	g2429062
Method	BLASTX
NCBI GI	g6006895
BLAST score	197
E value	1.0e-18
Match length	68
% identity	68
NCBI Description	(AC008153) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396406
Contig ID	74037_1.R1084
5'-most EST	g2428214
Method	BLASTX
NCBI GI	g1353193
BLAST score	220
E value	2.0e-19
Match length	118
% identity	53
NCBI Description	O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No.	396407
Contig ID	74047_1.R1084
5'-most EST	g5455391
Method	BLASTX
NCBI GI	g3033375
BLAST score	262
E value	2.0e-22
Match length	82
% identity	59
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No.	396408
Contig ID	74074_1.R1084
5'-most EST	g4879663

Seq. No.	396409
Contig ID	74081_1.R1084
5'-most EST	g2442821
Method	BLASTX
NCBI GI	g3289002
BLAST score	470
E value	1.0e-53
Match length	124
% identity	16
NCBI Description	(AF073522) CRP1 [Zea mays]

Seq. No.	396410
Contig ID	74085_1.R1084
5'-most EST	g3107645
Method	BLASTX
NCBI GI	g1054843
BLAST score	345
E value	3.0e-42
Match length	107
% identity	78
NCBI Description	(X92847) D12 oleate desaturase [Solanum commersonii]

Seq. No.	396411
Contig ID	74110_1.R1084
5'-most EST	g4968828
Method	BLASTN
NCBI GI	g5922603
BLAST score	323
E value	0.0e+00
Match length	368
% identity	62
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No.	396412
Contig ID	74117_1.R1084
5'-most EST	g2427527
Method	BLASTX
NCBI GI	g4204258
BLAST score	543
E value	4.0e-61
Match length	213
% identity	57
NCBI Description	(AC005223) 14409 [Arabidopsis thaliana]

Seq. No.	396413
Contig ID	74149_1.R1084
5'-most EST	g3061192
Method	BLASTX
NCBI GI	g3641838
BLAST score	268
E value	2.0e-29

Match length	101
% identity	62
NCBI Description	(AL023094) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	396414
Contig ID	74204_1.R1084
5'-most EST	g2427602
Method	BLASTX
NCBI GI	g2760323
BLAST score	545
E value	5.0e-59
Match length	196
% identity	66
NCBI Description	(AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No.	396415
Contig ID	74211_1.R1084
5'-most EST	g2427609

Seq. No.	396416
Contig ID	74226_1.R1084
5'-most EST	g2428395

Seq. No.	396417
Contig ID	74236_1.R1084
5'-most EST	g2427999

Seq. No.	396418
Contig ID	74241_1.R1084
5'-most EST	g2427639
Method	BLASTX
NCBI GI	g4895170
BLAST score	581
E value	4.0e-60
Match length	137
% identity	85
NCBI Description	(AC007662) putative plasma membrane ATPase [Arabidopsis thaliana]

Seq. No.	396419
Contig ID	74245_1.R1084
5'-most EST	g5003677
Method	BLASTX
NCBI GI	g3298441
BLAST score	337
E value	5.0e-33
Match length	130
% identity	53
NCBI Description	(AB010879) chloroplast ribosomal protein L10 [Nicotiana tabacum]

Seq. No.	396420
Contig ID	74261_1.R1084
5'-most EST	g2427659
Method	BLASTX
NCBI GI	g2244888

BLAST score	201
E value	2.0e-15
Match length	92
% identity	40
NCBI Description	(Z97338) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	396421
Contig ID	74328_1.R1084
5'-most EST	g2442718
Method	BLASTX
NCBI GI	g4220481
BLAST score	204
E value	9.0e-16
Match length	88
% identity	51
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	396422
Contig ID	74345_1.R1084
5'-most EST	g4715225
Method	BLASTX
NCBI GI	g4895190
BLAST score	304
E value	3.0e-27
Match length	98
% identity	60
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No.	396423
Contig ID	74390_1.R1084
5'-most EST	g5004988

Seq. No.	396424
Contig ID	74416_1.R1084
5'-most EST	g5004336

Seq. No.	396425
Contig ID	74480_1.R1084
5'-most EST	g4879505
Method	BLASTX
NCBI GI	g5052007
BLAST score	1277
E value	1.0e-141
Match length	344
% identity	65
NCBI Description	(AF155121) apoplastic invertase [Oryza sativa subsp. indica]

Seq. No.	396426
Contig ID	74489_1.R1084
5'-most EST	g2427888

Seq. No.	396427
Contig ID	74519_1.R1084
5'-most EST	g2427919

Seq. No.	396428
Contig ID	74587_1.R1084
5'-most EST	g4880156
Method	BLASTX
NCBI GI	g3834325
BLAST score	557
E value	6.0e-57
Match length	204
% identity	55
NCBI Description	(AC005679) Strong similarity to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_R83955, gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No.	396429
Contig ID	74617_1.R1084
5'-most EST	g2428017
Method	BLASTX
NCBI GI	g4033431
BLAST score	218
E value	2.0e-17
Match length	86
% identity	56
NCBI Description	PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK) >gi_2982467_emb_CAA18231.1_ (AL022223) pyruvate kinase like protein [Arabidopsis thaliana]

Seq. No.	396430
Contig ID	74626_1.R1084
5'-most EST	g2442645

Seq. No.	396431
Contig ID	74641_1.R1084
5'-most EST	g5005050

Seq. No.	396432
Contig ID	74696_1.R1084
5'-most EST	g2428097
Method	BLASTX
NCBI GI	g2196878
BLAST score	575
E value	2.0e-59
Match length	138
% identity	82
NCBI Description	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]

Seq. No.	396433
Contig ID	74733_1.R1084
5'-most EST	g2800682
Method	BLASTX
NCBI GI	g3786009
BLAST score	347
E value	4.0e-45
Match length	172
% identity	62
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	396434
Contig ID	74741_1.R1084
5'-most EST	g2428143
Method	BLASTX
NCBI GI	g6091729
BLAST score	455
E value	8.0e-47
Match length	141
% identity	68
NCBI Description	(AC010797) unknown protein [Arabidopsis thaliana]

Seq. No.	396435
Contig ID	74744_1.R1084
5'-most EST	g2428146
Method	BLASTX
NCBI GI	g4538929
BLAST score	228
E value	1.0e-18
Match length	55
% identity	71
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	396436
Contig ID	74873_1.R1084
5'-most EST	g4715341
Method	BLASTX
NCBI GI	g3953475
BLAST score	242
E value	3.0e-20
Match length	99
% identity	48
NCBI Description	(AC002328) F22O2.20 [Arabidopsis thaliana]

Seq. No.	396437
Contig ID	74877_1.R1084
5'-most EST	g2428279
Method	BLASTX
NCBI GI	g1710151
BLAST score	287
E value	1.0e-25
Match length	69
% identity	74
NCBI Description	(U72711) proline iminopeptidase [Arabidopsis thaliana]

Seq. No.	396438
Contig ID	74949_1.R1084
5'-most EST	g2428352

Seq. No.	396439
Contig ID	74951_1.R1084
5'-most EST	g2428354
Method	BLASTX
NCBI GI	g4586049
BLAST score	233
E value	5.0e-26

Match length	121
% identity	51
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396440
Contig ID	74967_1.R1084
5'-most EST	g3107570

Seq. No.	396441
Contig ID	74975_1.R1084
5'-most EST	g6012827
Method	BLASTX
NCBI GI	g6069648
BLAST score	323
E value	1.0e-29
Match length	168
% identity	40
NCBI Description	(AP000616) ESTs AU078644(E0685),C72841(E2351),AU078645(E0685), AU030746(E60179) correspond to a region of the predicted gene.; similar to Arabidopsis thaliana BAC F1104; similar to Medicago truncatula MtN21 (AF096370) [Oryza

Seq. No.	396442
Contig ID	74998_1.R1084
5'-most EST	g2428401
Method	BLASTX
NCBI GI	g5051771
BLAST score	170
E value	6.0e-12
Match length	82
% identity	46
NCBI Description	(AL078637) putative protein [Arabidopsis thaliana]

Seq. No.	396443
Contig ID	75000_1.R1084
5'-most EST	g4715686

Seq. No.	396444
Contig ID	75035_1.R1084
5'-most EST	g2428704

Seq. No.	396445
Contig ID	75091_1.R1084
5'-most EST	g2428607
Method	BLASTX
NCBI GI	g2145358
BLAST score	144
E value	9.0e-09
Match length	29
% identity	90
NCBI Description	(Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq. No.	396446
Contig ID	75106_1.R1084
5'-most EST	g2428509

Seq. No. 396447
Contig ID 75163_1.R1084
5'-most EST g2428566

Seq. No. 396448
Contig ID 75192_1.R1084
5'-most EST g5667641

Seq. No. 396449
Contig ID 75223_1.R1084
5'-most EST g3763797
Method BLASTX
NCBI GI g4455363
BLAST score 174
E value 2.0e-12
Match length 93
% identity 44
NCBI Description (AL035524) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No. 396450
Contig ID 75245_1.R1084
5'-most EST g2428650
Method BLASTX
NCBI GI g2723496
BLAST score 141
E value 7.0e-18
Match length 179
% identity 34
NCBI Description (AB009972) beta-1,4-xylosidase [Aspergillus oryzae]

Seq. No. 396451
Contig ID 75249_1.R1084
5'-most EST g2428654

Seq. No. 396452
Contig ID 75279_1.R1084
5'-most EST g2428684
Method BLASTX
NCBI GI g3386604
BLAST score 230
E value 9.0e-19
Match length 65
% identity 65
NCBI Description (AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No. 396453
Contig ID 75345_1.R1084
5'-most EST g2428750

Seq. No. 396454
Contig ID 75350_1.R1084
5'-most EST g2442857

Seq. No. 396455
Contig ID 75374_1.R1084
5'-most EST g2442836

Seq. No.	396456
Contig ID	75391_1.R1084
5'-most EST	g2428796

Seq. No.	396457
Contig ID	75411_1.R1084
5'-most EST	g4880566
Method	BLASTX
NCBI GI	g2245125
BLAST score	153
E value	6.0e-10
Match length	39
% identity	74
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396458
Contig ID	75429_1.R1084
5'-most EST	g2428835

Seq. No.	396459
Contig ID	75483_1.R1084
5'-most EST	g5003052

Seq. No.	396460
Contig ID	75483_2.R1084
5'-most EST	g2428890
Method	BLASTX
NCBI GI	g2462781
BLAST score	681
E value	1.0e-71
Match length	159
% identity	74
NCBI Description	(U73175) carbamoyl phosphate synthetase small subunit [Arabidopsis thaliana]

Seq. No.	396461
Contig ID	75501_1.R1084
5'-most EST	g2442842

Seq. No.	396462
Contig ID	75505_1.R1084
5'-most EST	g4716022
Method	BLASTX
NCBI GI	g1652649
BLAST score	181
E value	1.0e-19
Match length	140
% identity	43
NCBI Description	(D90907) hypothetical protein [Synechocystis sp.]

Seq. No.	396463
Contig ID	75505_2.R1084
5'-most EST	g4714855
Method	BLASTX
NCBI GI	g1652649
BLAST score	226

E value	2.0e-22
Match length	96
% identity	59
NCBI Description	(D90907) hypothetical protein [Synechocystis sp.]

Seq. No.	396464
Contig ID	75558_1.R1084
5'-most EST	g2428966
Method	BLASTX
NCBI GI	g3421413
BLAST score	657
E value	5.0e-69
Match length	143
% identity	85
NCBI Description	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No.	396465
Contig ID	75582_1.R1084
5'-most EST	g2428991

Seq. No.	396466
Contig ID	75583_1.R1084
5'-most EST	g4880359

Seq. No.	396467
Contig ID	75591_1.R1084
5'-most EST	g2429004
Method	BLASTX
NCBI GI	g3318615
BLAST score	415
E value	6.0e-45
Match length	101
% identity	92
NCBI Description	(AB016065) mitochondrial phosphate transporter [Oryza sativa]

Seq. No.	396468
Contig ID	75625_1.R1084
5'-most EST	g2442517
Method	BLASTX
NCBI GI	g1346388
BLAST score	167
E value	8.0e-12
Match length	40
% identity	78
NCBI Description	HOMEOBOX PROTEIN KNOTTED-1 LIKE 4 (KNAT4) >gi_1045044_emb_CAA63131_ (X92393) KNAT4 homeobox protein [Arabidopsis thaliana]

Seq. No.	396469
Contig ID	75638_1.R1084
5'-most EST	g5004104

Seq. No.	396470
Contig ID	75655_1.R1084

5'-most EST	g3761856
Method	BLASTN
NCBI GI	g559342
BLAST score	114
E value	4.0e-57
Match length	155
% identity	96
NCBI Description	Human TBXAS1 gene for thromboxane synthase, exon

Seq. No.	396471
Contig ID	75656_1.R1084
5'-most EST	g2431505
Method	BLASTX
NCBI GI	g1076758
BLAST score	334
E value	9.0e-31
Match length	114
% identity	57
NCBI Description	heat-shock protein precursor - rye >gi_2130093_pir__S65776 heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]

Seq. No.	396472
Contig ID	75662_1.R1084
5'-most EST	g4879908

Seq. No.	396473
Contig ID	75699_1.R1084
5'-most EST	g2431151
Method	BLASTX
NCBI GI	g1781042
BLAST score	221
E value	1.0e-30
Match length	133
% identity	49
NCBI Description	(Y10373) chitinase [Medicago truncatula]

Seq. No.	396474
Contig ID	75725_1.R1084
5'-most EST	g3107229

Seq. No.	396475
Contig ID	75727_1.R1084
5'-most EST	g2801247
Method	BLASTX
NCBI GI	g1431629
BLAST score	150
E value	1.0e-09
Match length	46
% identity	52
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	396476
Contig ID	75752_1.R1084
5'-most EST	g2431205

Seq. No. 396477
Contig ID 75757_1.R1084
5'-most EST g2431211

Seq. No. 396478
Contig ID 75760_1.R1084
5'-most EST g2431213

Seq. No. 396479
Contig ID 75773_1.R1084
5'-most EST g4879482

Seq. No. 396480
Contig ID 75776_1.R1084
5'-most EST g2431230
Method BLASTX
NCBI GI g4503719
BLAST score 270
E value 1.0e-23
Match length 115
% identity 47
NCBI Description fragile histidine triad gene >gi_1706794_sp_P49789_FHIT_HUMAN BIS(5'-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE 5',5'''-P1,P3-TRIPHOSPHATE HYDROLASE) (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE) (FRAGILE HISTIDINE TRIAD PROTEIN) >gi_3114520_pdb_4FIT_ Fhit-Apo >gi_3114524_pdb_6FIT_ Fhit-Transition State Analog >gi_3318895_pdb_1FHI_ Substrate Analog (Ib2) Complex With The Fragile Histidine Triad Protein, Fhit >gi_1203836 (U46922) member of the histidine triad (HIT) gene family; similar to the S. pombe diadenosine 5',5'''-P1,P4-tetraphosphate asymmetrical hydrolase [Homo sapiens] >gi_1945066 (U76272) diadenosine triphosphate (Ap3A) hydrolase [Homo sapiens]

Seq. No. 396481
Contig ID 75825_1.R1084
5'-most EST g3760903
Method BLASTX
NCBI GI g4454464
BLAST score 711
E value 4.0e-75
Match length 172
% identity 76
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 396482
Contig ID 75830_1.R1084
5'-most EST g2431285

Seq. No. 396483
Contig ID 75834_1.R1084
5'-most EST g3763693
Method BLASTX
NCBI GI g5816992
BLAST score 221

E value 9.0e-18
Match length 60
% identity 62
NCBI Description (AL110123) putative protein [Arabidopsis thaliana]

Seq. No. 396484
Contig ID 75839_1.R1084
5'-most EST g2431294
Method BLASTX
NCBI GI g6016691
BLAST score 375
E value 1.0e-35
Match length 194
% identity 38
NCBI Description (AC009991) unknown protein [Arabidopsis thaliana]

Seq. No. 396485
Contig ID 75848_1.R1084
5'-most EST g2431303

Seq. No. 396486
Contig ID 75856_1.R1084
5'-most EST g3762264

Seq. No. 396487
Contig ID 75862_1.R1084
5'-most EST g2431319
Method BLASTX
NCBI GI g166949
BLAST score 184
E value 1.0e-38
Match length 295
% identity 35
NCBI Description (M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea americana]

Seq. No. 396488
Contig ID 75875_1.R1084
5'-most EST g4878548

Seq. No. 396489
Contig ID 75877_1.R1084
5'-most EST g4880001
Method BLASTX
NCBI GI g2501555
BLAST score 1014
E value 1.0e-114
Match length 235
% identity 88
NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 396490
Contig ID 75888_1.R1084
5'-most EST g3762459
Method BLASTX
NCBI GI g5882749

BLAST score 252
E value 2.0e-21
Match length 116
% identity 54
NCBI Description (AC008263) Contains 2 PF_00612 IQ calmodulin-binding motif domains. [Arabidopsis thaliana]

Seq. No. 396491
Contig ID 75895_1.R1084
5'-most EST g2431352

Seq. No. 396492
Contig ID 75901_1.R1084
5'-most EST g2431358

Seq. No. 396493
Contig ID 75916_1.R1084
5'-most EST g2431373

Seq. No. 396494
Contig ID 75918_1.R1084
5'-most EST g3061266
Method BLASTX
NCBI GI g4406782
BLAST score 166
E value 4.0e-11
Match length 83
% identity 47
NCBI Description (AC006532) hypothetical protein [Arabidopsis thaliana]

Seq. No. 396495
Contig ID 75921_1.R1084
5'-most EST g2442371
Method BLASTN
NCBI GI g5852170
BLAST score 345
E value 0.0e+00
Match length 378
% identity 98
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No. 396496
Contig ID 75933_1.R1084
5'-most EST g3762727

Seq. No. 396497
Contig ID 75950_1.R1084
5'-most EST g2431407

Seq. No. 396498
Contig ID 75977_1.R1084
5'-most EST g3768317
Method BLASTN
NCBI GI g5042437
BLAST score 39
E value 2.0e-12

Match length	70
% identity	60
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	396499
Contig ID	76003_1.R1084
5'-most EST	g3762368

Seq. No.	396500
Contig ID	76005_1.R1084
5'-most EST	g2431463
Method	BLASTX
NCBI GI	g2746086
BLAST score	141
E value	1.0e-08
Match length	60
% identity	50
NCBI Description	(AF025292) putative high-affinity potassium transporter [Hordeum vulgare]

Seq. No.	396501
Contig ID	76016_1.R1084
5'-most EST	g3762266

Seq. No.	396502
Contig ID	76027_1.R1084
5'-most EST	g2431502
Method	BLASTX
NCBI GI	g4432839
BLAST score	217
E value	1.0e-17
Match length	46
% identity	43
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	396503
Contig ID	76034_1.R1084
5'-most EST	g2431494
Method	BLASTX
NCBI GI	g4512674
BLAST score	136
E value	3.0e-14
Match length	75
% identity	56
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396504
Contig ID	76043_1.R1084
5'-most EST	g3762384

Seq. No.	396505
Contig ID	76061_1.R1084
5'-most EST	g2431524

Seq. No.	396506
Contig ID	76069_1.R1084
5'-most EST	g3762490

Method	BLASTX
NCBI GI	g3548801
BLAST score	266
E value	1.0e-29
Match length	184
% identity	39
NCBI Description	(AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	396507
Contig ID	76071_1.R1084
5'-most EST	g2442184

Seq. No.	396508
Contig ID	76077_1.R1084
5'-most EST	g3762508
Method	BLASTN
NCBI GI	g5257255
BLAST score	273
E value	1.0e-152
Match length	544
% identity	86
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	396509
Contig ID	76078_1.R1084
5'-most EST	g4878793

Seq. No.	396510
Contig ID	76082_1.R1084
5'-most EST	g2442196
Method	BLASTX
NCBI GI	g2842486
BLAST score	277
E value	1.0e-27
Match length	123
% identity	56
NCBI Description	(AL021749) putative protein [Arabidopsis thaliana]

Seq. No.	396511
Contig ID	76087_1.R1084
5'-most EST	g2442201

Seq. No.	396512
Contig ID	76114_1.R1084
5'-most EST	g2442230

Seq. No.	396513
Contig ID	76119_1.R1084
5'-most EST	g2442235

Seq. No.	396514
Contig ID	76122_1.R1084
5'-most EST	g2442238

Seq. No.	396515

Contig ID	76129_1.R1084
5'-most EST	g5003964
Method	BLASTX
NCBI GI	g1352681
BLAST score	313
E value	2.0e-28
Match length	95
% identity	78
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana] >gi_6006880_gb_AAF00655.1_AC008153_7 (AC008153) protein phosphatase 2C (PP2C) [Arabidopsis thaliana]

Seq. No.	396516
Contig ID	76141_1.R1084
5'-most EST	g2442402

Seq. No.	396517
Contig ID	76147_1.R1084
5'-most EST	g2442264
Method	BLASTX
NCBI GI	g5734637
BLAST score	363
E value	4.0e-64
Match length	184
% identity	74
NCBI Description	(AP000391) ESTs AU029348(E30206),C74035(E30206) correspond to a region of the predicted gene.; Similar to lipase (U38916) [Oryza sativa]

Seq. No.	396518
Contig ID	76173_1.R1084
5'-most EST	g3762644
Method	BLASTX
NCBI GI	g1729980
BLAST score	111
E value	3.0e-12
Match length	56
% identity	58
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175 thaumatin-like protein - Arabidopsis thaliana >gi_536825 (L34693) thaumatin-like protein [Arabidopsis thaliana] >gi_1094863_prf__2106421A thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	396519
Contig ID	76178_1.R1084
5'-most EST	g4880078

Seq. No.	396520
Contig ID	76182_1.R1084
5'-most EST	g3767355
Method	BLASTX
NCBI GI	g2117615
BLAST score	165

E value	5.0e-11
Match length	30
% identity	93
NCBI Description	catalase - Campylobacter jejuni >gi_2120538_pir__S71937 catalase - Campylobacter jejuni >gi_984737_emb_CAA59444_ (X85130) catalase [Campylobacter jejuni]

Seq. No.	396521
Contig ID	76194_1.R1084
5'-most EST	g2442316

Seq. No.	396522
Contig ID	76195_1.R1084
5'-most EST	g3763264
Method	BLASTX
NCBI GI	g129350
BLAST score	229
E value	1.0e-18
Match length	75
% identity	56
NCBI Description	PROBABLE PROTEASE INHIBITOR P322 PRECURSOR >gi_82278_pir__S05594 pseudothionin St1 - potato (strain cv. Bintje) >gi_21394_emb_CAA31577_ (X13180) put. preprotein (AA -27 to 47) [Solanum tuberosum]

Seq. No.	396523
Contig ID	76224_1.R1084
5'-most EST	g2799685

Seq. No.	396524
Contig ID	76231_1.R1084
5'-most EST	g2442353

Seq. No.	396525
Contig ID	76282_1.R1084
5'-most EST	g3762853
Method	BLASTX
NCBI GI	g4262149
BLAST score	186
E value	7.0e-17
Match length	63
% identity	59
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	396526
Contig ID	76287_1.R1084
5'-most EST	g2442448

Seq. No.	396527
Contig ID	76290_1.R1084
5'-most EST	g2442413
Method	BLASTX
NCBI GI	g6091733
BLAST score	226
E value	2.0e-18
Match length	57

% identity	74
NCBI Description	(AC010797) unknown protein [Arabidopsis thaliana]

Seq. No.	396528
Contig ID	76317_1.R1084
5'-most EST	g3769207
Method	BLASTX
NCBI GI	g5281050
BLAST score	194
E value	1.0e-14
Match length	60
% identity	67
NCBI Description	(AL080318) putative protein [Arabidopsis thaliana]

Seq. No.	396529
Contig ID	76331_1.R1084
5'-most EST	g2442455

Seq. No.	396530
Contig ID	76351_1.R1084
5'-most EST	g4969346

Seq. No.	396531
Contig ID	76386_1.R1084
5'-most EST	g5004465
Method	BLASTX
NCBI GI	g4263528
BLAST score	147
E value	6.0e-09
Match length	59
% identity	58
NCBI Description	(AC004044) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	396532
Contig ID	76412_1.R1084
5'-most EST	g2442537

Seq. No.	396533
Contig ID	76428_1.R1084
5'-most EST	g2442809

Seq. No.	396534
Contig ID	76460_1.R1084
5'-most EST	g2442586

Seq. No.	396535
Contig ID	76494_1.R1084
5'-most EST	g2442625

Seq. No.	396536
Contig ID	76520_1.R1084
5'-most EST	g2442652
Method	BLASTX
NCBI GI	g1171866
BLAST score	145
E value	4.0e-09

Match length	29
% identity	93
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No.	396537
Contig ID	76522_1.R1084
5'-most EST	g2443064
Method	BLASTX
NCBI GI	g461033
BLAST score	129
E value	2.0e-14
Match length	120
% identity	36
NCBI Description	(S68015) c6.1A [human, Peptide, 324 aa] [Homo sapiens]

Seq. No.	396538
Contig ID	76525_1.R1084
5'-most EST	g4714833
Method	BLASTX
NCBI GI	g5803272
BLAST score	297
E value	4.0e-32
Match length	119
% identity	64
NCBI Description	(AP000399) ESTs AU055950(S20175),C73125(E2952), AU055951(S20175) correspond to a region of the predicted gene; similar to acyl-ACP thioesterase (U92878) [Oryza sativa]

Seq. No.	396539
Contig ID	76542_1.R1084
5'-most EST	g2442675

Seq. No.	396540
Contig ID	76616_1.R1084
5'-most EST	g2442751
Method	BLASTX
NCBI GI	g2462756
BLAST score	146
E value	5.0e-09
Match length	100
% identity	41
NCBI Description	(AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	396541
Contig ID	76618_1.R1084
5'-most EST	g3768232

Seq. No.	396542
Contig ID	76626_1.R1084
5'-most EST	g2442761
Method	BLASTX
NCBI GI	g3150415

BLAST score	747
E value	6.0e-79
Match length	297
% identity	53
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	396543
Contig ID	76629_1.R1084
5'-most EST	g3061237
Method	BLASTN
NCBI GI	g1815680
BLAST score	54
E value	2.0e-21
Match length	124
% identity	85
NCBI Description	Oryza sativa expansin (Os-EXP4) mRNA, complete cds

Seq. No.	396544
Contig ID	76656_1.R1084
5'-most EST	g2442791

Seq. No.	396545
Contig ID	76678_1.R1084
5'-most EST	g5004871

Seq. No.	396546
Contig ID	76691_1.R1084
5'-most EST	g2442826

Seq. No.	396547
Contig ID	76703_1.R1084
5'-most EST	g5004879
Method	BLASTX
NCBI GI	g5042177
BLAST score	315
E value	6.0e-29
Match length	120
% identity	53
NCBI Description	(AL078620) putative protein [Arabidopsis thaliana]

Seq. No.	396548
Contig ID	76713_1.R1084
5'-most EST	g3761748

Seq. No.	396549
Contig ID	76724_1.R1084
5'-most EST	g5667430

Seq. No.	396550
Contig ID	76730_1.R1084
5'-most EST	g4880746
Method	BLASTX
NCBI GI	g3044212
BLAST score	602
E value	1.0e-62

Match length	152
% identity	77
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	396551
Contig ID	76732_1.R1084
5'-most EST	g2442870
Method	BLASTN
NCBI GI	g5830029
BLAST score	34
E value	2.0e-09
Match length	38
% identity	97
NCBI Description	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

Seq. No.	396552
Contig ID	76739_1.R1084
5'-most EST	g4969263
Method	BLASTX
NCBI GI	g1041815
BLAST score	194
E value	2.0e-14
Match length	53
% identity	62
NCBI Description	(U16721) lipid transfer protein [Oryza sativa]

Seq. No.	396553
Contig ID	76740_1.R1084
5'-most EST	g2442878
Method	BLASTX
NCBI GI	g3894172
BLAST score	315
E value	8.0e-29
Match length	159
% identity	38
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	396554
Contig ID	76748_1.R1084
5'-most EST	g2442886

Seq. No.	396555
Contig ID	76783_1.R1084
5'-most EST	g5003531

Seq. No.	396556
Contig ID	76798_1.R1084
5'-most EST	g3763308
Method	BLASTX
NCBI GI	g773414
BLAST score	187
E value	1.0e-13
Match length	46
% identity	80
NCBI Description	(U23751) beta galactosidase [Cloning vector pBBR1MCS-2]

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	>gi_833819 (U25059) LacZ alpha peptide [Cloning vector pBBR1MCS-3] >gi_833823 (U25060) LacZ alpha peptide [Cloning vector pBBR1MCS-4] >gi_833827 (U25061) LacZ alpha peptide [Cloning vector pBBR1MCS-5]
Seq. No.	396557
Contig ID	76820_1.R1084
5'-most EST	g2442959
Seq. No.	396558
Contig ID	76827_1.R1084
5'-most EST	g4714404
Seq. No.	396559
Contig ID	76854_1.R1084
5'-most EST	g2442993
Method	BLASTX
NCBI GI	g3668115
BLAST score	222
E value	4.0e-18
Match length	80
% identity	59
NCBI Description	(Y15069) cinnamoyl-CoA reductase [Zea mays]
Seq. No.	396560
Contig ID	76856_1.R1084
5'-most EST	g4968726
Seq. No.	396561
Contig ID	76882_1.R1084
5'-most EST	g4714416
Method	BLASTX
NCBI GI	g2500026
BLAST score	383
E value	3.0e-43
Match length	105
% identity	80
NCBI Description	ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE LIGASE) >gi_1616657 (U49389) adenylosuccinate synthetase [Arabidopsis thaliana] >gi_4678286_emb_CAB41194.1_ (AL049660) adenylosuccinate synthetase [Arabidopsis thaliana]
Seq. No.	396562
Contig ID	76884_1.R1084
5'-most EST	g2443025
Seq. No.	396563
Contig ID	76924_1.R1084
5'-most EST	g2443065
Method	BLASTX
NCBI GI	g2618688
BLAST score	538
E value	1.0e-54
Match length	132
% identity	73
NCBI Description	(AC002510) putative esterase D [Arabidopsis thaliana]

Seq. No.	396564
Contig ID	76980_1.R1084
5'-most EST	g3766939
Method	BLASTX
NCBI GI	g4914430
BLAST score	143
E value	8.0e-09
Match length	38
% identity	66
NCBI Description	(AL050351) SEC14-like protein [Arabidopsis thaliana]

Seq. No.	396565
Contig ID	76990_1.R1084
5'-most EST	g5607586
Method	BLASTX
NCBI GI	g2224933
BLAST score	156
E value	6.0e-10
Match length	107
% identity	41
NCBI Description	(AF004216) ethylene-insensitive3 [Arabidopsis thaliana] >gi_2224935 (AF004217) ethylene-insensitive3 [Arabidopsis thaliana]

Seq. No.	396566
Contig ID	76997_1.R1084
5'-most EST	g2443138
Method	BLASTX
NCBI GI	g4587558
BLAST score	438
E value	6.0e-43
Match length	184
% identity	46
NCBI Description	(AC006577) Contains similarity to gb_U45880 X-linked inhibitor of apotosis protein from Homo sapiens and contains PF_00097 Zinc finger C3HC4 (Ring finger) domain. [Arabidopsis thaliana]

Seq. No.	396567
Contig ID	77008_1.R1084
5'-most EST	g3766838

Seq. No.	396568
Contig ID	77037_1.R1084
5'-most EST	g3767137
Method	BLASTN
NCBI GI	g6041757
BLAST score	459
E value	0.0e+00
Match length	467
% identity	100
NCBI Description	Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence

Seq. No.	396569
Contig ID	77048_1.R1084

5'-most EST	g2443190
Method	BLASTX
NCBI GI	g3395938
BLAST score	292
E value	6.0e-26
Match length	82
% identity	38
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	396570
Contig ID	77050_1.R1084
5'-most EST	g2443192
Method	BLASTX
NCBI GI	g2130944
BLAST score	275
E value	7.0e-34
Match length	123
% identity	59
NCBI Description	(AB004060) sulfate transporter [Arabidopsis thaliana] >gi_2262137_gb_AAC78252.1_AAC78252 (AC002330) sulfate transporter protein [Arabidopsis thaliana]

Seq. No.	396571
Contig ID	77066_1.R1084
5'-most EST	g3762477
Method	BLASTN
NCBI GI	g1724113
BLAST score	116
E value	3.0e-58
Match length	318
% identity	85
NCBI Description	Avena fatua Af10-protein mRNA, complete cds

Seq. No.	396572
Contig ID	77081_1.R1084
5'-most EST	g2799518
Method	BLASTX
NCBI GI	g3309082
BLAST score	216
E value	2.0e-17
Match length	51
% identity	75
NCBI Description	(AF076251) calcineurin B-like protein 1 [Arabidopsis thaliana]

Seq. No.	396573
Contig ID	77104_1.R1084
5'-most EST	g2796279
Method	BLASTX
NCBI GI	g2947068
BLAST score	147
E value	6.0e-09
Match length	92
% identity	37
NCBI Description	(AC002521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 396574
Contig ID 77121_1.R1084
5'-most EST g2796298

Seq. No. 396575
Contig ID 77139_1.R1084
5'-most EST g5038551

Seq. No. 396576
Contig ID 77143_1.R1084
5'-most EST g3107432
Method BLASTX
NCBI GI g4406372
BLAST score 433
E value 5.0e-43
Match length 97
% identity 82
NCBI Description (AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No. 396577
Contig ID 77158_1.R1084
5'-most EST g2799229
Method BLASTX
NCBI GI g544400
BLAST score 341
E value 9.0e-32
Match length 119
% identity 58
NCBI Description GLUTELIN TYPE-B 2 PRECURSOR >gi_100676_pir__S17763 glutelin gluB-2 precursor - rice >gi_20212_emb_CAA38110_ (X54192) glutelin [Oryza sativa]

Seq. No. 396578
Contig ID 77159_1.R1084
5'-most EST g3769224

Seq. No. 396579
Contig ID 77182_1.R1084
5'-most EST g3759104

Seq. No. 396580
Contig ID 77202_1.R1084
5'-most EST g2796389
Method BLASTX
NCBI GI g3482971
BLAST score 143
E value 1.0e-13
Match length 48
% identity 69
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 396581
Contig ID 77222_1.R1084
5'-most EST g2799920

Seq. No. 396582

Contig ID	77222_3.R1084
5'-most EST	g2800794
Method	BLASTX
NCBI GI	g4538978
BLAST score	327
E value	4.0e-30
Match length	104
% identity	58
NCBI Description	(AL049487) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396583
Contig ID	77222_4.R1084
5'-most EST	g2800668

Seq. No.	396584
Contig ID	77236_1.R1084
5'-most EST	g2796423
Method	BLASTX
NCBI GI	g4584520
BLAST score	193
E value	1.0e-14
Match length	71
% identity	62
NCBI Description	(AL049607) enoyl-CoA hydratase-like protein [Arabidopsis thaliana]

Seq. No.	396585
Contig ID	77250_1.R1084
5'-most EST	g2796441

Seq. No.	396586
Contig ID	77252_1.R1084
5'-most EST	g2799514

Seq. No.	396587
Contig ID	77255_1.R1084
5'-most EST	g2798954
Method	BLASTX
NCBI GI	g3075394
BLAST score	362
E value	6.0e-35
Match length	78
% identity	82
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	396588
Contig ID	77256_1.R1084
5'-most EST	g3762126

Seq. No.	396589
Contig ID	77266_1.R1084
5'-most EST	g3761974

Seq. No.	396590
Contig ID	77275_1.R1084

5'-most EST	g2796462
Seq. No.	396591
Contig ID	77280_1.R1084
5'-most EST	g2799348
Method	BLASTN
NCBI GI	g5689237
BLAST score	66
E value	7.0e-29
Match length	129
% identity	88
NCBI Description	Zea mays ZmHP2 mRNA for histidine-containing phosphotransfer protein, complete cds
Seq. No.	396592
Contig ID	77293_1.R1084
5'-most EST	g5005127
Seq. No.	396593
Contig ID	77294_1.R1084
5'-most EST	g2797246
Method	BLASTX
NCBI GI	g2119013
BLAST score	296
E value	3.0e-27
Match length	76
% identity	78
NCBI Description	histone H3.2 protein - shrew mouse >gi_515005_emb_CAA56575_ (X80327) histone H3.2 protein [Mus pahari]
Seq. No.	396594
Contig ID	77336_1.R1084
5'-most EST	g2796528
Seq. No.	396595
Contig ID	77385_1.R1084
5'-most EST	g4715948
Method	BLASTX
NCBI GI	g2131347
BLAST score	163
E value	8.0e-11
Match length	80
% identity	50
NCBI Description	hypothetical protein YDL153c - yeast (Saccharomyces cerevisiae) >gi_1431240_emb_CAA98726_ (Z74201) ORF YDL153c [Saccharomyces cerevisiae] >gi_1480820 (U63063) something about silencing 10 [Saccharomyces cerevisiae]
Seq. No.	396596
Contig ID	77398_1.R1084
5'-most EST	g2799346
Method	BLASTX
NCBI GI	g225174
BLAST score	444
E value	3.0e-85
Match length	255
% identity	60

NCBI Description	glutelin precursor [Oryza sativa]
Seq. No.	396597
Contig ID	77398_2.R1084
5'-most EST	g2798422
Method	BLASTX
NCBI GI	g2764800
BLAST score	284
E value	8.0e-31
Match length	103
% identity	67
NCBI Description	(X76738) 12s globulin [Avena sativa]
Seq. No.	396598
Contig ID	77434_1.R1084
5'-most EST	g2797628
Seq. No.	396599
Contig ID	77469_1.R1084
5'-most EST	g2797974
Seq. No.	396600
Contig ID	77510_1.R1084
5'-most EST	g2797476
Seq. No.	396601
Contig ID	77525_1.R1084
5'-most EST	g2796728
Seq. No.	396602
Contig ID	77568_1.R1084
5'-most EST	g5038797
Method	BLASTX
NCBI GI	g3142294
BLAST score	656
E value	1.0e-68
Match length	138
% identity	93
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]
Seq. No.	396603
Contig ID	77578_1.R1084
5'-most EST	g2796784
Seq. No.	396604
Contig ID	77580_1.R1084
5'-most EST	g2796786
Method	BLASTN
NCBI GI	g940048
BLAST score	34
E value	1.0e-09
Match length	38
% identity	97
NCBI Description	Phaseolus vulgaris clone XZT-205 mRNA, partial cds

Seq. No.	396605
Contig ID	77634_1.R1084
5'-most EST	g3767673
Method	BLASTX
NCBI GI	g2760543
BLAST score	291
E value	6.0e-26
Match length	69
% identity	77
NCBI Description	(Z97060) L-galactono-1,4-lactone dehydrogenase [Brassica oleracea]

Seq. No.	396606
Contig ID	77644_1.R1084
5'-most EST	g2798093

Seq. No.	396607
Contig ID	77653_1.R1084
5'-most EST	g2797390

Seq. No.	396608
Contig ID	77685_1.R1084
5'-most EST	g2796899

Seq. No.	396609
Contig ID	77712_1.R1084
5'-most EST	g2797854

Seq. No.	396610
Contig ID	77744_1.R1084
5'-most EST	g2796973

Seq. No.	396611
Contig ID	77747_1.R1084
5'-most EST	g2796970

Seq. No.	396612
Contig ID	77784_1.R1084
5'-most EST	g5038959

Seq. No.	396613
Contig ID	77788_1.R1084
5'-most EST	g2800747
Method	BLASTN
NCBI GI	g313764
BLAST score	54
E value	3.0e-21
Match length	62
% identity	97
NCBI Description	C.longicaudatus mRNA for cyclin B

Seq. No.	396614
Contig ID	77798_1.R1084
5'-most EST	g2797023

Seq. No.	396615
Contig ID	77828_1.R1084

5'-most EST g2801227

Seq. No. 396616
Contig ID 77843_1.R1084
5'-most EST g3760873

Seq. No. 396617
Contig ID 77858_1.R1084
5'-most EST g2797084

Seq. No. 396618
Contig ID 77880_1.R1084
5'-most EST g4714723

Seq. No. 396619
Contig ID 77883_1.R1084
5'-most EST g3760835
Method BLASTX
NCBI GI g282994
BLAST score 224
E value 5.0e-18
Match length 122
% identity 39
NCBI Description Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No. 396620
Contig ID 77918_1.R1084
5'-most EST g2797415
Method BLASTX
NCBI GI g3980264
BLAST score 352
E value 1.0e-33
Match length 71
% identity 96
NCBI Description (AJ011383) 20S proteasome beta subunit [Cicer arietinum]

Seq. No. 396621
Contig ID 77937_1.R1084
5'-most EST g2797167

Seq. No. 396622
Contig ID 77938_1.R1084
5'-most EST g2798192
Method BLASTX
NCBI GI g1168940
BLAST score 520
E value 7.0e-53
Match length 155
% identity 63
NCBI Description CHORISMATE MUTASE PRECURSOR (CM-1) >gi_629509_pir__S38958 chorismate mutase precursor - Arabidopsis thaliana >gi_429153_emb_CAA81286_ (Z26519) chorismate mutase precursor [Arabidopsis thaliana]

Seq. No. 396623
Contig ID 77975_1.R1084

5'-most EST	g2797206
Seq. No.	396624
Contig ID	77977_1.R1084
5'-most EST	g3763776
Method	BLASTN
NCBI GI	g2149018
BLAST score	470
E value	0.0e+00
Match length	638
% identity	97
NCBI Description	Oryza sativa putative ADP-glucose pyrophosphorylase subunit SH2 and putative NADPH-dependent reductase A1 genes, complete cds
Seq. No.	396625
Contig ID	77979_1.R1084
5'-most EST	g2797211
Method	BLASTX
NCBI GI	g2244876
BLAST score	187
E value	2.0e-24
Match length	89
% identity	64
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]
Seq. No.	396626
Contig ID	78009_1.R1084
5'-most EST	g3763794
Method	BLASTX
NCBI GI	g4732123
BLAST score	285
E value	1.0e-25
Match length	118
% identity	57
NCBI Description	(AF129087) mitogen-activated protein kinase homologue [Medicago sativa]
Seq. No.	396627
Contig ID	78046_1.R1084
5'-most EST	g2797279
Seq. No.	396628
Contig ID	78078_1.R1084
5'-most EST	g2797311
Seq. No.	396629
Contig ID	78099_1.R1084
5'-most EST	g4714598
Seq. No.	396630
Contig ID	78101_1.R1084
5'-most EST	g2797336
Seq. No.	396631
Contig ID	78110_1.R1084
5'-most EST	g2800450

Seq. No.	396632
Contig ID	78120_1.R1084
5'-most EST	g5003075

Seq. No.	396633
Contig ID	78203_1.R1084
5'-most EST	g2797444
Method	BLASTN
NCBI GI	g218196
BLAST score	115
E value	5.0e-58
Match length	184
% identity	94
NCBI Description	Rice RA5 gene for allergenic protein, complete cds

Seq. No.	396634
Contig ID	78266_1.R1084
5'-most EST	g3759027

Seq. No.	396635
Contig ID	78284_1.R1084
5'-most EST	g3762113

Seq. No.	396636
Contig ID	78294_1.R1084
5'-most EST	g2797544

Seq. No.	396637
Contig ID	78308_1.R1084
5'-most EST	g2797955
Method	BLASTX
NCBI GI	g975888
BLAST score	167
E value	9.0e-25
Match length	65
% identity	94
NCBI Description	(U32511) myo-inositol-1-phosphate synthase [Mesembryanthemum crystallinum]

Seq. No.	396638
Contig ID	78313_1.R1084
5'-most EST	g3762171

Seq. No.	396639
Contig ID	78333_1.R1084
5'-most EST	g2797588

Seq. No.	396640
Contig ID	78378_1.R1084
5'-most EST	g2798012

Seq. No.	396641
Contig ID	78448_1.R1084
5'-most EST	g3761906
Method	BLASTX
NCBI GI	g4455177

BLAST score 245
E value 1.0e-20
Match length 76
% identity 64
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 396642
Contig ID 78454_1.R1084
5'-most EST g5455311
Method BLASTX
NCBI GI g4314378
BLAST score 198
E value 1.0e-18
Match length 90
% identity 51
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana] >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative lipase [Arabidopsis thaliana]

Seq. No. 396643
Contig ID 78461_1.R1084
5'-most EST g5667522

Seq. No. 396644
Contig ID 78518_1.R1084
5'-most EST g3761928
Method BLASTX
NCBI GI g2911058
BLAST score 223
E value 3.0e-18
Match length 47
% identity 72
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 396645
Contig ID 78550_1.R1084
5'-most EST g2797820

Seq. No. 396646
Contig ID 78613_1.R1084
5'-most EST g2800661

Seq. No. 396647
Contig ID 78700_1.R1084
5'-most EST g3761301
Method BLASTX
NCBI GI g2443751
BLAST score 263
E value 1.0e-22
Match length 65
% identity 83
NCBI Description (AF020303) fumarase [Arabidopsis thaliana] >gi_2529676 (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No. 396648
Contig ID 78702_1.R1084
5'-most EST g3107249

Method	BLASTX
NCBI GI	g4510348
BLAST score	254
E value	1.0e-26
Match length	122
% identity	54
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	396649
Contig ID	78721_1.R1084
5'-most EST	g5002917
Method	BLASTX
NCBI GI	g4038034
BLAST score	415
E value	2.0e-40
Match length	89
% identity	87
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	396650
Contig ID	78743_1.R1084
5'-most EST	g3762538

Seq. No.	396651
Contig ID	78759_1.R1084
5'-most EST	g2798040

Seq. No.	396652
Contig ID	78765_1.R1084
5'-most EST	g3106879
Method	BLASTX
NCBI GI	g2500378
BLAST score	228
E value	6.0e-24
Match length	88
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	396653
Contig ID	78815_1.R1084
5'-most EST	g3762874
Method	BLASTX
NCBI GI	g2982297
BLAST score	444
E value	1.0e-43
Match length	162
% identity	68
NCBI Description	(AF051233) KIAA0107-like protein [Picea mariana]

Seq. No.	396654
Contig ID	78819_1.R1084
5'-most EST	g2798103

Seq. No.	396655
Contig ID	78873_1.R1084
5'-most EST	g2798158
Method	BLASTX

NCBI GI	g3402817
BLAST score	233
E value	4.0e-19
Match length	51
% identity	84
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	396656
Contig ID	78950_1.R1084
5'-most EST	g6025159
Method	BLASTX
NCBI GI	g1176081
BLAST score	201
E value	2.0e-15
Match length	100
% identity	40
NCBI Description	HYPOTHETICAL PROTEIN HI0671 >gi_1074478_pir__F64156 hypothetical protein HI0671 - Haemophilus influenzae (strain Rd KW20) >gi_1573672 (U32750) conserved hypothetical protein [Haemophilus influenzae Rd]

Seq. No.	396657
Contig ID	78978_1.R1084
5'-most EST	g2799135
Method	BLASTN
NCBI GI	g5764544
BLAST score	39
E value	3.0e-12
Match length	42
% identity	98
NCBI Description	Shuttle vector pSLIRES11, complete sequence

Seq. No.	396658
Contig ID	79021_1.R1084
5'-most EST	g2798325

Seq. No.	396659
Contig ID	79030_1.R1084
5'-most EST	g2798335

Seq. No.	396660
Contig ID	79038_1.R1084
5'-most EST	g2799434

Seq. No.	396661
Contig ID	79046_1.R1084
5'-most EST	g3769110

Seq. No.	396662
Contig ID	79078_1.R1084
5'-most EST	g2799078
Method	BLASTX
NCBI GI	g3057122
BLAST score	187
E value	1.0e-13
Match length	52
% identity	69

NCBI Description (AF023160) starch synthase DULL1 [Zea mays]

Seq. No. 396663
Contig ID 79085_1.R1084
5'-most EST g4714068
Method BLASTX
NCBI GI g3152603
BLAST score 166
E value 2.0e-11
Match length 72
% identity 43
NCBI Description (AC004482) unknown protein [Arabidopsis thaliana]

Seq. No. 396664
Contig ID 79169_1.R1084
5'-most EST g3760595
Method BLASTX
NCBI GI g2827552
BLAST score 611
E value 3.0e-63
Match length 129
% identity 41
NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 396665
Contig ID 79178_1.R1084
5'-most EST g3767788

Seq. No. 396666
Contig ID 79231_1.R1084
5'-most EST g4879336

Seq. No. 396667
Contig ID 79261_1.R1084
5'-most EST g2798590

Seq. No. 396668
Contig ID 79264_1.R1084
5'-most EST g6025067
Method BLASTX
NCBI GI g3283057
BLAST score 243
E value 2.0e-20
Match length 63
% identity 70
NCBI Description (AF054617) one helix protein [Arabidopsis thaliana]

Seq. No. 396669
Contig ID 79290_1.R1084
5'-most EST g3762784
Method BLASTX
NCBI GI g4558673
BLAST score 276
E value 4.0e-24
Match length 91
% identity 52
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

>gi_4726112_gb_AAD28312.1_AC006436_3 (AC006436)
hypothetical protein [Arabidopsis thaliana]

Seq. No.	396670
Contig ID	79512_3.R1084
5'-most EST	g3762170

Seq. No.	396671
Contig ID	79593_1.R1084
5'-most EST	g2798952
Method	BLASTX
NCBI GI	g2213584
BLAST score	214
E value	2.0e-17
Match length	78
% identity	55
NCBI Description	(AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No.	396672
Contig ID	79598_1.R1084
5'-most EST	g2798945
Method	BLASTX
NCBI GI	g5669638
BLAST score	327
E value	1.0e-30
Match length	92
% identity	71
NCBI Description	(AF096248) ethylene-responsive RNA helicase [Lycopersicon esculentum]

Seq. No.	396673
Contig ID	79659_1.R1084
5'-most EST	g2799316
Method	BLASTX
NCBI GI	g2388580
BLAST score	336
E value	8.0e-32
Match length	80
% identity	75
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	396674
Contig ID	79712_1.R1084
5'-most EST	g3106819

Seq. No.	396675
Contig ID	79766_1.R1084
5'-most EST	g2799425
Method	BLASTX
NCBI GI	g3914136
BLAST score	175
E value	2.0e-12
Match length	93
% identity	42
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein

[Cicer arietinum]

Seq. No.	396676
Contig ID	79912_1.R1084
5'-most EST	g3760105
Method	BLASTX
NCBI GI	g2270994
BLAST score	249
E value	7.0e-35
Match length	145
% identity	56
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	396677
Contig ID	80015_1.R1084
5'-most EST	g3766806

Seq. No.	396678
Contig ID	80050_1.R1084
5'-most EST	g5667198

Seq. No.	396679
Contig ID	80062_1.R1084
5'-most EST	g2800865
Method	BLASTN
NCBI GI	g2280517
BLAST score	60
E value	9.0e-25
Match length	68
% identity	99
NCBI Description	Nicotiana tabacum mRNA for BYJ15, partial cds

Seq. No.	396680
Contig ID	80079_1.R1084
5'-most EST	g2799746
Method	BLASTX
NCBI GI	g4734007
BLAST score	225
E value	2.0e-18
Match length	93
% identity	42
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396681
Contig ID	80083_1.R1084
5'-most EST	g2799814

Seq. No.	396682
Contig ID	80123_1.R1084
5'-most EST	g2799792

Seq. No.	396683
Contig ID	80174_1.R1084
5'-most EST	g5003879
Method	BLASTN
NCBI GI	g169818
BLAST score	814

E value	0.0e+00
Match length	907
% identity	98
NCBI Description	Rice 25S ribosomal RNA gene

Seq. No.	396684
Contig ID	80174_2.R1084
5'-most EST	g5455472
Method	BLASTN
NCBI GI	g5441872
BLAST score	88
E value	2.0e-41
Match length	238
% identity	85
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig a)

Seq. No.	396685
Contig ID	80190_1.R1084
5'-most EST	g2800309
Method	BLASTX
NCBI GI	g4580759
BLAST score	188
E value	7.0e-14
Match length	157
% identity	31
NCBI Description	(AF061087) P-glycoprotein [Gossypium hirsutum]

Seq. No.	396686
Contig ID	80214_1.R1084
5'-most EST	g2799885
Method	BLASTN
NCBI GI	g722320
BLAST score	34
E value	3.0e-09
Match length	46
% identity	93
NCBI Description	Oryza sativa (Osem) gene, complete cds

Seq. No.	396687
Contig ID	80218_1.R1084
5'-most EST	g2800937

Seq. No.	396688
Contig ID	80268_1.R1084
5'-most EST	g4880141
Method	BLASTX
NCBI GI	g4006934
BLAST score	305
E value	2.0e-27
Match length	124
% identity	48
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	396689
Contig ID	80325_1.R1084
5'-most EST	g2799998

Seq. No.	396690
Contig ID	80420_1.R1084
5'-most EST	g2800095
Method	BLASTX
NCBI GI	g4973431
BLAST score	622
E value	1.0e-64
Match length	169
% identity	66
NCBI Description	(AF148877) putative aldehyde dehydrogenase OS-ALDH [Oryza sativa subsp. indica]

Seq. No.	396691
Contig ID	80455_1.R1084
5'-most EST	g2800131

Seq. No.	396692
Contig ID	80488_1.R1084
5'-most EST	g4715955

Seq. No.	396693
Contig ID	80519_1.R1084
5'-most EST	g2800195

Seq. No.	396694
Contig ID	80535_1.R1084
5'-most EST	g2800211
Method	BLASTX
NCBI GI	g4585994
BLAST score	390
E value	2.0e-50
Match length	145
% identity	76
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	396695
Contig ID	80578_1.R1084
5'-most EST	g2800254
Method	BLASTX
NCBI GI	g3892051
BLAST score	201
E value	2.0e-15
Match length	55
% identity	67
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]

Seq. No.	396696
Contig ID	80594_1.R1084
5'-most EST	g2799002
Method	BLASTN
NCBI GI	g1698774
BLAST score	50
E value	9.0e-19
Match length	53
% identity	98

NCBI Description	Filamentous phage display expression cloning vector pZGT5 with murine Ig kappa light chain fragment insert, complete sequence
Seq. No.	396697
Contig ID	80662_1.R1084
5'-most EST	g2800261
Seq. No.	396698
Contig ID	80722_1.R1084
5'-most EST	g2800323
Method	BLASTX
NCBI GI	g5803167
BLAST score	164
E value	4.0e-11
Match length	53
% identity	51
NCBI Description	pre-mRNA splicing factor SF3a (60kD), similar to S. cerevisiae PRP9 (spliceosome-associated protein 61) >gi_1082798_pir__A55749 spliceosome-associated protein SAP 61 - human >gi_508723 (U08815) SAP 61 [Homo sapiens]
Seq. No.	396699
Contig ID	80728_1.R1084
5'-most EST	g2800435
Seq. No.	396700
Contig ID	80738_1.R1084
5'-most EST	g5038667
Method	BLASTX
NCBI GI	g2190992
BLAST score	358
E value	1.0e-33
Match length	156
% identity	47
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]
Seq. No.	396701
Contig ID	80754_1.R1084
5'-most EST	g2799198
Method	BLASTN
NCBI GI	g984907
BLAST score	34
E value	3.0e-09
Match length	34
% identity	100
NCBI Description	Plasmid pBSL159 cloning vector, complete sequence
Seq. No.	396702
Contig ID	80849_1.R1084
5'-most EST	g3760737
Method	BLASTX
NCBI GI	g2129742
BLAST score	232
E value	5.0e-19
Match length	70

% identity	56
NCBI Description	stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	396703
Contig ID	80900_1.R1084
5'-most EST	g2800461
Method	BLASTX
NCBI GI	g3068809
BLAST score	169
E value	1.0e-11
Match length	69
% identity	52
NCBI Description	(AF059295) Skp1 homolog [Arabidopsis thaliana]

Seq. No.	396704
Contig ID	80987_1.R1084
5'-most EST	g2800658

Seq. No.	396705
Contig ID	81019_1.R1084
5'-most EST	g2800466

Seq. No.	396706
Contig ID	81037_1.R1084
5'-most EST	g4714837
Method	BLASTX
NCBI GI	g3063449
BLAST score	719
E value	7.0e-76
Match length	216
% identity	63
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No.	396707
Contig ID	81056_1.R1084
5'-most EST	g2800667

Seq. No.	396708
Contig ID	81061_1.R1084
5'-most EST	g2800510
Method	BLASTX
NCBI GI	g2642446
BLAST score	352
E value	2.0e-43
Match length	145
% identity	69
NCBI Description	(AC002391) similar to auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	396709
Contig ID	81069_1.R1084
5'-most EST	g2800573

Seq. No.	396710
Contig ID	81139_1.R1084
5'-most EST	g5055943
Method	BLASTX
NCBI GI	g5295941
BLAST score	643
E value	5.0e-71
Match length	143
% identity	99
NCBI Description	(AB026295) ESTs AU075322(C11109),D22430(C11109) correspond to a region of the predicted gene.; Similar to Medicago sativa early nodule-specific protein (ENOD8) gene, complete cds.(L18899) [Oryza sativa]

Seq. No.	396711
Contig ID	81209_1.R1084
5'-most EST	g2800592

Seq. No.	396712
Contig ID	81247_1.R1084
5'-most EST	g2800630

Seq. No.	396713
Contig ID	81542_1.R1084
5'-most EST	g5851007
Method	BLASTN
NCBI GI	g5777612
BLAST score	337
E value	0.0e+00
Match length	652
% identity	94
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	396714
Contig ID	81597_1.R1084
5'-most EST	g5667218

Seq. No.	396715
Contig ID	81603_1.R1084
5'-most EST	g2800994

Seq. No.	396716
Contig ID	81806_1.R1084
5'-most EST	g2801214

Seq. No.	396717
Contig ID	81855_1.R1084
5'-most EST	g4714866
Method	BLASTX
NCBI GI	g4587988
BLAST score	146
E value	3.0e-11
Match length	147
% identity	39
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396718
Contig ID	81856_1.R1084
5'-most EST	g2801259
Method	BLASTX
NCBI GI	g4559384
BLAST score	147
E value	3.0e-09
Match length	43
% identity	65
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	396719
Contig ID	81861_1.R1084
5'-most EST	g2801264

Seq. No.	396720
Contig ID	81862_1.R1084
5'-most EST	g2801265

Seq. No.	396721
Contig ID	81907_1.R1084
5'-most EST	g3762133
Method	BLASTX
NCBI GI	g1173555
BLAST score	247
E value	5.0e-21
Match length	52
% identity	77
NCBI Description	(U31544) UDP-galactose-4-epimerase [Pisum sativum]

Seq. No.	396722
Contig ID	81918_1.R1084
5'-most EST	g3767674

Seq. No.	396723
Contig ID	81962_1.R1084
5'-most EST	g4715414
Method	BLASTX
NCBI GI	g3929325
BLAST score	321
E value	2.0e-40
Match length	125
% identity	68
NCBI Description	(AF100333) putative DNA-binding protein [Dendrobium grex Madame Thong-IN]

Seq. No.	396724
Contig ID	82001_1.R1084
5'-most EST	g3060965

Seq. No.	396725
Contig ID	82016_1.R1084
5'-most EST	g6012812
Method	BLASTX
NCBI GI	g3551954
BLAST score	365
E value	1.0e-34

Match length	162
% identity	42
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	396726
Contig ID	82020_1.R1084
5'-most EST	g4879993
Method	BLASTX
NCBI GI	g4191791
BLAST score	335
E value	3.0e-31
Match length	84
% identity	73
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

Seq. No.	396727
Contig ID	82047_1.R1084
5'-most EST	g3762875
Method	BLASTX
NCBI GI	g4678261
BLAST score	205
E value	4.0e-16
Match length	110
% identity	39
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	396728
Contig ID	82060_1.R1084
5'-most EST	g3762779
Method	BLASTX
NCBI GI	g5419927
BLAST score	379
E value	2.0e-36
Match length	85
% identity	82
NCBI Description	(AJ243340) expansin9 [Lycopersicon esculentum]

Seq. No.	396729
Contig ID	82068_1.R1084
5'-most EST	g4968580
Method	BLASTX
NCBI GI	g3928084
BLAST score	343
E value	5.0e-32
Match length	195
% identity	43
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No.	396730
Contig ID	82073_1.R1084
5'-most EST	g3061044

Seq. No.	396731

Contig ID	82081_1.R1084
5'-most EST	g3762928
Seq. No.	396732
Contig ID	82104_1.R1084
5'-most EST	g3061194
Seq. No.	396733
Contig ID	82110_1.R1084
5'-most EST	g3061083
Method	BLASTX
NCBI GI	g2129770
BLAST score	421
E value	6.0e-41
Match length	130
% identity	58
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana] >gi_5533311_gb_AAD45124.1_AF163820_1 (AF163820) endoxyloglucan transferase [Arabidopsis thaliana]
Seq. No.	396734
Contig ID	82177_1.R1084
5'-most EST	g3760416
Seq. No.	396735
Contig ID	82202_1.R1084
5'-most EST	g3061175
Seq. No.	396736
Contig ID	82212_1.R1084
5'-most EST	g4879940
Seq. No.	396737
Contig ID	82303_1.R1084
5'-most EST	g3090444
Method	BLASTX
NCBI GI	g5903051
BLAST score	120
E value	2.0e-10
Match length	60
% identity	60
NCBI Description	(AC008016) Contains PF_00069 Eukaryotic protein kinase domain. ESTs gb_W43822, gb_T20475 and gb_AA586152 come from this gene. [Arabidopsis thaliana]
Seq. No.	396738
Contig ID	82333_1.R1084
5'-most EST	g3090476
Method	BLASTX
NCBI GI	g99809
BLAST score	239
E value	5.0e-20
Match length	105

% identity	48
NCBI Description	gene Bp10 protein - rape >gi_17795_emb_CAA47177_ (X66608) Bplo [Brassica napus]

Seq. No.	396739
Contig ID	82455_1.R1084
5'-most EST	g3762523

Seq. No.	396740
Contig ID	82539_1.R1084
5'-most EST	g3106548
Method	BLASTN
NCBI GI	g303536
BLAST score	166
E value	2.0e-88
Match length	192
% identity	77
NCBI Description	Carrot gene for ribosomal DNA

Seq. No.	396741
Contig ID	82543_1.R1084
5'-most EST	g3106476
Method	BLASTN
NCBI GI	g3851589
BLAST score	108
E value	2.0e-53
Match length	408
% identity	82
NCBI Description	Oryza sativa 33 kDa secretory protein mRNA, complete cds

Seq. No.	396742
Contig ID	82598_1.R1084
5'-most EST	g5038558

Seq. No.	396743
Contig ID	82655_1.R1084
5'-most EST	g3762747

Seq. No.	396744
Contig ID	82668_1.R1084
5'-most EST	g5005131

Seq. No.	396745
Contig ID	82673_1.R1084
5'-most EST	g3106628

Seq. No.	396746
Contig ID	82678_1.R1084
5'-most EST	g3768029
Method	BLASTX
NCBI GI	g4249382
BLAST score	189
E value	5.0e-14
Match length	51
% identity	67
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC

gb_AC004481. [Arabidopsis thaliana]

Seq. No.	396747
Contig ID	82732_1.R1084
5'-most EST	g5004701

Seq. No.	396748
Contig ID	82767_1.R1084
5'-most EST	g4878451
Method	BLASTX
NCBI GI	g2149640
BLAST score	157
E value	4.0e-17
Match length	125
% identity	48
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana] >gi_5733867_gb_AAD49755.1_AC007932_3 (AC007932) Identical to gb_U91995 Argonaute protein from Arabidopsis thaliana. ESTs gb_H76075, gb_AA720232, gb_N65911 and gb_AA651494 come from this gene

Seq. No.	396749
Contig ID	82785_1.R1084
5'-most EST	g3763043
Method	BLASTX
NCBI GI	g4325369
BLAST score	172
E value	5.0e-13
Match length	63
% identity	62
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	396750
Contig ID	82810_1.R1084
5'-most EST	g3762639

Seq. No.	396751
Contig ID	82875_1.R1084
5'-most EST	g3106847
Method	BLASTX
NCBI GI	g2921158
BLAST score	136
E value	2.0e-12
Match length	145
% identity	33
NCBI Description	(AF022909) ClpC [Arabidopsis thaliana]

Seq. No.	396752
Contig ID	82907_1.R1084
5'-most EST	g6062510
Method	BLASTX
NCBI GI	g6056194
BLAST score	186
E value	2.0e-13
Match length	110
% identity	36
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	396753
Contig ID	82921_1.R1084
5'-most EST	g3760585
Seq. No.	396754
Contig ID	82947_1.R1084
5'-most EST	g3106920
Seq. No.	396755
Contig ID	82955_1.R1084
5'-most EST	g3759949
Seq. No.	396756
Contig ID	82977_1.R1084
5'-most EST	g3767318
Method	BLASTX
NCBI GI	g1709205
BLAST score	347
E value	1.0e-36
Match length	121
% identity	64
NCBI Description	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMP 3) (INOSITOL MONOPHOSPHATASE 3) >gi_1098971 (U39059) myo-inositol monophosphatase 3 [Lycopersicon esculentum]
Seq. No.	396757
Contig ID	83021_1.R1084
5'-most EST	g4714177
Seq. No.	396758
Contig ID	83032_1.R1084
5'-most EST	g5002856
Method	BLASTN
NCBI GI	g4521194
BLAST score	420
E value	0.0e+00
Match length	663
% identity	91
NCBI Description	Oryza sativa DNA, centromere sequence RCB11
Seq. No.	396759
Contig ID	83126_1.R1084
5'-most EST	g5667193
Method	BLASTX
NCBI GI	g5281034
BLAST score	220
E value	2.0e-17
Match length	131
% identity	44
NCBI Description	(AL080318) putative protein [Arabidopsis thaliana]
Seq. No.	396760
Contig ID	83139_1.R1084
5'-most EST	g3760246
Seq. No.	396761

Contig ID	83141_1.R1084
5'-most EST	g3107114
Method	BLASTX
NCBI GI	g3150415
BLAST score	238
E value	9.0e-20
Match length	93
% identity	34
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	396762
Contig ID	83162_1.R1084
5'-most EST	g3107135
Method	BLASTN
NCBI GI	g6063530
BLAST score	234
E value	1.0e-129
Match length	335
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	396763
Contig ID	83197_1.R1084
5'-most EST	g4878498

Seq. No.	396764
Contig ID	83231_1.R1084
5'-most EST	g3760141
Method	BLASTX
NCBI GI	g2982724
BLAST score	287
E value	2.0e-25
Match length	99
% identity	59
NCBI Description	(AB012222) tryptophan-tRNA synthetase [Cavia porcellus]

Seq. No.	396765
Contig ID	83238_1.R1084
5'-most EST	g5004100

Seq. No.	396766
Contig ID	83269_1.R1084
5'-most EST	g3767959

Seq. No.	396767
Contig ID	83434_1.R1084
5'-most EST	g3107444
Method	BLASTX
NCBI GI	g4769012
BLAST score	188
E value	5.0e-14
Match length	73
% identity	55
NCBI Description	(AF143746) CER1 [Oryza sativa]

Seq. No.	396768
Contig ID	83456_1.R1084
5'-most EST	g3107487

Seq. No.	396769
Contig ID	83489_1.R1084
5'-most EST	g3107499
Method	BLASTX
NCBI GI	g4558591
BLAST score	287
E value	1.0e-25
Match length	106
% identity	58
NCBI Description	(AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana] >gi_4662638_gb_AAD26909.1_AC007233_1 (AC007233) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	396770
Contig ID	83492_1.R1084
5'-most EST	g3107502

Seq. No.	396771
Contig ID	83529_1.R1084
5'-most EST	g3760291
Method	BLASTN
NCBI GI	g4521194
BLAST score	151
E value	6.0e-79
Match length	563
% identity	85
NCBI Description	Oryza sativa DNA, centromere sequence RCB11

Seq. No.	396772
Contig ID	83552_1.R1084
5'-most EST	g3107689

Seq. No.	396773
Contig ID	83559_1.R1084
5'-most EST	g3762929
Method	BLASTX
NCBI GI	g6056396
BLAST score	403
E value	4.0e-39
Match length	103
% identity	79
NCBI Description	(AC009324) Similar to initiation factor 2 subunit [Arabidopsis thaliana] >gi_6056397_gb_AAF02861.1_AC009324_10 (AC009324) Similar to initiation factor 2 subunit [Arabidopsis thaliana]

Seq. No.	396774
Contig ID	83571_1.R1084
5'-most EST	g3107590

Seq. No.	396775
Contig ID	83588_2.R1084
5'-most EST	g3761972

Method	BLASTX
NCBI GI	g1172557
BLAST score	507
E value	3.0e-51
Match length	104
% identity	91
NCBI Description	OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_422030_pir__S34146 porin por1 - maize >gi_626044_pir__A55017 porin, plastid - maize >gi_313136_emb_CAA51828_ (X73429) porin [Zea mays]

Seq. No.	396776
Contig ID	83619_1.R1084
5'-most EST	g4716330

Seq. No.	396777
Contig ID	83666_1.R1084
5'-most EST	g3107715

Seq. No.	396778
Contig ID	83668_1.R1084
5'-most EST	g3107693

Seq. No.	396779
Contig ID	83756_1.R1084
5'-most EST	g5607602

Seq. No.	396780
Contig ID	83775_1.R1084
5'-most EST	g3768048

Seq. No.	396781
Contig ID	83838_1.R1084
5'-most EST	g3341810

Seq. No.	396782
Contig ID	83889_1.R1084
5'-most EST	g5002844
Method	BLASTX
NCBI GI	g2129626
BLAST score	385
E value	4.0e-56
Match length	256
% identity	51
NCBI Description	J-domain protein - Arabidopsis thaliana >gi_928936_emb_CAA89204_ (Z49238) J-domain protein [Arabidopsis thaliana] >gi_1585434_prf__2124427A diamide resistance gene [Arabidopsis thaliana]

Seq. No.	396783
Contig ID	83907_1.R1084
5'-most EST	g3462543
Method	BLASTX
NCBI GI	g1491710
BLAST score	157
E value	5.0e-14

Match length	71
% identity	59
NCBI Description	(X96506) alpha subunit; forms heterodimer with NC2 alpha/Dr1 [Homo sapiens]

Seq. No.	396784
Contig ID	83917_1.R1084
5'-most EST	g3462553

Seq. No.	396785
Contig ID	83947_1.R1084
5'-most EST	g3762851

Seq. No.	396786
Contig ID	83985_1.R1084
5'-most EST	g4715661

Seq. No.	396787
Contig ID	84014_1.R1084
5'-most EST	g3767087
Method	BLASTX
NCBI GI	g1930079
BLAST score	161
E value	7.0e-19
Match length	82
% identity	66
NCBI Description	(U92877) acyl-ACP thioesterase [Garcinia mangostana]

Seq. No.	396788
Contig ID	84086_1.R1084
5'-most EST	g3762589

Seq. No.	396789
Contig ID	84112_1.R1084
5'-most EST	g4714316

Seq. No.	396790
Contig ID	84114_1.R1084
5'-most EST	g5004793

Seq. No.	396791
Contig ID	84135_1.R1084
5'-most EST	g3760012
Method	BLASTX
NCBI GI	g1729980
BLAST score	145
E value	6.0e-09
Match length	42
% identity	69
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175 thaumatin-like protein - Arabidopsis thaliana >gi_536825 (L34693) thaumatin-like protein [Arabidopsis thaliana] >gi_1094863_prf__2106421A thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	396792
Contig ID	84207_1.R1084

5'-most EST	g5004728
Method	BLASTX
NCBI GI	g3402817
BLAST score	213
E value	9.0e-17
Match length	62
% identity	58
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	396793
Contig ID	84225_1.R1084
5'-most EST	g3762729

Seq. No.	396794
Contig ID	84230_1.R1084
5'-most EST	g4878928

Seq. No.	396795
Contig ID	84241_1.R1084
5'-most EST	g3762745
Method	BLASTX
NCBI GI	g4883603
BLAST score	225
E value	4.0e-18
Match length	130
% identity	37
NCBI Description	(AC006922) putative xyloglucan endo-transglycosylase [Arabidopsis thaliana]

Seq. No.	396796
Contig ID	84246_1.R1084
5'-most EST	g3762750

Seq. No.	396797
Contig ID	84256_1.R1084
5'-most EST	g3763824
Method	BLASTX
NCBI GI	g4155128
BLAST score	167
E value	4.0e-13
Match length	142
% identity	37
NCBI Description	(AE001491) putative 3-HYDROXYACID DEHYDROGENASE [Helicobacter pylori J99]

Seq. No.	396798
Contig ID	84285_1.R1084
5'-most EST	g3763316
Method	BLASTX
NCBI GI	g3402817
BLAST score	255
E value	1.0e-27
Match length	71
% identity	84
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	396799

Contig ID	84295_1.R1084
5'-most EST	g3759060
Method	BLASTN
NCBI GI	g949979
BLAST score	121
E value	2.0e-61
Match length	306
% identity	85
NCBI Description	Z.mays Glossy2 locus DNA

Seq. No.	396800
Contig ID	84301_1.R1084
5'-most EST	g3762806

Seq. No.	396801
Contig ID	84321_1.R1084
5'-most EST	g5038817

Seq. No.	396802
Contig ID	84326_1.R1084
5'-most EST	g3762831

Seq. No.	396803
Contig ID	84339_1.R1084
5'-most EST	g3762844
Method	BLASTX
NCBI GI	g5804817
BLAST score	102
E value	1.0e-10
Match length	63
% identity	53
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	396804
Contig ID	84392_1.R1084
5'-most EST	g3762897

Seq. No.	396805
Contig ID	84400_1.R1084
5'-most EST	g3766588

Seq. No.	396806
Contig ID	84417_1.R1084
5'-most EST	g3762922

Seq. No.	396807
Contig ID	84420_1.R1084
5'-most EST	g3762934

Seq. No.	396808
Contig ID	84435_1.R1084
5'-most EST	g3758965

Seq. No.	396809
Contig ID	84483_1.R1084
5'-most EST	g3762989
Method	BLASTX

NCBI GI	g2660677
BLAST score	255
E value	5.0e-22
Match length	66
% identity	71
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	396810
Contig ID	84487_1.R1084
5'-most EST	g3762993

Seq. No.	396811
Contig ID	84498_1.R1084
5'-most EST	g3766602

Seq. No.	396812
Contig ID	84501_1.R1084
5'-most EST	g5607322
Method	BLASTX
NCBI GI	g1546696
BLAST score	236
E value	5.0e-32
Match length	107
% identity	63
NCBI Description	(X98807) peroxidase ATP21a [Arabidopsis thaliana]

Seq. No.	396813
Contig ID	84518_1.R1084
5'-most EST	g3767237

Seq. No.	396814
Contig ID	84553_1.R1084
5'-most EST	g3763060

Seq. No.	396815
Contig ID	84554_1.R1084
5'-most EST	g3763072

Seq. No.	396816
Contig ID	84556_1.R1084
5'-most EST	g3763063

Seq. No.	396817
Contig ID	84557_1.R1084
5'-most EST	g3761752
Method	BLASTN
NCBI GI	g2879844
BLAST score	54
E value	2.0e-21
Match length	75
% identity	93
NCBI Description	Loligo pealei mRNA for putative N-ethylmaleimide-sensitive fusion protein (NSF)

Seq. No.	396818
Contig ID	84566_1.R1084
5'-most EST	g3761743

Method	BLASTN
NCBI GI	g2352027
BLAST score	119
E value	4.0e-60
Match length	200
% identity	93
NCBI Description	Cloning vector pRS402 with ADE2 marker, complete sequence

Seq. No.	396819
Contig ID	84583_1.R1084
5'-most EST	g3763091
Method	BLASTX
NCBI GI	g2854153
BLAST score	152
E value	9.0e-10
Match length	42
% identity	62
NCBI Description	(AF045640) No definition line found [Caenorhabditis elegans]

Seq. No.	396820
Contig ID	84600_1.R1084
5'-most EST	g3763107

Seq. No.	396821
Contig ID	84612_1.R1084
5'-most EST	g3763119

Seq. No.	396822
Contig ID	84632_1.R1084
5'-most EST	g3763140

Seq. No.	396823
Contig ID	84642_1.R1084
5'-most EST	g3763151

Seq. No.	396824
Contig ID	84650_1.R1084
5'-most EST	g3763158

Seq. No.	396825
Contig ID	84661_1.R1084
5'-most EST	g3763169
Method	BLASTX
NCBI GI	g3915189
BLAST score	256
E value	8.0e-29
Match length	92
% identity	66
NCBI Description	UBIQUITIN-CONJUGATING ENZYME X (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN)

Seq. No.	396826
Contig ID	84668_1.R1084
5'-most EST	g3767661
Method	BLASTX
NCBI GI	g5123701

BLAST score	235
E value	2.0e-19
Match length	62
% identity	69
NCBI Description	(AL079347) putative protein [Arabidopsis thaliana]

Seq. No.	396827
Contig ID	84691_1.R1084
5'-most EST	g3764114
Method	BLASTX
NCBI GI	g4490737
BLAST score	385
E value	6.0e-37
Match length	118
% identity	64
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	396828
Contig ID	84748_1.R1084
5'-most EST	g4881004
Method	BLASTX
NCBI GI	g6006361
BLAST score	781
E value	3.0e-83
Match length	160
% identity	93
NCBI Description	(AP000559) ESTs AU030008(E50477),AU078239(E50477) correspond to a region of the predicted gene.; Similar to peptidyl-prolyl cis-trans isomerase 10 &CELB0252_4 (P52017) [Oryza sativa]

Seq. No.	396829
Contig ID	84748_2.R1084
5'-most EST	g3759879
Method	BLASTX
NCBI GI	g6006361
BLAST score	385
E value	4.0e-37
Match length	130
% identity	52
NCBI Description	(AP000559) ESTs AU030008(E50477),AU078239(E50477) correspond to a region of the predicted gene.; Similar to peptidyl-prolyl cis-trans isomerase 10 &CELB0252_4 (P52017) [Oryza sativa]

Seq. No.	396830
Contig ID	84767_1.R1084
5'-most EST	g3763276
Method	BLASTX
NCBI GI	g4580461
BLAST score	337
E value	6.0e-35
Match length	94
% identity	83
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 396831

Contig ID	84772_1.R1084
5'-most EST	g3763280
Seq. No.	396832
Contig ID	84785_1.R1084
5'-most EST	g3763294
Method	BLASTX
NCBI GI	g728777
BLAST score	175
E value	2.0e-12
Match length	102
% identity	43
NCBI Description	ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (A1 36 KD SUBUNIT) (RF-C 36 KD SUBUNIT) (RFC36) >gi_1498257 (L07540) replication factor C, 36-kDa subunit [Homo sapiens]
Seq. No.	396833
Contig ID	84801_1.R1084
5'-most EST	g3763309
Method	BLASTX
NCBI GI	g3402817
BLAST score	255
E value	1.0e-21
Match length	51
% identity	96
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]
Seq. No.	396834
Contig ID	84818_1.R1084
5'-most EST	g3763327
Method	BLASTX
NCBI GI	g1419388
BLAST score	345
E value	2.0e-33
Match length	87
% identity	83
NCBI Description	(X98925) stromal ascorbate peroxidase [Arabidopsis thaliana]
Seq. No.	396835
Contig ID	84821_1.R1084
5'-most EST	g3763329
Seq. No.	396836
Contig ID	84841_1.R1084
5'-most EST	g3763350
Seq. No.	396837
Contig ID	84850_1.R1084
5'-most EST	g3763359
Method	BLASTN
NCBI GI	g5441876
BLAST score	362
E value	0.0e+00
Match length	413
% identity	97

NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	396838
Contig ID	84856_1.R1084
5'-most EST	g5803568
Method	BLASTX
NCBI GI	g1732515
BLAST score	195
E value	2.0e-14
Match length	139
% identity	34
NCBI Description	(U62744) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No.	396839
Contig ID	84862_1.R1084
5'-most EST	g4715210
Method	BLASTX
NCBI GI	g2289003
BLAST score	356
E value	3.0e-41
Match length	114
% identity	74
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No.	396840
Contig ID	84865_1.R1084
5'-most EST	g3763374
Method	BLASTX
NCBI GI	g3292831
BLAST score	190
E value	4.0e-14
Match length	66
% identity	52
NCBI Description	(AL031018) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	396841
Contig ID	84911_1.R1084
5'-most EST	g3763419

Seq. No.	396842
Contig ID	84917_1.R1084
5'-most EST	g4714431

Seq. No.	396843
Contig ID	84922_1.R1084
5'-most EST	g3763430

Seq. No.	396844
Contig ID	84936_1.R1084
5'-most EST	g3763444

Seq. No.	396845
Contig ID	84941_1.R1084

5'-most EST	g4714407
Seq. No.	396846
Contig ID	84952_1.R1084
5'-most EST	g3763460
Seq. No.	396847
Contig ID	84978_1.R1084
5'-most EST	g5003478
Method	BLASTX
NCBI GI	g4938501
BLAST score	179
E value	1.0e-12
Match length	58
% identity	62
NCBI Description	(AL078465) putative protein [Arabidopsis thaliana]
Seq. No.	396848
Contig ID	84995_1.R1084
5'-most EST	g3763503
Method	BLASTX
NCBI GI	g1001379
BLAST score	217
E value	2.0e-25
Match length	109
% identity	55
NCBI Description	(D64006) aspartate beta-semialdehyde dehydrogenese [Synechocystis sp.]
Seq. No.	396849
Contig ID	85013_1.R1084
5'-most EST	g3763521
Seq. No.	396850
Contig ID	85039_1.R1084
5'-most EST	g3763548
Method	BLASTN
NCBI GI	g415261
BLAST score	60
E value	8.0e-25
Match length	63
% identity	98
NCBI Description	Schizosaccharomyces pombe (clone pJK210) DNA sequence
Seq. No.	396851
Contig ID	85048_1.R1084
5'-most EST	g4968762
Method	BLASTX
NCBI GI	g4580398
BLAST score	400
E value	2.0e-38
Match length	215
% identity	42
NCBI Description	(AC007171) putative protein kinase APK1A [Arabidopsis thaliana]
Seq. No.	396852

Contig ID	85058_1.R1084
5'-most EST	g3763566
Method	BLASTX
NCBI GI	g3402697
BLAST score	298
E value	1.0e-26
Match length	69
% identity	77
NCBI Description	(AC004261) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]

Seq. No.	396853
Contig ID	85110_1.R1084
5'-most EST	g4968831
Method	BLASTX
NCBI GI	g1711512
BLAST score	449
E value	1.0e-44
Match length	122
% identity	76
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54) >gi_1076577_pir__S51598 signal recognition particle 54K protein - tomato (cv. UC82-B) >gi_556902_emb_CAA84288_ (Z34527) 54-kD signal recognition particle (SRP) specific protein [Lycopersicon esculentum]

Seq. No.	396854
Contig ID	85128_1.R1084
5'-most EST	g3763637

Seq. No.	396855
Contig ID	85209_1.R1084
5'-most EST	g4968814

Seq. No.	396856
Contig ID	85222_1.R1084
5'-most EST	g3763732

Seq. No.	396857
Contig ID	85238_1.R1084
5'-most EST	g3768147
Method	BLASTX
NCBI GI	g1174470
BLAST score	298
E value	1.0e-26
Match length	88
% identity	62
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	396858
Contig ID	85267_1.R1084
5'-most EST	g3763778
Method	BLASTX
NCBI GI	g1711512

BLAST score	165
E value	4.0e-11
Match length	102
% identity	45
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54) >gi_1076577_pir__S51598 signal recognition particle 54K protein - tomato (cv. UC82-B) >gi_556902_emb_CAA84288_ (Z34527) 54-kD signal recognition particle (SRP) specific protein [Lycopersicon esculentum]

Seq. No.	396859
Contig ID	85284_1.R1084
5'-most EST	g4714623

Seq. No.	396860
Contig ID	85347_1.R1084
5'-most EST	g3764142
Method	BLASTX
NCBI GI	g629592
BLAST score	384
E value	1.0e-39
Match length	172
% identity	50
NCBI Description	hypothetical protein - rape >gi_6065752_emb_CAB58175.1_ (X74225) putative pod-specific dehydrogenase SAC25 [Brassica napus]

Seq. No.	396861
Contig ID	85364_1.R1084
5'-most EST	g3764127

Seq. No.	396862
Contig ID	85389_1.R1084
5'-most EST	g3766542
Method	BLASTX
NCBI GI	g4507375
BLAST score	173
E value	8.0e-12
Match length	211
% identity	30
NCBI Description	tubulin-specific chaperone e >gi_1465772 (U61232) cofactor E [Homo sapiens]

Seq. No.	396863
Contig ID	85449_1.R1084
5'-most EST	g3766604
Method	BLASTX
NCBI GI	g773414
BLAST score	296
E value	2.0e-26
Match length	90
% identity	69
NCBI Description	(U23751) beta galactosidase [Cloning vector pBBR1MCS-2] >gi_833819 (U25059) LacZ alpha peptide [Cloning vector pBBR1MCS-3] >gi_833823 (U25060) LacZ alpha peptide [Cloning vector pBBR1MCS-4] >gi_833827 (U25061) LacZ alpha peptide [Cloning vector pBBR1MCS-5]

Seq. No.	396864
Contig ID	85464_1.R1084
5'-most EST	g3766618
Method	BLASTX
NCBI GI	g3892057
BLAST score	296
E value	5.0e-36
Match length	95
% identity	44
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396865
Contig ID	85467_1.R1084
5'-most EST	g3766621
Method	BLASTX
NCBI GI	g4263510
BLAST score	262
E value	2.0e-29
Match length	146
% identity	60
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396866
Contig ID	85494_1.R1084
5'-most EST	g4715475

Seq. No.	396867
Contig ID	85507_1.R1084
5'-most EST	g4878365
Method	BLASTX
NCBI GI	g3176673
BLAST score	187
E value	1.0e-13
Match length	100
% identity	42
NCBI Description	(AC003671) Similar to serine/threonine kinase gb_Y12531 from Brassica oleracea. [Arabidopsis thaliana]

Seq. No.	396868
Contig ID	85517_1.R1084
5'-most EST	g3766671
Method	BLASTN
NCBI GI	g5091496
BLAST score	59
E value	4.0e-24
Match length	83
% identity	93
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	396869
Contig ID	85543_1.R1084
5'-most EST	g3766697

Seq. No.	396870
Contig ID	85551_1.R1084

5'-most EST	g3766705
Seq. No.	396871
Contig ID	85575_1.R1084
5'-most EST	g3766738
Seq. No.	396872
Contig ID	85606_1.R1084
5'-most EST	g3766760
Seq. No.	396873
Contig ID	85687_1.R1084
5'-most EST	g3766842
Seq. No.	396874
Contig ID	85690_1.R1084
5'-most EST	g3766845
Method	BLASTX
NCBI GI	g5302796
BLAST score	178
E value	2.0e-28
Match length	181
% identity	44
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.	396875
Contig ID	85718_1.R1084
5'-most EST	g3766895
Seq. No.	396876
Contig ID	85719_1.R1084
5'-most EST	g3762488
Method	BLASTN
NCBI GI	g6002775
BLAST score	301
E value	1.0e-168
Match length	682
% identity	98
NCBI Description	Oryza sativa hypothetical protein, fertilin alpha subunit, membrane protein homolog, and Myb-related protein genes, complete cds; and unknown gene
Seq. No.	396877
Contig ID	85798_1.R1084
5'-most EST	g3767879
Seq. No.	396878
Contig ID	85860_1.R1084
5'-most EST	g4714059
Seq. No.	396879
Contig ID	85878_1.R1084
5'-most EST	g3767042
Seq. No.	396880
Contig ID	85912_1.R1084
5'-most EST	g3767077

Method	BLASTN
NCBI GI	g4324617
BLAST score	79
E value	4.0e-36
Match length	138
% identity	92
NCBI Description	Cloning vector pDR1149 complete sequence

Seq. No.	396881
Contig ID	85914_1.R1084
5'-most EST	g3767078

Seq. No.	396882
Contig ID	85918_1.R1084
5'-most EST	g5038868

Seq. No.	396883
Contig ID	85956_1.R1084
5'-most EST	g3767121

Seq. No.	396884
Contig ID	85984_1.R1084
5'-most EST	g3767150
Method	BLASTX
NCBI GI	g4240122
BLAST score	154
E value	1.0e-09
Match length	79
% identity	44
NCBI Description	(AB007802) cytochrome b5 [Arabidopsis thaliana]

Seq. No.	396885
Contig ID	86002_1.R1084
5'-most EST	g3767167

Seq. No.	396886
Contig ID	86026_1.R1084
5'-most EST	g3767192
Method	BLASTX
NCBI GI	g2462744
BLAST score	248
E value	5.0e-21
Match length	87
% identity	56
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	396887
Contig ID	86052_1.R1084
5'-most EST	g3767218

Seq. No.	396888
Contig ID	86080_1.R1084
5'-most EST	g3767901
Method	BLASTX
NCBI GI	g4803960
BLAST score	227
E value	1.0e-18

Match length	64
% identity	59
NCBI Description	(AC006202) putative carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	396889
Contig ID	86128_1.R1084
5'-most EST	g4714556
Method	BLASTX
NCBI GI	g1402906
BLAST score	202
E value	4.0e-26
Match length	104
% identity	60
NCBI Description	(X98314) peroxidase [Arabidopsis thaliana] >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2 [Arabidopsis thaliana]

Seq. No.	396890
Contig ID	86139_1.R1084
5'-most EST	g5667189
Method	BLASTX
NCBI GI	g2982331
BLAST score	816
E value	2.0e-87
Match length	174
% identity	98
NCBI Description	(AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No.	396891
Contig ID	86147_1.R1084
5'-most EST	g6012896

Seq. No.	396892
Contig ID	86158_1.R1084
5'-most EST	g4716894
Method	BLASTN
NCBI GI	g5295936
BLAST score	89
E value	5.0e-42
Match length	266
% identity	37
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	396893
Contig ID	86185_1.R1084
5'-most EST	g3767353
Method	BLASTX
NCBI GI	g2653285
BLAST score	265
E value	2.0e-23
Match length	79
% identity	84
NCBI Description	(AJ003025) enoyl-ACP reductase [Oryza sativa]

Seq. No. 396894

Contig ID 86190_1.R1084
5'-most EST g3767960

Seq. No. 396895
Contig ID 86207_1.R1084
5'-most EST g4714573
Method BLASTX
NCBI GI g5777627
BLAST score 329
E value 2.0e-30
Match length 80
% identity 84
NCBI Description (AJ245900) CAA303715.1 protein [Oryza sativa]

Seq. No. 396896
Contig ID 86220_1.R1084
5'-most EST g3768887

Seq. No. 396897
Contig ID 86245_1.R1084
5'-most EST g5038704

Seq. No. 396898
Contig ID 86248_1.R1084
5'-most EST g3767418

Seq. No. 396899
Contig ID 86286_1.R1084
5'-most EST g3767456
Method BLASTX
NCBI GI g4884932
BLAST score 275
E value 6.0e-24
Match length 113
% identity 45
NCBI Description (AF141659) AtHVA22a [Arabidopsis thaliana]
>gi_4884944_gb_AAD31885.1_AF141977_1 (AF141977) AtHVA22a
[Arabidopsis thaliana]

Seq. No. 396900
Contig ID 86315_1.R1084
5'-most EST g3767485
Method BLASTX
NCBI GI g3080405
BLAST score 217
E value 1.0e-18
Match length 86
% identity 59
NCBI Description (AL022603) Lsd1 like protein [Arabidopsis thaliana]
>gi_4455269_emb_CAB36805.1_ (AL035527) Lsd1 like protein
[Arabidopsis thaliana]

Seq. No. 396901
Contig ID 86434_1.R1084
5'-most EST g3767687

Seq. No. 396902

Contig ID	86500_1.R1084
5'-most EST	g3767755
Method	BLASTX
NCBI GI	g4588003
BLAST score	363
E value	5.0e-59
Match length	173
% identity	75
NCBI Description	(AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana]

Seq. No.	396903
Contig ID	86516_1.R1084
5'-most EST	g3767770

Seq. No.	396904
Contig ID	86575_1.R1084
5'-most EST	g3767829

Seq. No.	396905
Contig ID	86576_1.R1084
5'-most EST	g4714533

Seq. No.	396906
Contig ID	86580_1.R1084
5'-most EST	g4880612
Method	BLASTX
NCBI GI	g5823576
BLAST score	439
E value	3.0e-43
Match length	93
% identity	86
NCBI Description	(AL049730) putative protein [Arabidopsis thaliana]

Seq. No.	396907
Contig ID	86592_1.R1084
5'-most EST	g3767847

Seq. No.	396908
Contig ID	86649_1.R1084
5'-most EST	g4714523

Seq. No.	396909
Contig ID	86704_1.R1084
5'-most EST	g3767962

Seq. No.	396910
Contig ID	86740_1.R1084
5'-most EST	g3761394

Seq. No.	396911
Contig ID	86767_1.R1084
5'-most EST	g3768026

Seq. No.	396912
Contig ID	86821_1.R1084
5'-most EST	g5038659

Seq. No.	396913
Contig ID	86837_1.R1084
5'-most EST	g5005343
Method	BLASTX
NCBI GI	g3822036
BLAST score	648
E value	1.0e-67
Match length	193
% identity	66
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	396914
Contig ID	86873_1.R1084
5'-most EST	g3760219
Method	BLASTX
NCBI GI	g5091624
BLAST score	272
E value	1.0e-23
Match length	88
% identity	56
NCBI Description	(AC007454) Similar to gb_X92204 NAM gene product from Petunia hybrida. ESTs gb_H36656 and gb_AA651216 come from this gene. [Arabidopsis thaliana]

Seq. No.	396915
Contig ID	87034_1.R1084
5'-most EST	g5455590
Method	BLASTN
NCBI GI	g6006355
BLAST score	118
E value	2.0e-59
Match length	237
% identity	45
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	396916
Contig ID	87037_1.R1084
5'-most EST	g4716554

Seq. No.	396917
Contig ID	87053_1.R1084
5'-most EST	g4714820
Method	BLASTX
NCBI GI	g4826399
BLAST score	155
E value	3.0e-22
Match length	196
% identity	34
NCBI Description	(AJ012423) wall-associated kinase 2 [Arabidopsis thaliana]

Seq. No.	396918
Contig ID	87126_1.R1084
5'-most EST	g4878167

Seq. No.	396919
Contig ID	87175_1.R1084
5'-most EST	g4716631

Method	BLASTX
NCBI GI	g4106340
BLAST score	211
E value	1.0e-31
Match length	146
% identity	51
NCBI Description	(AF062396) protein phosphatase 2A regulatory subunit isoform B' delta [Arabidopsis thaliana]

Seq. No.	396920
Contig ID	87186_1.R1084
5'-most EST	g3768450
Method	BLASTX
NCBI GI	g1816410
BLAST score	152
E value	3.0e-18
Match length	95
% identity	49
NCBI Description	(AB000585) pod storage protein [Phaseolus vulgaris]

Seq. No.	396921
Contig ID	87289_1.R1084
5'-most EST	g3761139
Method	BLASTX
NCBI GI	g4490702
BLAST score	191
E value	2.0e-31
Match length	146
% identity	45
NCBI Description	(AL035680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	396922
Contig ID	87294_1.R1084
5'-most EST	g3768561

Seq. No.	396923
Contig ID	87304_1.R1084
5'-most EST	g4714519
Method	BLASTX
NCBI GI	g167527
BLAST score	201
E value	2.0e-15
Match length	76
% identity	55
NCBI Description	(M91375) This sequence shows homology with Cucumber peroxidase.; peroxidase; putative [Cucumis sativus]

Seq. No.	396924
Contig ID	87330_1.R1084
5'-most EST	g3768599

Seq. No.	396925
Contig ID	87351_1.R1084
5'-most EST	g3768621

Seq. No.	396926
Contig ID	87378_1.R1084

5'-most EST	g3768648
Method	BLASTN
NCBI GI	g287400
BLAST score	44
E value	2.0e-15
Match length	68
% identity	91
NCBI Description	Rice mRNA for peroxidase, complete cds

Seq. No.	396927
Contig ID	87380_1.R1084
5'-most EST	g3768665

Seq. No.	396928
Contig ID	87384_1.R1084
5'-most EST	g3768654

Seq. No.	396929
Contig ID	87465_1.R1084
5'-most EST	g5455613

Seq. No.	396930
Contig ID	87493_1.R1084
5'-most EST	g5803361

Seq. No.	396931
Contig ID	87586_1.R1084
5'-most EST	g4969044

Seq. No.	396932
Contig ID	87587_1.R1084
5'-most EST	g5002772
Method	BLASTX
NCBI GI	g2501499
BLAST score	299
E value	7.0e-27
Match length	175
% identity	42
NCBI Description	INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE (IAA-GLU SYNTHETASE) ((URIDINE 5'-DIPHOSPHATE-GLUCOSE:INDOL-3-YLACETYL)-BETA-D-GLUCOSYL TRANSFERASE) >gi_626043_pir__A54739 indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) - maize >gi_548195 (L34847) IAA-glu synthetase [Zea mays]

Seq. No.	396933
Contig ID	87644_1.R1084
5'-most EST	g3768932

Seq. No.	396934
Contig ID	87700_1.R1084
5'-most EST	g3768988

Seq. No.	396935
Contig ID	87712_1.R1084
5'-most EST	g4715540
Method	BLASTX

NCBI GI g4432860
BLAST score 565
E value 5.0e-58
Match length 210
% identity 13
NCBI Description (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No. 396936
Contig ID 87838_1.R1084
5'-most EST g3769147

Seq. No. 396937
Contig ID 87845_1.R1084
5'-most EST g4716094
Method BLASTX
NCBI GI g2982301
BLAST score 224
E value 3.0e-18
Match length 66
% identity 68
NCBI Description (AF051235) YGL010w-like protein [Picea mariana]

Seq. No. 396938
Contig ID 87881_1.R1084
5'-most EST g4716640
Method BLASTX
NCBI GI g2464913
BLAST score 247
E value 2.0e-20
Match length 119
% identity 46
NCBI Description (Z99708) sugar transporter like protein [Arabidopsis thaliana]

Seq. No. 396939
Contig ID 87900_1.R1084
5'-most EST g3769214

Seq. No. 396940
Contig ID 87937_1.R1084
5'-most EST g3769228

Seq. No. 396941
Contig ID 87945_1.R1084
5'-most EST g3769236

Seq. No. 396942
Contig ID 87968_1.R1084
5'-most EST g5005444

Seq. No. 396943
Contig ID 87997_1.R1084
5'-most EST g3769290
Method BLASTN
NCBI GI g5777612
BLAST score 318

E value	1.0e-179
Match length	368
% identity	97
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	396944
Contig ID	88002_1.R1084
5'-most EST	g6062503

Seq. No.	396945
Contig ID	88038_1.R1084
5'-most EST	g3758952

Seq. No.	396946
Contig ID	88052_1.R1084
5'-most EST	g3758966

Seq. No.	396947
Contig ID	88061_1.R1084
5'-most EST	g4715527

Seq. No.	396948
Contig ID	88100_1.R1084
5'-most EST	g3759014

Seq. No.	396949
Contig ID	88252_1.R1084
5'-most EST	g4714489

Seq. No.	396950
Contig ID	88288_1.R1084
5'-most EST	g3759646

Seq. No.	396951
Contig ID	88292_1.R1084
5'-most EST	g5038771

Seq. No.	396952
Contig ID	88348_1.R1084
5'-most EST	g3759707

Seq. No.	396953
Contig ID	88356_1.R1084
5'-most EST	g3759715

Seq. No.	396954
Contig ID	88427_1.R1084
5'-most EST	g5455339

Seq. No.	396955
Contig ID	88445_1.R1084
5'-most EST	g3759813

Seq. No.	396956
Contig ID	88463_1.R1084
5'-most EST	g4878623

Seq. No.	396957
Contig ID	88637_1.R1084
5'-most EST	g3760015

Seq. No.	396958
Contig ID	88673_1.R1084
5'-most EST	g3760038
Method	BLASTX
NCBI GI	g462234
BLAST score	157
E value	2.0e-10
Match length	40
% identity	78
NCBI Description	HISTONE H2A >gi_419741_pir__S30155 histone H2A - Norway spruce >gi_297871_emb_CAA48030_ (X67819) histone H2A [Picea abies]

Seq. No.	396959
Contig ID	88724_1.R1084
5'-most EST	g3760453

Seq. No.	396960
Contig ID	88736_1.R1084
5'-most EST	g4879198
Method	BLASTX
NCBI GI	g6016871
BLAST score	167
E value	2.0e-11
Match length	104
% identity	39
NCBI Description	(AP000570) EST C98565(E0414) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	396961
Contig ID	88748_1.R1084
5'-most EST	g3760113
Method	BLASTX
NCBI GI	g3176667
BLAST score	162
E value	2.0e-13
Match length	58
% identity	67
NCBI Description	(AC004393) Similar to hypothetical 41.9KD protein gb_1001369 from sequence of Synechocystis sp. gb_D64006. [Arabidopsis thaliana]

Seq. No.	396962
Contig ID	88764_1.R1084
5'-most EST	g3760129
Method	BLASTX
NCBI GI	g4263707
BLAST score	261
E value	8.0e-24
Match length	116
% identity	56
NCBI Description	(AC006223) putative 70kD heat shock protein [Arabidopsis thaliana]

Seq. No. 396963
Contig ID 88822_1.R1084
5'-most EST g3760188

Seq. No. 396964
Contig ID 88904_1.R1084
5'-most EST g3760274
Method BLASTX
NCBI GI g3063695
BLAST score 471
E value 5.0e-57
Match length 245
% identity 53
NCBI Description (AL022537) hypothetical protein [Arabidopsis thaliana]

Seq. No. 396965
Contig ID 88928_1.R1084
5'-most EST g3760297

Seq. No. 396966
Contig ID 88929_1.R1084
5'-most EST g3760310
Method BLASTX
NCBI GI g4584957
BLAST score 429
E value 4.0e-59
Match length 152
% identity 84
NCBI Description (AF077337) heat shock protein 101; 101 kDa heat shock protein [Zea mays] >gi_4928488_gb_AAD33606.1_AF133840_1 (AF133840) heat shock protein HSP101 [Zea mays]

Seq. No. 396967
Contig ID 88953_1.R1084
5'-most EST g3760325

Seq. No. 396968
Contig ID 88974_1.R1084
5'-most EST g5771045
Method BLASTX
NCBI GI g4115559
BLAST score 108
E value 7.0e-12
Match length 47
% identity 79
NCBI Description (AB013596) UDP-glucose:anthocysnin 5-O-glucosyltransferase [Perilla frutescens]

Seq. No. 396969
Contig ID 88983_1.R1084
5'-most EST g3760356
Method BLASTX
NCBI GI g4468806
BLAST score 146
E value 6.0e-20
Match length 131

% identity	46
NCBI Description	(AL035601) cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana]
Seq. No.	396970
Contig ID	89027_1.R1084
5'-most EST	g3760437
Seq. No.	396971
Contig ID	89039_1.R1084
5'-most EST	g4879136
Seq. No.	396972
Contig ID	89067_1.R1084
5'-most EST	g4714862
Method	BLASTX
NCBI GI	g2827713
BLAST score	471
E value	6.0e-47
Match length	106
% identity	86
NCBI Description	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]
Seq. No.	396973
Contig ID	89095_1.R1084
5'-most EST	g3760472
Method	BLASTX
NCBI GI	g2245131
BLAST score	252
E value	1.0e-21
Match length	87
% identity	64
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.	396974
Contig ID	89099_1.R1084
5'-most EST	g5003584
Seq. No.	396975
Contig ID	89103_1.R1084
5'-most EST	g3760480
Seq. No.	396976
Contig ID	89122_1.R1084
5'-most EST	g4880891
Seq. No.	396977
Contig ID	89124_1.R1084
5'-most EST	g5002905
Seq. No.	396978
Contig ID	89150_1.R1084
5'-most EST	g5002973
Method	BLASTX
NCBI GI	g1361979
BLAST score	518

E value	2.0e-52
Match length	126
% identity	80
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) - watermelon >gi_1350550_dbj_BAA12843_ (D85624) serine acetyltransferase [Citrullus lanatus] >gi_1841312_dbj_BAA08479_ (D49535) serine acetyltransferase. [Citrullus lanatus] >gi_2337772_dbj_BAA21827_ (AB006530) serine acetyltransferase [Citrullus lanatus]

Seq. No.	396979
Contig ID	89170_1.R1084
5'-most EST	g3760549
Method	BLASTN
NCBI GI	g3015620
BLAST score	78
E value	9.0e-36
Match length	98
% identity	95
NCBI Description	Zea mays low molecular weight heat shock protein precursor (hsp22) mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	396980
Contig ID	89225_1.R1084
5'-most EST	g3760605
Method	BLASTX
NCBI GI	g4775576
BLAST score	448
E value	3.0e-44
Match length	156
% identity	57
NCBI Description	(AJ238785) MUS1 protein [Zea mays]

Seq. No.	396981
Contig ID	89228_1.R1084
5'-most EST	g3760608
Method	BLASTX
NCBI GI	g4006917
BLAST score	345
E value	4.0e-32
Match length	142
% identity	48
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	396982
Contig ID	89243_1.R1084
5'-most EST	g3760624
Method	BLASTX
NCBI GI	g4415941
BLAST score	364
E value	3.0e-42
Match length	170
% identity	45
NCBI Description	(AC006418) putative arginine-serine rich splicing factor [Arabidopsis thaliana]

Seq. No.	396983
Contig ID	89269_1.R1084
5'-most EST	g5004075

Seq. No.	396984
Contig ID	89308_1.R1084
5'-most EST	g3762065
Method	BLASTX
NCBI GI	g2827544
BLAST score	238
E value	8.0e-20
Match length	59
% identity	76
NCBI Description	(AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No.	396985
Contig ID	89458_1.R1084
5'-most EST	g3761002
Method	BLASTX
NCBI GI	g4325369
BLAST score	553
E value	1.0e-56
Match length	137
% identity	72
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	396986
Contig ID	89505_1.R1084
5'-most EST	g3760889
Method	BLASTX
NCBI GI	g4097547
BLAST score	331
E value	1.0e-30
Match length	126
% identity	34
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	396987
Contig ID	89636_1.R1084
5'-most EST	g4714320

Seq. No.	396988
Contig ID	89744_1.R1084
5'-most EST	g3762193
Method	BLASTX
NCBI GI	g477815
BLAST score	132
E value	1.0e-10
Match length	49
% identity	65
NCBI Description	ubiquitin-ribosomal protein fusion protein - Eimeria bovis

Seq. No.	396989
Contig ID	89764_1.R1084
5'-most EST	g5055952
Method	BLASTX

NCBI GI	g3953471
BLAST score	556
E value	6.0e-57
Match length	131
% identity	78
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	396990
Contig ID	89800_1.R1084
5'-most EST	g3761194

Seq. No.	396991
Contig ID	89874_1.R1084
5'-most EST	g3761270

Seq. No.	396992
Contig ID	89959_1.R1084
5'-most EST	g3761386

Seq. No.	396993
Contig ID	90035_1.R1084
5'-most EST	g4715395

Seq. No.	396994
Contig ID	90068_1.R1084
5'-most EST	g5607309

Seq. No.	396995
Contig ID	90099_1.R1084
5'-most EST	g3761497

Seq. No.	396996
Contig ID	90112_1.R1084
5'-most EST	g4715520

Seq. No.	396997
Contig ID	90138_1.R1084
5'-most EST	g3761536

Seq. No.	396998
Contig ID	90224_1.R1084
5'-most EST	g3761623

Seq. No.	396999
Contig ID	90238_1.R1084
5'-most EST	g3761636

Seq. No.	397000
Contig ID	90251_1.R1084
5'-most EST	g5002889

Seq. No.	397001
Contig ID	90269_1.R1084
5'-most EST	g4714834
Method	BLASTN
NCBI GI	g5803242
BLAST score	649

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E value	0.0e+00
Match length	694
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	397002
Contig ID	90321_1.R1084
5'-most EST	g3761719
Method	BLASTX
NCBI GI	g4803955
BLAST score	286
E value	2.0e-25
Match length	100
% identity	58
NCBI Description	(AC006202) putative cyclic nucleotide and calmodulin-regulated ion channel protein [Arabidopsis thaliana]

Seq. No.	397003
Contig ID	90324_1.R1084
5'-most EST	g4715221
Method	BLASTX
NCBI GI	g4557093
BLAST score	215
E value	5.0e-17
Match length	73
% identity	64
NCBI Description	(AF001136) zinc finger protein [Pinus radiata]

Seq. No.	397004
Contig ID	90328_1.R1084
5'-most EST	g3761726

Seq. No.	397005
Contig ID	90329_1.R1084
5'-most EST	g3761727

Seq. No.	397006
Contig ID	90361_1.R1084
5'-most EST	g4880692
Method	BLASTN
NCBI GI	g559342
BLAST score	41
E value	1.0e-13
Match length	72
% identity	92
NCBI Description	Human TBXAS1 gene for thromboxane synthase, exon

Seq. No.	397007
Contig ID	90362_1.R1084
5'-most EST	g4715392

Seq. No.	397008
Contig ID	90485_1.R1084
5'-most EST	g6062531

Seq. No. 397009

Contig ID 90497_1.R1084
5'-most EST g3761930

Seq. No. 397010
Contig ID 90498_1.R1084
5'-most EST g5900760

Seq. No. 397011
Contig ID 90620_1.R1084
5'-most EST g3762030
Method BLASTX
NCBI GI g3928150
BLAST score 493
E value 1.0e-56
Match length 131
% identity 92
NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 397012
Contig ID 90742_1.R1084
5'-most EST g5455520
Method BLASTN
NCBI GI g5734616
BLAST score 67
E value 4.0e-29
Match length 79
% identity 96
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No. 397013
Contig ID 90805_1.R1084
5'-most EST g6025148

Seq. No. 397014
Contig ID 90811_1.R1084
5'-most EST g4715518
Method BLASTX
NCBI GI g2388999
BLAST score 153
E value 8.0e-10
Match length 98
% identity 34
NCBI Description (Z98981) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 397015
Contig ID 90861_1.R1084
5'-most EST g3762313

Seq. No. 397016
Contig ID 90862_1.R1084
5'-most EST g3762277

Seq. No. 397017
Contig ID 90866_1.R1084
5'-most EST g3762383

Seq. No. 397018

Contig ID 90891_1.R1084
5'-most EST g4714138

Seq. No. 397019
Contig ID 90900_2.R1084
5'-most EST g3762315

Seq. No. 397020
Contig ID 90901_1.R1084
5'-most EST g3762316
Method BLASTX
NCBI GI g4262234
BLAST score 236
E value 9.0e-22
Match length 150
% identity 42
NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]

Seq. No. 397021
Contig ID 90903_1.R1084
5'-most EST g4714098

Seq. No. 397022
Contig ID 90905_1.R1084
5'-most EST g3762320

Seq. No. 397023
Contig ID 90925_1.R1084
5'-most EST g3762340

Seq. No. 397024
Contig ID 90978_1.R1084
5'-most EST g5004281
Method BLASTX
NCBI GI g6056388
BLAST score 239
E value 7.0e-20
Match length 137
% identity 32
NCBI Description (AC009324) 26S proteasome ATPase subunit [Arabidopsis thaliana]

Seq. No. 397025
Contig ID 90989_1.R1084
5'-most EST g4715153
Method BLASTX
NCBI GI g4558591
BLAST score 311
E value 3.0e-28
Match length 78
% identity 71
NCBI Description (AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana] >gi_4662638_gb_AAD26909.1_AC007233_1 (AC007233) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No. 397026
Contig ID 90998_1.R1084

5'-most EST	g3762476
Method	BLASTX
NCBI GI	g4512674
BLAST score	254
E value	1.0e-21
Match length	159
% identity	26
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397027
Contig ID	91035_1.R1084
5'-most EST	g5038708

Seq. No.	397028
Contig ID	91070_1.R1084
5'-most EST	g3762487

Seq. No.	397029
Contig ID	91073_1.R1084
5'-most EST	g4107124

Seq. No.	397030
Contig ID	91076_1.R1084
5'-most EST	g4107127
Method	BLASTN
NCBI GI	g5295936
BLAST score	100
E value	7.0e-49
Match length	211
% identity	87
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	397031
Contig ID	91129_1.R1084
5'-most EST	g4714758
Method	BLASTX
NCBI GI	g4415923
BLAST score	286
E value	3.0e-25
Match length	149
% identity	43
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No.	397032
Contig ID	91195_1.R1084
5'-most EST	g4714673

Seq. No.	397033
Contig ID	91217_1.R1084
5'-most EST	g4714728
Method	BLASTX
NCBI GI	g5052007
BLAST score	438
E value	2.0e-43
Match length	97

% identity	79
NCBI Description	(AF155121) apoplastic invertase [Oryza sativa subsp. indica]

Seq. No.	397034
Contig ID	91254_1.R1084
5'-most EST	g4880971

Seq. No.	397035
Contig ID	91289_1.R1084
5'-most EST	g4714767
Method	BLASTX
NCBI GI	g4102839
BLAST score	627
E value	1.0e-103
Match length	328
% identity	60
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	397036
Contig ID	91299_1.R1084
5'-most EST	g4714777

Seq. No.	397037
Contig ID	91351_1.R1084
5'-most EST	g4716687

Seq. No.	397038
Contig ID	91369_1.R1084
5'-most EST	g4714847
Method	BLASTX
NCBI GI	g5732066
BLAST score	192
E value	4.0e-29
Match length	168
% identity	32
NCBI Description	(AF147263) contains similarity to Medicago truncatula N7 protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No.	397039
Contig ID	91397_1.R1084
5'-most EST	g4716059

Seq. No.	397040
Contig ID	91430_1.R1084
5'-most EST	g4714910

Seq. No.	397041
Contig ID	91457_1.R1084
5'-most EST	g4714937

Seq. No.	397042
Contig ID	91573_1.R1084
5'-most EST	g4715053

Seq. No.	397043
Contig ID	91580_1.R1084

5'-most EST	g4715060
Seq. No.	397044
Contig ID	91586_1.R1084
5'-most EST	g4715066
Method	BLASTX
NCBI GI	g2980770
BLAST score	169
E value	1.0e-11
Match length	47
% identity	68
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.	397045
Contig ID	91759_1.R1084
5'-most EST	g4715699
Seq. No.	397046
Contig ID	91798_1.R1084
5'-most EST	g5803502
Seq. No.	397047
Contig ID	91820_1.R1084
5'-most EST	g4714153
Seq. No.	397048
Contig ID	91834_1.R1084
5'-most EST	g4715317
Method	BLASTX
NCBI GI	g5080773
BLAST score	220
E value	2.0e-17
Match length	98
% identity	46
NCBI Description	(AC007576) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	397049
Contig ID	91852_1.R1084
5'-most EST	g4878568
Method	BLASTX
NCBI GI	g5911685
BLAST score	753
E value	4.0e-80
Match length	179
% identity	79
NCBI Description	(Y11996) PRT1 protein [Nicotiana tabacum]
Seq. No.	397050
Contig ID	91891_1.R1084
5'-most EST	g4716610
Method	BLASTX
NCBI GI	g5107831
BLAST score	265
E value	1.0e-30
Match length	145
% identity	53
NCBI Description	(AF149413) contains similarity to protein kinase domains

(Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]

Seq. No.	397051
Contig ID	91897_1.R1084
5'-most EST	g4715565
Method	BLASTX
NCBI GI	g3860263
BLAST score	279
E value	3.0e-29
Match length	102
% identity	67
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	397052
Contig ID	91923_1.R1084
5'-most EST	g4714441
Method	BLASTN
NCBI GI	g5257255
BLAST score	57
E value	3.0e-23
Match length	318
% identity	64
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	397053
Contig ID	91978_1.R1084
5'-most EST	g5607300

Seq. No.	397054
Contig ID	91997_1.R1084
5'-most EST	g4715482

Seq. No.	397055
Contig ID	92055_1.R1084
5'-most EST	g4715541
Method	BLASTX
NCBI GI	g5802576
BLAST score	499
E value	5.0e-50
Match length	237
% identity	44
NCBI Description	(AF174294) (+)-delta-cadinene sythase [Gossypium arboreum]

Seq. No.	397056
Contig ID	92063_1.R1084
5'-most EST	g5803524

Seq. No.	397057
Contig ID	92081_1.R1084
5'-most EST	g4715568
Method	BLASTX
NCBI GI	g1931644
BLAST score	238
E value	2.0e-19

Match length 110
% identity 39
NCBI Description (U95973) membrane protein PTM1 precursor isolog [Arabidopsis thaliana]

Seq. No. 397058
Contig ID 92100_1.R1084
5'-most EST g4716745

Seq. No. 397059
Contig ID 92118_1.R1084
5'-most EST g4715605
Method BLASTX
NCBI GI g4581163
BLAST score 246
E value 2.0e-20
Match length 106
% identity 53
NCBI Description (AC006220) unknown protein [Arabidopsis thaliana]

Seq. No. 397060
Contig ID 92179_1.R1084
5'-most EST g5005244

Seq. No. 397061
Contig ID 92216_1.R1084
5'-most EST g4715703
Method BLASTX
NCBI GI g1502430
BLAST score 878
E value 1.0e-94
Match length 213
% identity 77
NCBI Description (U62331) phosphate transporter [Arabidopsis thaliana] >gi_2564661 (AF022872) phosphate transporter [Arabidopsis thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770) phosphate transporter, AtPT2 [Arabidopsis thaliana]

Seq. No. 397062
Contig ID 92226_1.R1084
5'-most EST g4716474

Seq. No. 397063
Contig ID 92272_1.R1084
5'-most EST g4715759
Method BLASTN
NCBI GI g5091496
BLAST score 684
E value 0.0e+00
Match length 760
% identity 99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No. 397064
Contig ID 92334_1.R1084

5'-most EST	g4715821
Method	BLASTX
NCBI GI	g2618687
BLAST score	296
E value	8.0e-27
Match length	105
% identity	40
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397065
Contig ID	92335_1.R1084
5'-most EST	g4715937

Seq. No.	397066
Contig ID	92345_1.R1084
5'-most EST	g4715832

Seq. No.	397067
Contig ID	92353_1.R1084
5'-most EST	g5002955

Seq. No.	397068
Contig ID	92362_1.R1084
5'-most EST	g4715850

Seq. No.	397069
Contig ID	92401_1.R1084
5'-most EST	g4715889

Seq. No.	397070
Contig ID	92426_1.R1084
5'-most EST	g4715914

Seq. No.	397071
Contig ID	92432_1.R1084
5'-most EST	g4715920
Method	BLASTX
NCBI GI	g1805254
BLAST score	494
E value	1.0e-49
Match length	140
% identity	73
NCBI Description	(U62622) monogalactosyldiacylglycerol synthase [Cucumis sativus]

Seq. No.	397072
Contig ID	92471_1.R1084
5'-most EST	g4715960

Seq. No.	397073
Contig ID	92487_1.R1084
5'-most EST	g4715977
Method	BLASTX
NCBI GI	g2822483
BLAST score	463
E value	6.0e-46
Match length	149

% identity	61
NCBI Description	(AF039709) 14-3-3 protein homolog [Maackia amurensis]

Seq. No.	397074
Contig ID	92551_1.R1084
5'-most EST	g4716042

Seq. No.	397075
Contig ID	92580_1.R1084
5'-most EST	g4716071
Method	BLASTX
NCBI GI	g4874309
BLAST score	297
E value	2.0e-26
Match length	88
% identity	60
NCBI Description	(AC006053) biotin holocarboxylase synthetase [Arabidopsis thaliana]

Seq. No.	397076
Contig ID	92637_1.R1084
5'-most EST	g4716128

Seq. No.	397077
Contig ID	92639_1.R1084
5'-most EST	g4716130

Seq. No.	397078
Contig ID	92653_1.R1084
5'-most EST	g4716144

Seq. No.	397079
Contig ID	92673_1.R1084
5'-most EST	g4716164

Seq. No.	397080
Contig ID	92678_1.R1084
5'-most EST	g4716171
Method	BLASTN
NCBI GI	g6069643
BLAST score	130
E value	9.0e-67
Match length	336
% identity	13
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0514G12

Seq. No.	397081
Contig ID	92707_1.R1084
5'-most EST	g4716200
Method	BLASTX
NCBI GI	g4580513
BLAST score	406
E value	2.0e-39
Match length	112
% identity	66
NCBI Description	(AF036300) scarecrow-like 1 [Arabidopsis thaliana]

Seq. No.	397082
Contig ID	92748_1.R1084
5'-most EST	g4716241
Method	BLASTX
NCBI GI	g2828296
BLAST score	154
E value	6.0e-10
Match length	30
% identity	93
NCBI Description	(AL021687) RNase L inhibitor-like protein [Arabidopsis thaliana]

Seq. No.	397083
Contig ID	92753_1.R1084
5'-most EST	g4716246
Method	BLASTX
NCBI GI	g3128217
BLAST score	296
E value	1.0e-26
Match length	84
% identity	74
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana] >gi_3337374 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397084
Contig ID	92792_1.R1084
5'-most EST	g4716285

Seq. No.	397085
Contig ID	92800_1.R1084
5'-most EST	g4716293
Method	BLASTX
NCBI GI	g6006874
BLAST score	230
E value	6.0e-19
Match length	105
% identity	45
NCBI Description	(AC008153) putative UDP-glucuronosyltransferase, 5' partial [Arabidopsis thaliana]

Seq. No.	397086
Contig ID	92807_1.R1084
5'-most EST	g4716300

Seq. No.	397087
Contig ID	92846_1.R1084
5'-most EST	g4716339
Method	BLASTX
NCBI GI	g5803264
BLAST score	725
E value	1.0e-76
Match length	136
% identity	100
NCBI Description	(AP000399) ESTs AU057456(S21460),AU057455(S21460) correspond to a region of the predicted gene; similar to cytochrome c oxidase subunit Vb precursor (D85381) [Oryza

sativa]

Seq. No. 397088
Contig ID 92875_1.R1084
5'-most EST g4716601
Method BLASTX
NCBI GI g2213611
BLAST score 396
E value 9.0e-54
Match length 179
% identity 66
NCBI Description (AC000103) F21J9.5 [Arabidopsis thaliana]

Seq. No. 397089
Contig ID 92913_1.R1084
5'-most EST g4716762
Method BLASTX
NCBI GI g2801538
BLAST score 152
E value 4.0e-12
Match length 99
% identity 45
NCBI Description (AF039532) harpin induced gene 1 homolog [Oryza sativa]

Seq. No. 397090
Contig ID 92980_1.R1084
5'-most EST g4716476

Seq. No. 397091
Contig ID 92981_1.R1084
5'-most EST g4716477
Method BLASTX
NCBI GI g4510375
BLAST score 169
E value 2.0e-21
Match length 107
% identity 72
NCBI Description (AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]

Seq. No. 397092
Contig ID 92988_1.R1084
5'-most EST g4716484

Seq. No. 397093
Contig ID 92996_1.R1084
5'-most EST g4716493
Method BLASTX
NCBI GI g2245118
BLAST score 277
E value 2.0e-24
Match length 80
% identity 69
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 397094
Contig ID 93138_1.R1084

5'-most EST	g4716638
Method	BLASTX
NCBI GI	g5732079
BLAST score	188
E value	9.0e-14
Match length	71
% identity	49
NCBI Description	(AF162444) No definition line found [Arabidopsis thaliana]

Seq. No.	397095
Contig ID	93276_1.R1084
5'-most EST	g4716779

Seq. No.	397096
Contig ID	93307_1.R1084
5'-most EST	g4716811

Seq. No.	397097
Contig ID	93342_1.R1084
5'-most EST	g4716848

Seq. No.	397098
Contig ID	93348_1.R1084
5'-most EST	g4716854

Seq. No.	397099
Contig ID	93349_1.R1084
5'-most EST	g4716882

Seq. No.	397100
Contig ID	93396_1.R1084
5'-most EST	g4714393
Method	BLASTX
NCBI GI	g3608481
BLAST score	185
E value	2.0e-13
Match length	66
% identity	58
NCBI Description	(AF088913) ribosomal protein L27a [Petunia x hybrida]

Seq. No.	397101
Contig ID	93424_1.R1084
5'-most EST	g5607368

Seq. No.	397102
Contig ID	93437_1.R1084
5'-most EST	g4969378
Method	BLASTX
NCBI GI	g3334441
BLAST score	204
E value	1.0e-15
Match length	98
% identity	29
NCBI Description	HYPOTHETICAL 47.9 KD PROTEIN T5I7.9 IN CHROMOSOME II >gi_2642161 (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 397103
Contig ID 93512_1.R1084
5'-most EST g4714170

Seq. No. 397104
Contig ID 93604_1.R1084
5'-most EST g4714265

Seq. No. 397105
Contig ID 93725_1.R1084
5'-most EST g5003210

Seq. No. 397106
Contig ID 93775_1.R1084
5'-most EST g4714442

Seq. No. 397107
Contig ID 93779_1.R1084
5'-most EST g4714447

Seq. No. 397108
Contig ID 93859_1.R1084
5'-most EST g4714559
Method BLASTX
NCBI GI g1890311
BLAST score 236
E value 1.0e-19
Match length 76
% identity 66
NCBI Description (Y11789) peroxidase ATP23b [Arabidopsis thaliana]

Seq. No. 397109
Contig ID 93887_1.R1084
5'-most EST g4714572

Seq. No. 397110
Contig ID 93988_1.R1084
5'-most EST g4878184

Seq. No. 397111
Contig ID 93991_1.R1084
5'-most EST g4878187
Method BLASTX
NCBI GI g2435511
BLAST score 166
E value 2.0e-11
Match length 71
% identity 46
NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No. 397112
Contig ID 94015_1.R1084
5'-most EST g4878214
Method BLASTX
NCBI GI g5106764
BLAST score 345

E value 2.0e-32
Match length 136
% identity 57
NCBI Description (AF073329) eukaryotic translation initiation factor 3 large subunit [Zea mays]

Seq. No. 397113
Contig ID 94033_1.R1084
5'-most EST g4878240

Seq. No. 397114
Contig ID 94051_1.R1084
5'-most EST g4878252

Seq. No. 397115
Contig ID 94060_1.R1084
5'-most EST g4878328

Seq. No. 397116
Contig ID 94077_1.R1084
5'-most EST g4878311
Method BLASTX
NCBI GI g2746086
BLAST score 563
E value 5.0e-58
Match length 121
% identity 88
NCBI Description (AF025292) putative high-affinity potassium transporter [Hordeum vulgare]

Seq. No. 397117
Contig ID 94086_1.R1084
5'-most EST g4878288
Method BLASTX
NCBI GI g2098778
BLAST score 183
E value 9.0e-19
Match length 65
% identity 78
NCBI Description (U96045) APS reductase [Arabidopsis thaliana]

Seq. No. 397118
Contig ID 94105_1.R1084
5'-most EST g4878313

Seq. No. 397119
Contig ID 94231_1.R1084
5'-most EST g5003481
Method BLASTX
NCBI GI g2244990
BLAST score 904
E value 1.0e-97
Match length 231
% identity 74
NCBI Description (Z97340) putative protein [Arabidopsis thaliana]

Seq. No. 397120

Contig ID	94245_1.R1084
5'-most EST	g4878452
Seq. No.	397121
Contig ID	94255_1.R1084
5'-most EST	g5003466
Method	BLASTX
NCBI GI	g4733981
BLAST score	180
E value	3.0e-15
Match length	58
% identity	58
NCBI Description	(AC007268) putative serine carboxypeptidase [Arabidopsis thaliana]
Seq. No.	397122
Contig ID	94299_1.R1084
5'-most EST	g5701686
Seq. No.	397123
Contig ID	94301_1.R1084
5'-most EST	g4878510
Seq. No.	397124
Contig ID	94304_1.R1084
5'-most EST	g4878520
Seq. No.	397125
Contig ID	94395_1.R1084
5'-most EST	g4878613
Method	BLASTX
NCBI GI	g1857447
BLAST score	149
E value	1.0e-09
Match length	92
% identity	42
NCBI Description	(U82367) UDP-glucose glucosyltransferase [Solanum tuberosum]
Seq. No.	397126
Contig ID	94436_1.R1084
5'-most EST	g4878657
Method	BLASTX
NCBI GI	g3063698
BLAST score	379
E value	1.0e-40
Match length	137
% identity	65
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]
Seq. No.	397127
Contig ID	94445_1.R1084
5'-most EST	g4878711
Method	BLASTX
NCBI GI	g6094552
BLAST score	214
E value	5.0e-17

Match length	156
% identity	37
NCBI Description	(AC010676) unknown protein [Arabidopsis thaliana]

Seq. No.	397128
Contig ID	94549_1.R1084
5'-most EST	g4878774
Method	BLASTX
NCBI GI	g1871187
BLAST score	302
E value	1.0e-27
Match length	114
% identity	54
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	397129
Contig ID	94554_1.R1084
5'-most EST	g4878779

Seq. No.	397130
Contig ID	94559_1.R1084
5'-most EST	g4878783

Seq. No.	397131
Contig ID	94588_1.R1084
5'-most EST	g5803392
Method	BLASTX
NCBI GI	g4884860
BLAST score	299
E value	5.0e-27
Match length	133
% identity	53
NCBI Description	(AF133118) nucleic acid binding protein [Oryza sativa]

Seq. No.	397132
Contig ID	94657_1.R1084
5'-most EST	g4878884

Seq. No.	397133
Contig ID	94670_1.R1084
5'-most EST	g4878894

Seq. No.	397134
Contig ID	94682_1.R1084
5'-most EST	g4878907

Seq. No.	397135
Contig ID	94688_1.R1084
5'-most EST	g4878915

Seq. No.	397136
Contig ID	94783_1.R1084
5'-most EST	g4879012

Seq. No.	397137
Contig ID	94811_1.R1084
5'-most EST	g5701698

Method	BLASTX
NCBI GI	g4510349
BLAST score	260
E value	2.0e-22
Match length	125
% identity	52
NCBI Description	(AC006921) putative bZIP transcription factor [Arabidopsis thaliana]

Seq. No.	397138
Contig ID	94825_1.R1084
5'-most EST	g4879140
Method	BLASTX
NCBI GI	g5777683
BLAST score	151
E value	1.0e-09
Match length	81
% identity	44
NCBI Description	(AL109989) hypothetical protein SCJ12.22 [Streptomyces coelicolor A3(2)]

Seq. No.	397139
Contig ID	94833_1.R1084
5'-most EST	g4879138
Method	BLASTX
NCBI GI	g4309734
BLAST score	336
E value	3.0e-31
Match length	166
% identity	44
NCBI Description	(AC006439) putative 26S proteosome regulatory subunit 8 [Arabidopsis thaliana]

Seq. No.	397140
Contig ID	94866_1.R1084
5'-most EST	g4879095

Seq. No.	397141
Contig ID	94883_1.R1084
5'-most EST	g4879112

Seq. No.	397142
Contig ID	94899_1.R1084
5'-most EST	g6062538
Method	BLASTX
NCBI GI	g4538911
BLAST score	191
E value	3.0e-18
Match length	84
% identity	57
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397143
Contig ID	94900_1.R1084
5'-most EST	g4879129
Method	BLASTX
NCBI GI	g3540179

BLAST score	160
E value	7.0e-11
Match length	36
% identity	83
NCBI Description	(AC004122) putative amino acid permease [Arabidopsis thaliana]

Seq. No.	397144
Contig ID	94906_1.R1084
5'-most EST	g5004180

Seq. No.	397145
Contig ID	94922_1.R1084
5'-most EST	g4879166

Seq. No.	397146
Contig ID	94945_1.R1084
5'-most EST	g4879267
Method	BLASTN
NCBI GI	g4521194
BLAST score	239
E value	1.0e-132
Match length	416
% identity	91
NCBI Description	Oryza sativa DNA, centromere sequence RCB11

Seq. No.	397147
Contig ID	94959_1.R1084
5'-most EST	g4879192

Seq. No.	397148
Contig ID	95074_1.R1084
5'-most EST	g5004513
Method	BLASTX
NCBI GI	g1763972
BLAST score	196
E value	1.0e-17
Match length	69
% identity	74
NCBI Description	(U81385) heat shock protein [Oryza sativa]

Seq. No.	397149
Contig ID	95136_1.R1084
5'-most EST	g5004944

Seq. No.	397150
Contig ID	95228_1.R1084
5'-most EST	g4879478

Seq. No.	397151
Contig ID	95234_1.R1084
5'-most EST	g5004829
Method	BLASTX
NCBI GI	g4514716
BLAST score	211
E value	1.0e-16
Match length	102

% identity	32
NCBI Description	(AB017533) EPc [Nicotiana tabacum]

Seq. No.	397152
Contig ID	95235_1.R1084
5'-most EST	g4879533
Method	BLASTX
NCBI GI	g3142303
BLAST score	265
E value	5.0e-23
Match length	139
% identity	44
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	397153
Contig ID	95245_1.R1084
5'-most EST	g4880391

Seq. No.	397154
Contig ID	95265_1.R1084
5'-most EST	g4880605

Seq. No.	397155
Contig ID	95302_1.R1084
5'-most EST	g4879557
Method	BLASTX
NCBI GI	g3152731
BLAST score	403
E value	3.0e-39
Match length	120
% identity	69
NCBI Description	(AF056325) myo-inositol 1-phosphate synthase; INO1 [Hordeum vulgare]

Seq. No.	397156
Contig ID	95318_1.R1084
5'-most EST	g4879665
Method	BLASTX
NCBI GI	g322752
BLAST score	591
E value	2.0e-65
Match length	153
% identity	81
NCBI Description	auxin-independent growth promoter - Nicotiana tabacum >gi_559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]

Seq. No.	397157
Contig ID	95321_1.R1084
5'-most EST	g4879634
Method	BLASTX
NCBI GI	g5262796
BLAST score	293
E value	2.0e-26
Match length	106

% identity	60
NCBI Description	(AL080282) putative protein [Arabidopsis thaliana]

Seq. No.	397158
Contig ID	95327_1.R1084
5'-most EST	g4879584

Seq. No.	397159
Contig ID	95375_1.R1084
5'-most EST	g4879637
Method	BLASTX
NCBI GI	g4138581
BLAST score	126
E value	7.0e-11
Match length	111
% identity	24
NCBI Description	(X98474) mitochondrial energy transfer protein [Solanum tuberosum]

Seq. No.	397160
Contig ID	95376_1.R1084
5'-most EST	g4879649
Method	BLASTX
NCBI GI	g4467124
BLAST score	160
E value	1.0e-10
Match length	143
% identity	27
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397161
Contig ID	95377_1.R1084
5'-most EST	g4879641

Seq. No.	397162
Contig ID	95401_1.R1084
5'-most EST	g4879666
Method	BLASTX
NCBI GI	g5734781
BLAST score	143
E value	1.0e-08
Match length	105
% identity	35
NCBI Description	(AC007980) 89719 [Arabidopsis thaliana]

Seq. No.	397163
Contig ID	95404_1.R1084
5'-most EST	g4879689

Seq. No.	397164
Contig ID	95437_1.R1084
5'-most EST	g4879706
Method	BLASTN
NCBI GI	g4512226
BLAST score	243
E value	1.0e-134
Match length	465

% identity	90
NCBI Description	Oryza sativa gypsy-type retrotransposon RIRE3 DNA, internal region, complete sequence

Seq. No.	397165
Contig ID	95453_1.R1084
5'-most EST	g4880460
Method	BLASTX
NCBI GI	g5764630
BLAST score	316
E value	3.0e-29
Match length	61
% identity	93
NCBI Description	(AF173816) bell-like homeodomain 2 [Arabidopsis thaliana]

Seq. No.	397166
Contig ID	95454_1.R1084
5'-most EST	g4879753

Seq. No.	397167
Contig ID	95474_1.R1084
5'-most EST	g4880266

Seq. No.	397168
Contig ID	95504_1.R1084
5'-most EST	g5004651

Seq. No.	397169
Contig ID	95509_1.R1084
5'-most EST	g5004880

Seq. No.	397170
Contig ID	95515_1.R1084
5'-most EST	g4880530

Seq. No.	397171
Contig ID	95527_1.R1084
5'-most EST	g4880653

Seq. No.	397172
Contig ID	95535_1.R1084
5'-most EST	g4879805
Method	BLASTN
NCBI GI	g2780745
BLAST score	50
E value	6.0e-19
Match length	57
% identity	96
NCBI Description	Oryza sativa mRNA for plastid RNA polymerase sigma factor, complete cds

Seq. No.	397173
Contig ID	95537_1.R1084
5'-most EST	g4879812

Seq. No.	397174
Contig ID	95560_1.R1084

5'-most EST g5607451

Seq. No. 397175
Contig ID 95562_1.R1084
5'-most EST g4880730

Seq. No. 397176
Contig ID 95566_1.R1084
5'-most EST g4879836

Seq. No. 397177
Contig ID 95574_1.R1084
5'-most EST g4879844
Method BLASTX
NCBI GI g4455171
BLAST score 173
E value 2.0e-12
Match length 76
% identity 50
NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 397178
Contig ID 95577_1.R1084
5'-most EST g4879847
Method BLASTX
NCBI GI g2245036
BLAST score 244
E value 1.0e-20
Match length 109
% identity 56
NCBI Description (Z97342) triacylglycerol lipase like protein [Arabidopsis thaliana]

Seq. No. 397179
Contig ID 95583_1.R1084
5'-most EST g4879853

Seq. No. 397180
Contig ID 95669_1.R1084
5'-most EST g4879941

Seq. No. 397181
Contig ID 95672_1.R1084
5'-most EST g4879944
Method BLASTX
NCBI GI g3122313
BLAST score 330
E value 2.0e-30
Match length 100
% identity 62
NCBI Description LEC14B HOMOLOG >gi_2351587 (U82760) LEC14B homolog [Prunus armeniaca]

Seq. No. 397182
Contig ID 95674_1.R1084
5'-most EST g4879992

Seq. No. 397183
Contig ID 95678_1.R1084
5'-most EST g4879979

Seq. No. 397184
Contig ID 95692_1.R1084
5'-most EST g4879975

Seq. No. 397185
Contig ID 95698_1.R1084
5'-most EST g4879974
Method BLASTX
NCBI GI g4581047
BLAST score 124
E value 7.0e-19
Match length 212
% identity 39
NCBI Description (AF134807) putative dihydroflavonol reductase [Oryza sativa]

Seq. No. 397186
Contig ID 95722_1.R1084
5'-most EST g4880000
Method BLASTX
NCBI GI g6090879
BLAST score 432
E value 1.0e-50
Match length 137
% identity 69
NCBI Description (AF169966) putative cycloartenol synthase [Oryza sativa]

Seq. No. 397187
Contig ID 95754_1.R1084
5'-most EST g4880032

Seq. No. 397188
Contig ID 95852_1.R1084
5'-most EST g4880148

Seq. No. 397189
Contig ID 95874_1.R1084
5'-most EST g4880169

Seq. No. 397190
Contig ID 95942_1.R1084
5'-most EST g4880242
Method BLASTX
NCBI GI g4587595
BLAST score 148
E value 2.0e-13
Match length 78
% identity 47
NCBI Description (AC006951) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No. 397191
Contig ID 96420_1.R1084

5'-most EST	g5816522
Method	BLASTN
NCBI GI	g5922603
BLAST score	44
E value	3.0e-15
Match length	134
% identity	93
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No.	397192
Contig ID	96537_1.R1084
5'-most EST	g4880865
Method	BLASTX
NCBI GI	g3335378
BLAST score	309
E value	3.0e-28
Match length	78
% identity	78
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	397193
Contig ID	96544_1.R1084
5'-most EST	g4880872
Method	BLASTX
NCBI GI	g3786007
BLAST score	242
E value	3.0e-20
Match length	149
% identity	35
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397194
Contig ID	96555_1.R1084
5'-most EST	g4880884

Seq. No.	397195
Contig ID	96603_1.R1084
5'-most EST	g4880931
Method	BLASTX
NCBI GI	g2494116
BLAST score	569
E value	4.0e-83
Match length	193
% identity	79
NCBI Description	(AC002376) Similar to Synechocystis hypothetical protein (gb_D90915). [Arabidopsis thaliana]

Seq. No.	397196
Contig ID	96696_1.R1084
5'-most EST	g4881030

Seq. No.	397197
Contig ID	96731_1.R1084
5'-most EST	g4881060

Seq. No. 397198

Contig ID	96732_1.R1084
5'-most EST	g4881138
Method	BLASTX
NCBI GI	g1514643
BLAST score	439
E value	2.0e-43
Match length	134
% identity	63
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	397199
Contig ID	96783_1.R1084
5'-most EST	g4881112

Seq. No.	397200
Contig ID	96815_1.R1084
5'-most EST	g4881148
Method	BLASTX
NCBI GI	g294845
BLAST score	301
E value	9.0e-38
Match length	101
% identity	74
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	397201
Contig ID	96886_1.R1084
5'-most EST	g6012825
Method	BLASTX
NCBI GI	g4836931
BLAST score	169
E value	8.0e-19
Match length	99
% identity	37
NCBI Description	(AC006085) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	397202
Contig ID	96989_1.R1084
5'-most EST	g4968805
Method	BLASTX
NCBI GI	g4503521
BLAST score	331
E value	7.0e-36
Match length	111
% identity	66
NCBI Description	murine mammary tumor integration site 6 (oncogene homolog) >gi_2498490_sp_Q64252_INT6_MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens]

Seq. No.	397203
Contig ID	96990_1.R1084
5'-most EST	g4968822

Seq. No. 397204
Contig ID 96992_1.R1084
5'-most EST g4968816

Seq. No. 397205
Contig ID 97026_1.R1084
5'-most EST g4968776
Method BLASTX
NCBI GI g2760323
BLAST score 233
E value 2.0e-19
Match length 57
% identity 33
NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No. 397206
Contig ID 97240_1.R1084
5'-most EST g4968989

Seq. No. 397207
Contig ID 97344_1.R1084
5'-most EST g4969095
Method BLASTX
NCBI GI g2934884
BLAST score 115
E value 5.0e-09
Match length 72
% identity 60
NCBI Description (L28003) TGACG-motif binding factor [Glycine max]

Seq. No. 397208
Contig ID 97396_1.R1084
5'-most EST g5002819
Method BLASTX
NCBI GI g5733885
BLAST score 520
E value 1.0e-101
Match length 265
% identity 73
NCBI Description (AC007932) ESTs gb_H37217 and gb_T22141 come from this gene. [Arabidopsis thaliana]

Seq. No. 397209
Contig ID 97415_1.R1084
5'-most EST g4969169
Method BLASTX
NCBI GI g166341
BLAST score 261
E value 8.0e-37
Match length 171
% identity 49
NCBI Description (M98267) alliinase [Allium cepa] >gi_1044969 (L48614) allinase [Allium cepa]

Seq. No. 397210
Contig ID 97426_1.R1084

5'-most EST	g4969180
Seq. No.	397211
Contig ID	97436_1.R1084
5'-most EST	g4969205
Method	BLASTX
NCBI GI	g138132
BLAST score	463
E value	1.0e-46
Match length	89
% identity	98
NCBI Description	A AND A* PROTEINS (GPA) >gi_75748_pir__ZABPF4 gene A protein - phage phi-X174 >gi_216020 (J02482) A (rf replication, viral strand synthesis) [Bacteriophage phi-X174] >gi_1667374_emb_CAA24351_ (V01128) RF DNA replication [coliphage phiX174]
Seq. No.	397212
Contig ID	97472_1.R1084
5'-most EST	g4969226
Seq. No.	397213
Contig ID	97515_1.R1084
5'-most EST	g5607567
Seq. No.	397214
Contig ID	97536_1.R1084
5'-most EST	g4969435
Seq. No.	397215
Contig ID	97548_1.R1084
5'-most EST	g4969309
Seq. No.	397216
Contig ID	97565_1.R1084
5'-most EST	g4969320
Seq. No.	397217
Contig ID	97577_1.R1084
5'-most EST	g5455356
Method	BLASTN
NCBI GI	g5295936
BLAST score	419
E value	0.0e+00
Match length	608
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence
Seq. No.	397218
Contig ID	97653_1.R1084
5'-most EST	g4969425
Seq. No.	397219
Contig ID	97662_1.R1084
5'-most EST	g4969419

Seq. No.	397220
Contig ID	97722_1.R1084
5'-most EST	g5002760
Method	BLASTX
NCBI GI	g5734759
BLAST score	373
E value	8.0e-36
Match length	129
% identity	52
NCBI Description	(AC007651) Similar to Cytochrome P450 [Arabidopsis thaliana]

Seq. No.	397221
Contig ID	97819_1.R1084
5'-most EST	g5607543

Seq. No.	397222
Contig ID	97864_1.R1084
5'-most EST	g5002904
Method	BLASTX
NCBI GI	g1707017
BLAST score	255
E value	3.0e-46
Match length	120
% identity	70
NCBI Description	(U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	397223
Contig ID	97917_1.R1084
5'-most EST	g5004800
Method	BLASTX
NCBI GI	g4140398
BLAST score	395
E value	3.0e-38
Match length	118
% identity	64
NCBI Description	(AF081794) sterol-C5(6)-desaturase [Nicotiana tabacum]

Seq. No.	397224
Contig ID	97938_1.R1084
5'-most EST	g5002979
Method	BLASTX
NCBI GI	g3183413
BLAST score	214
E value	5.0e-17
Match length	135
% identity	44
NCBI Description	HYPOTHETICAL PROTEIN MTH1505 >gi_2622622 (AE000910) N-ethylammeline chlorohydrolase homolog [Methanobacterium thermoautotrophicum]

Seq. No.	397225
Contig ID	97943_1.R1084
5'-most EST	g5002984
Method	BLASTX
NCBI GI	g2980790
BLAST score	205

E value	9.0e-16
Match length	96
% identity	43
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397226
Contig ID	97954_1.R1084
5'-most EST	g5003057

Seq. No.	397227
Contig ID	98043_1.R1084
5'-most EST	g5003731
Method	BLASTX
NCBI GI	g5733874
BLAST score	192
E value	1.0e-14
Match length	52
% identity	75
NCBI Description	(AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No.	397228
Contig ID	98160_1.R1084
5'-most EST	g5005000
Method	BLASTN
NCBI GI	g5803242
BLAST score	34
E value	4.0e-09
Match length	87
% identity	85
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	397229
Contig ID	98258_1.R1084
5'-most EST	g5443704
Method	BLASTX
NCBI GI	g266944
BLAST score	474
E value	7.0e-48
Match length	90
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2) >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic - tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein L2 [Lycopersicon esculentum]

Seq. No.	397230
Contig ID	98342_1.R1084
5'-most EST	g5003352

Seq. No.	397231
Contig ID	98536_1.R1084
5'-most EST	g6012901

Seq. No.	397232
Contig ID	98607_1.R1084
5'-most EST	g5003635
Method	BLASTX

NCBI GI g3293031
BLAST score 360
E value 9.0e-34
Match length 191
% identity 35
NCBI Description (AJ007574) amino acid carrier [Ricinus communis]

Seq. No. 397233
Contig ID 98611_1.R1084
5'-most EST g5003639
Method BLASTX
NCBI GI g5670315
BLAST score 580
E value 1.0e-65
Match length 161
% identity 80
NCBI Description (AF170909) SYNC1 protein [Arabidopsis thaliana]

Seq. No. 397234
Contig ID 98678_1.R1084
5'-most EST g5003709
Method BLASTX
NCBI GI g3549671
BLAST score 211
E value 5.0e-19
Match length 157
% identity 46
NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No. 397235
Contig ID 98684_1.R1084
5'-most EST g5003715
Method BLASTX
NCBI GI g2245125
BLAST score 199
E value 6.0e-15
Match length 87
% identity 45
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 397236
Contig ID 98693_1.R1084
5'-most EST g5003724

Seq. No. 397237
Contig ID 98709_1.R1084
5'-most EST g5003742
Method BLASTX
NCBI GI g3386603
BLAST score 221
E value 1.0e-17
Match length 64
% identity 66
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 397238
Contig ID 99002_1.R1084

5'-most EST	g5004108
Method	BLASTN
NCBI GI	g287392
BLAST score	343
E value	0.0e+00
Match length	343
% identity	100
NCBI Description	Oryza sativa mitochondrial gene for tRNAs, complete sequences

Seq. No.	397239
Contig ID	99083_1.R1084
5'-most EST	g5004194
Method	BLASTX
NCBI GI	g477226
BLAST score	802
E value	6.0e-91
Match length	181
% identity	93
NCBI Description	heat shock protein HSP82 - maize >gi_300083_bbs_130886 (S59780) HSP82=82 kda heat shock protein [Zea mays, seedling, leaves, Peptide, 715 aa] [Zea mays]

Seq. No.	397240
Contig ID	99094_1.R1084
5'-most EST	g5004306
Method	BLASTX
NCBI GI	g4138912
BLAST score	331
E value	6.0e-31
Match length	93
% identity	62
NCBI Description	(AF059487) expansin precursor [Lycopersicon esculentum]

Seq. No.	397241
Contig ID	99156_1.R1084
5'-most EST	g5004273

Seq. No.	397242
Contig ID	99195_1.R1084
5'-most EST	g5851002
Method	BLASTN
NCBI GI	g6063530
BLAST score	36
E value	2.0e-10
Match length	155
% identity	55
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	397243
Contig ID	99198_1.R1084
5'-most EST	g5004316
Method	BLASTN
NCBI GI	g5042437
BLAST score	135
E value	1.0e-69
Match length	405

% identity	98
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	397244
Contig ID	99213_1.R1084
5'-most EST	g5667164
Method	BLASTX
NCBI GI	g5734621
BLAST score	726
E value	5.0e-77
Match length	163
% identity	89
NCBI Description	(AP000391) ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892) [Oryza sativa]

Seq. No.	397245
Contig ID	99479_1.R1084
5'-most EST	g5455425

Seq. No.	397246
Contig ID	99484_1.R1084
5'-most EST	g5455432

Seq. No.	397247
Contig ID	99541_1.R1084
5'-most EST	g5005109

Seq. No.	397248
Contig ID	99632_1.R1084
5'-most EST	g5004774

Seq. No.	397249
Contig ID	99661_1.R1084
5'-most EST	g5004809

Seq. No.	397250
Contig ID	99737_1.R1084
5'-most EST	g5667360

Seq. No.	397251
Contig ID	99762_1.R1084
5'-most EST	g5005136

Seq. No.	397252
Contig ID	99821_1.R1084
5'-most EST	g5004967
Method	BLASTX
NCBI GI	g1399307
BLAST score	183
E value	1.0e-13
Match length	63
% identity	54
NCBI Description	(U41475) phosphoinositide-specific phospholipase C P25 [Glycine max]

Seq. No.	397253

09604734.050599

Contig ID 99829_1.R1084
5'-most EST g5004971

Seq. No. 397254
Contig ID 99874_1.R1084
5'-most EST g5005493

Seq. No. 397255
Contig ID 100223_1.R1084
5'-most EST g5055992

Seq. No. 397256
Contig ID 100274_1.R1084
5'-most EST g5038931

Seq. No. 397257
Contig ID 100285_1.R1084
5'-most EST g5038601

Seq. No. 397258
Contig ID 100288_1.R1084
5'-most EST g5038654

Seq. No. 397259
Contig ID 100325_1.R1084
5'-most EST g5038946

Seq. No. 397260
Contig ID 100336_1.R1084
5'-most EST g5039052
Method BLASTX
NCBI GI g2370459
BLAST score 148
E value 4.0e-09
Match length 41
% identity 71
NCBI Description (Y11987) FPF1 protein [Sinapis alba]

Seq. No. 397261
Contig ID 100426_1.R1084
5'-most EST g5039153
Method BLASTX
NCBI GI g135440
BLAST score 638
E value 8.0e-67
Match length 123
% identity 98
NCBI Description TUBULIN ALPHA CHAIN >gi_71581_pir__UBUTA tubulin alpha chain - Trypanosoma brucei rhodesiense >gi_162320 (K02836) alpha tubulin [Trypanosoma brucei]

Seq. No. 397262
Contig ID 100479_1.R1084
5'-most EST g5038806

Seq. No. 397263
Contig ID 100487_1.R1084

5'-most EST	g5038809
Seq. No.	397264
Contig ID	100547_1.R1084
5'-most EST	g5038870
Method	BLASTN
NCBI GI	g5091496
BLAST score	54
E value	3.0e-21
Match length	183
% identity	39
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence
Seq. No.	397265
Contig ID	100648_1.R1084
5'-most EST	g5039022
Method	BLASTX
NCBI GI	g6056210
BLAST score	131
E value	4.0e-15
Match length	67
% identity	66
NCBI Description	(AC009400) calmodulin-like protein [Arabidopsis thaliana]
Seq. No.	397266
Contig ID	100806_1.R1084
5'-most EST	g5039141
Seq. No.	397267
Contig ID	100838_1.R1084
5'-most EST	g5055946
Method	BLASTX
NCBI GI	g422261
BLAST score	264
E value	7.0e-23
Match length	119
% identity	43
NCBI Description	DNA ligase (ATP) (EC 6.5.1.1) - Crithidia fasciculata (fragment) >gi_312384_emb_CAA80615_ (Z23078) DNA ligase I [Crithidia fasciculata]
Seq. No.	397268
Contig ID	100868_1.R1084
5'-most EST	g5055976
Seq. No.	397269
Contig ID	100936_1.R1084
5'-most EST	g5443698
Seq. No.	397270
Contig ID	100963_1.R1084
5'-most EST	g5771181
Method	BLASTX
NCBI GI	g2129770
BLAST score	117
E value	1.0e-08

Match length	51
% identity	67
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana] >gi_5533311_gb_AAD45124.1_AF163820_1 (AF163820) endoxyloglucan transferase [Arabidopsis thaliana]

Seq. No.	397271
Contig ID	101104_1.R1084
5'-most EST	g5455317

Seq. No.	397272
Contig ID	101147_1.R1084
5'-most EST	g5455359
Method	BLASTX
NCBI GI	g1707074
BLAST score	162
E value	1.0e-10
Match length	141
% identity	35
NCBI Description	(U80450) M01E11.2 [Caenorhabditis elegans]

Seq. No.	397273
Contig ID	101153_1.R1084
5'-most EST	g5455366
Method	BLASTN
NCBI GI	g5852170
BLAST score	212
E value	1.0e-115
Match length	363
% identity	42
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No.	397274
Contig ID	101164_1.R1084
5'-most EST	g5455485

Seq. No.	397275
Contig ID	101261_1.R1084
5'-most EST	g5851054
Method	BLASTX
NCBI GI	g481526
BLAST score	349
E value	3.0e-33
Match length	90
% identity	80
NCBI Description	probable ribosomal protein S1 - wheat mitochondrion

Seq. No.	397276
Contig ID	101268_1.R1084
5'-most EST	g6012881

Seq. No.	397277

Contig ID	101550_1.R1084
5'-most EST	g5607443
Method	BLASTN
NCBI GI	g2586089
BLAST score	39
E value	1.0e-12
Match length	132
% identity	58
NCBI Description	Oryza longistaminata receptor-like kinase protein (Xa21), family member F, pseudogene sequence

Seq. No.	397278
Contig ID	101553_1.R1084
5'-most EST	g5607390

Seq. No.	397279
Contig ID	101561_1.R1084
5'-most EST	g5851083
Method	BLASTX
NCBI GI	g3540196
BLAST score	151
E value	4.0e-15
Match length	124
% identity	38
NCBI Description	(AC004260) Putative amp-binding protein [Arabidopsis thaliana]

Seq. No.	397280
Contig ID	101567_1.R1084
5'-most EST	g5607491
Method	BLASTX
NCBI GI	g4567207
BLAST score	193
E value	7.0e-15
Match length	95
% identity	43
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	397281
Contig ID	101595_1.R1084
5'-most EST	g5607408
Method	BLASTX
NCBI GI	g3047066
BLAST score	201
E value	3.0e-15
Match length	127
% identity	30
NCBI Description	(AF058825) contains similarity to retrovirus-related POL polyproteins [Arabidopsis thaliana]

Seq. No.	397282
Contig ID	101599_1.R1084
5'-most EST	g6012858
Method	BLASTX
NCBI GI	g5777616
BLAST score	281
E value	7.0e-25

Match length	73
% identity	81
NCBI Description	(AJ245900) CAA30374.1 protein [Oryza sativa]

Seq. No.	397283
Contig ID	101603_1.R1084
5'-most EST	g5607416
Method	BLASTN
NCBI GI	g5670155
BLAST score	867
E value	0.0e+00
Match length	871
% identity	100
NCBI Description	Oryza sativa subsp. japonica BAC clone 34K24, complete sequence

Seq. No.	397284
Contig ID	101675_1.R1084
5'-most EST	g5607542
Method	BLASTN
NCBI GI	g1421782
BLAST score	76
E value	3.0e-34
Match length	109
% identity	94
NCBI Description	Cloning vector pKRX, complete sequence

Seq. No.	397285
Contig ID	101732_1.R1084
5'-most EST	g5771199

Seq. No.	397286
Contig ID	101781_1.R1084
5'-most EST	g5607625

Seq. No.	397287
Contig ID	101884_1.R1084
5'-most EST	g5667208

Seq. No.	397288
Contig ID	101990_1.R1084
5'-most EST	g5667365
Method	BLASTX
NCBI GI	g6056196
BLAST score	171
E value	3.0e-12
Match length	42
% identity	71
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	397289
Contig ID	102007_1.R1084
5'-most EST	g5667383
Method	BLASTX
NCBI GI	g5051771
BLAST score	177
E value	2.0e-12

Match length 132
% identity 48
NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 397290
Contig ID 102167_1.R1084
5'-most EST g5667258

Seq. No. 397291
Contig ID 102267_1.R1084
5'-most EST g5667628

Seq. No. 397292
Contig ID 102293_1.R1084
5'-most EST g5667654

Seq. No. 397293
Contig ID 102365_1.R1084
5'-most EST g5803395

Seq. No. 397294
Contig ID 102373_1.R1084
5'-most EST g5803403
Method BLASTX
NCBI GI g1644219
BLAST score 428
E value 3.0e-42
Match length 122
% identity 69
NCBI Description (D64127) RNA polymerase beta' subunit [Bacillus subtilis]

Seq. No. 397295
Contig ID 102469_1.R1084
5'-most EST g5803505

Seq. No. 397296
Contig ID 102499_1.R1084
5'-most EST g5803535

Seq. No. 397297
Contig ID 102514_1.R1084
5'-most EST g5803551
Method BLASTX
NCBI GI g1723182
BLAST score 167
E value 2.0e-11
Match length 40
% identity 65
NCBI Description SUGAR CARRIER PROTEIN A >gi_169736 (L08197) sugar carrier protein [Ricinus communis]

Seq. No. 397298
Contig ID 102568_1.R1084
5'-most EST g5701696

Seq. No. 397299
Contig ID 102684_1.R1084

5'-most EST	g5851096
Method	BLASTN
NCBI GI	g6006355
BLAST score	300
E value	1.0e-168
Match length	364
% identity	96
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	397300
Contig ID	102801_1.R1084
5'-most EST	g5816548

Seq. No.	397301
Contig ID	102860_1.R1084
5'-most EST	g5851089
Method	BLASTX
NCBI GI	g6006369
BLAST score	956
E value	1.0e-112
Match length	221
% identity	96
NCBI Description	(AP000559) ESTs C99670(E21043),C99671(E21043), AU078262(R10938),AU078261(R10938),D15282(C0402) correspond to a region of the predicted gene.; Similar to arginine decarboxylase (U52851) [Oryza sativa]

Seq. No.	397302
Contig ID	102998_1.R1084
5'-most EST	g5900672
Method	BLASTX
NCBI GI	g5091527
BLAST score	493
E value	2.0e-49
Match length	92
% identity	100
NCBI Description	(AB023482) Similar to Zea mays PRP gene.(X60432) [Oryza sativa]

Seq. No.	397303
Contig ID	103114_1.R1084
5'-most EST	g6012800

Seq. No.	397304
Contig ID	103159_1.R1084
5'-most EST	g6012845
Method	BLASTN
NCBI GI	g6069643
BLAST score	261
E value	1.0e-145
Match length	285
% identity	97
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0514G12

Seq. No.	397305
Contig ID	103203_1.R1084
5'-most EST	g6012891

Method	BLASTX
NCBI GI	g3510540
BLAST score	289
E value	2.0e-30
Match length	85
% identity	80
NCBI Description	(AF038815) expansin [Prunus armeniaca]

Seq. No.	397306
Contig ID	103206_1.R1084
5'-most EST	g6012895
Method	BLASTX
NCBI GI	g2497486
BLAST score	300
E value	1.0e-31
Match length	103
% identity	68
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]

Seq. No.	397307
Contig ID	103227_1.R1084
5'-most EST	g6012915
Method	BLASTX
NCBI GI	g4468993
BLAST score	146
E value	3.0e-09
Match length	43
% identity	60
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	397308
Contig ID	103273_1.R1084
5'-most EST	g6024895

Seq. No.	397309
Seq. ID	LIB3431-001-P1-K1-A11
Method	BLASTX
NCBI GI	g548605
BLAST score	171
E value	1.0e-12
Match length	73
% identity	55
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	397310
Seq. ID	LIB3431-001-P1-K1-A9
Method	BLASTX
NCBI GI	g4567262
BLAST score	150
E value	1.0e-09
Match length	54

% identity	54
NCBI Description	(AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No.	397311
Seq. ID	LIB3431-001-P1-K1-B11
Method	BLASTX
NCBI GI	g320618
BLAST score	158
E value	3.0e-11
Match length	58
% identity	62
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	397312
Seq. ID	LIB3431-001-P1-K1-B3
Method	BLASTX
NCBI GI	g100796
BLAST score	293
E value	1.0e-26
Match length	102
% identity	59
NCBI Description	phosphoribulokinase (EC 2.7.1.19) - wheat

Seq. No.	397313
Seq. ID	LIB3431-001-P1-K1-B4
Method	BLASTX
NCBI GI	g4960024
BLAST score	144
E value	2.0e-09
Match length	63
% identity	51
NCBI Description	(AF144079) S-adenosyl-L-methionine:L-methionine S-methyltransferase [Zea mays]

Seq. No.	397314
Seq. ID	LIB3431-001-P1-K1-B7
Method	BLASTX
NCBI GI	g3334144
BLAST score	397
E value	1.0e-38
Match length	117
% identity	68
NCBI Description	G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_ (D86925) C-type cyclin [Oryza sativa]

Seq. No.	397315
Seq. ID	LIB3431-001-P1-K1-B8
Method	BLASTX
NCBI GI	g132105
BLAST score	347
E value	6.0e-33
Match length	77
% identity	87

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397316
Seq. ID	LIB3431-001-P1-K1-B9
Method	BLASTX
NCBI GI	g5734636
BLAST score	165
E value	1.0e-11
Match length	58
% identity	53
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No.	397317
Seq. ID	LIB3431-001-P1-K1-C11
Method	BLASTX
NCBI GI	g3510256
BLAST score	171
E value	2.0e-12
Match length	78
% identity	50
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	397318
Seq. ID	LIB3431-001-P1-K1-C2
Method	BLASTX
NCBI GI	g132105
BLAST score	191
E value	1.0e-14
Match length	70
% identity	57
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397319
Seq. ID	LIB3431-001-P1-K1-C5
Method	BLASTX
NCBI GI	g2754849
BLAST score	199
E value	5.0e-16
Match length	69
% identity	64

NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	397320
Seq. ID	LIB3431-001-P1-K1-C7
Method	BLASTN
NCBI GI	g2072554
BLAST score	183
E value	2.0e-98
Match length	315
% identity	90
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397321
Seq. ID	LIB3431-001-P1-K1-C9
Method	BLASTX
NCBI GI	g3021274
BLAST score	292
E value	2.0e-26
Match length	109
% identity	54
NCBI Description	(AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]

Seq. No.	397322
Seq. ID	LIB3431-001-P1-K1-D11
Method	BLASTN
NCBI GI	g3789949
BLAST score	72
E value	2.0e-32
Match length	160
% identity	86
NCBI Description	Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No.	397323
Seq. ID	LIB3431-001-P1-K1-D3
Method	BLASTN
NCBI GI	g6006355
BLAST score	37
E value	1.0e-11
Match length	49
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	397324
Seq. ID	LIB3431-001-P1-K1-D7
Method	BLASTN
NCBI GI	g20262
BLAST score	161
E value	3.0e-85
Match length	337
% identity	88
NCBI Description	O.sativa light-induced mRNA

Seq. No.	397325

Seq. ID	LIB3431-001-P1-K1-D9
Method	BLASTX
NCBI GI	g320618
BLAST score	323
E value	5.0e-30
Match length	83
% identity	77
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	397326
Seq. ID	LIB3431-001-P1-K1-E11
Method	BLASTX
NCBI GI	g2501356
BLAST score	288
E value	4.0e-39
Match length	127
% identity	69
NCBI Description	TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK) >gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor [Solanum tuberosum]

Seq. No.	397327
Seq. ID	LIB3431-001-P1-K1-E5
Method	BLASTX
NCBI GI	g2570499
BLAST score	147
E value	7.0e-10
Match length	39
% identity	74
NCBI Description	(AF022732) 23kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	397328
Seq. ID	LIB3431-001-P1-K1-E7
Method	BLASTX
NCBI GI	g515616
BLAST score	360
E value	2.0e-34
Match length	110
% identity	69
NCBI Description	(X61608) LHC II Type III chlorophyll a /b binding protein [Brassica napus]

Seq. No.	397329
Seq. ID	LIB3431-001-P1-K1-E8
Method	BLASTN
NCBI GI	g1835730
BLAST score	136
E value	2.0e-70
Match length	204
% identity	92
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No.	397330
Seq. ID	LIB3431-001-P1-K1-F4
Method	BLASTX
NCBI GI	g132105
BLAST score	227
E value	7.0e-22
Match length	104
% identity	58
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397331
Seq. ID	LIB3431-001-P1-K1-F7
Method	BLASTX
NCBI GI	g129231
BLAST score	226
E value	4.0e-19
Match length	66
% identity	65
NCBI Description	ORYZAIN ALPHA CHAIN PRECURSOR >gi_67644_pir__KHRZOA oryzain (EC 3.4.22.-) alpha precursor - rice >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor [Oryza sativa]

Seq. No.	397332
Seq. ID	LIB3431-001-P1-K1-G10
Method	BLASTX
NCBI GI	g1519251
BLAST score	354
E value	9.0e-34
Match length	97
% identity	75
NCBI Description	(U65957) GF14-c protein [Oryza sativa]

Seq. No.	397333
Seq. ID	LIB3431-001-P1-K1-G12
Method	BLASTX
NCBI GI	g4887022
BLAST score	201
E value	8.0e-16
Match length	91
% identity	51
NCBI Description	(AF123509) Nt-iaa4.1 deduced protein [Nicotiana tabacum]

Seq. No.	397334
Seq. ID	LIB3431-001-P1-K1-G3
Method	BLASTN
NCBI GI	g20237
BLAST score	34

E value	7.0e-10
Match length	34
% identity	100
NCBI Description	O.sativa (rice) constitutive GOS2 gene

Seq. No.	397335
Seq. ID	LIB3431-001-P1-K1-G5
Method	BLASTN
NCBI GI	g218171
BLAST score	35
E value	8.0e-11
Match length	67
% identity	88
NCBI Description	Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No.	397336
Seq. ID	LIB3431-001-P1-K1-G9
Method	BLASTX
NCBI GI	g2264373
BLAST score	203
E value	3.0e-16
Match length	59
% identity	66
NCBI Description	(AC002354) putative NAM/no apical meristem protein [Arabidopsis thaliana]

Seq. No.	397337
Seq. ID	LIB3431-001-P1-K1-H8
Method	BLASTN
NCBI GI	g1835730
BLAST score	59
E value	6.0e-25
Match length	111
% identity	88
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No.	397338
Seq. ID	LIB3431-001-P1-N1-A10
Method	BLASTN
NCBI GI	g304219
BLAST score	47
E value	2.0e-17
Match length	78
% identity	92
NCBI Description	Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No.	397339
Seq. ID	LIB3431-001-P1-N1-A11
Method	BLASTX
NCBI GI	g671740
BLAST score	403
E value	2.0e-39
Match length	75

% identity	97
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397340
Seq. ID	LIB3431-001-P1-N1-B1
Method	BLASTN
NCBI GI	g6063530
BLAST score	68
E value	3.0e-30
Match length	68
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	397341
Seq. ID	LIB3431-001-P1-N1-B11
Method	BLASTN
NCBI GI	g20177
BLAST score	334
E value	0.0e+00
Match length	360
% identity	99
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	397342
Seq. ID	LIB3431-001-P1-N1-B2
Method	BLASTX
NCBI GI	g1173347
BLAST score	391
E value	6.0e-38
Match length	84
% identity	95
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	397343
Seq. ID	LIB3431-001-P1-N1-B3
Method	BLASTX
NCBI GI	g21839
BLAST score	290
E value	5.0e-26
Match length	61
% identity	95
NCBI Description	(X57952) phosphoribulokinase [Triticum aestivum]

Seq. No.	397344
Seq. ID	LIB3431-001-P1-N1-B4
Method	BLASTX
NCBI GI	g4960024
BLAST score	198
E value	2.0e-15
Match length	50

% identity	78
NCBI Description	(AF144079) S-adenosyl-L-methionine:L-methionine S-methyltransferase [Zea mays]

Seq. No.	397345
Seq. ID	LIB3431-001-P1-N1-B6
Method	BLASTN
NCBI GI	g1752830
BLAST score	56
E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Oryza sativa DNA for metallothionein-like protein, complete cds

Seq. No.	397346
Seq. ID	LIB3431-001-P1-N1-B7
Method	BLASTN
NCBI GI	g1695697
BLAST score	193
E value	1.0e-104
Match length	376
% identity	96
NCBI Description	Oryza sativa mRNA for C-type cyclin, complete cds

Seq. No.	397347
Seq. ID	LIB3431-001-P1-N1-B8
Method	BLASTX
NCBI GI	g671740
BLAST score	331
E value	8.0e-31
Match length	65
% identity	95
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397348
Seq. ID	LIB3431-001-P1-N1-C10
Method	BLASTX
NCBI GI	g3510256
BLAST score	143
E value	6.0e-09
Match length	34
% identity	71
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	397349
Seq. ID	LIB3431-001-P1-N1-C11
Method	BLASTX
NCBI GI	g3510256
BLAST score	166
E value	2.0e-11
Match length	54
% identity	61
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 397350

Seq. ID	LIB3431-001-P1-N1-C12
Method	BLASTX
NCBI GI	g3128168
BLAST score	258
E value	2.0e-22
Match length	71
% identity	58
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	397351
Seq. ID	LIB3431-001-P1-N1-C2
Method	BLASTX
NCBI GI	g347451
BLAST score	231
E value	5.0e-19
Match length	73
% identity	64
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	397352
Seq. ID	LIB3431-001-P1-N1-C3
Method	BLASTN
NCBI GI	g218207
BLAST score	268
E value	1.0e-149
Match length	280
% identity	99
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397353
Seq. ID	LIB3431-001-P1-N1-C5
Method	BLASTX
NCBI GI	g2754849
BLAST score	168
E value	9.0e-12
Match length	41
% identity	78
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	397354
Seq. ID	LIB3431-001-P1-N1-C6
Method	BLASTX
NCBI GI	g4115377
BLAST score	244
E value	1.0e-20
Match length	59
% identity	76
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	397355
Seq. ID	LIB3431-001-P1-N1-D11
Method	BLASTX

NCBI GI	g5918208
BLAST score	287
E value	1.0e-25
Match length	55
% identity	100
NCBI Description	(AJ249397) putative protein translation factor [Phleum pratense]

Seq. No.	397356
Seq. ID	LIB3431-001-P1-N1-D3
Method	BLASTN
NCBI GI	g6006355
BLAST score	211
E value	1.0e-115
Match length	443
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	397357
Seq. ID	LIB3431-001-P1-N1-D4
Method	BLASTX
NCBI GI	g131192
BLAST score	255
E value	4.0e-32
Match length	77
% identity	92
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937 photosystem I chain V precursor - barley >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide PSI-G precursor [Hordeum vulgare]

Seq. No.	397358
Seq. ID	LIB3431-001-P1-N1-D6
Method	BLASTX
NCBI GI	g399333
BLAST score	214
E value	3.0e-17
Match length	66
% identity	67
NCBI Description	CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8) precursor - pepper >gi_17944_emb_CAA46086_ (X64874) O-acetylserine (thiol)-lyase [Capsicum annuum]

Seq. No.	397359
Seq. ID	LIB3431-001-P1-N1-D7
Method	BLASTN
NCBI GI	g5091597
BLAST score	108
E value	1.0e-53
Match length	220
% identity	39
NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No.	397360

Seq. ID	LIB3431-001-P1-N1-D9
Method	BLASTX
NCBI GI	g289920
BLAST score	295
E value	1.0e-26
Match length	61
% identity	93
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	397361
Seq. ID	LIB3431-001-P1-N1-E2
Method	BLASTX
NCBI GI	g283008
BLAST score	378
E value	2.0e-36
Match length	73
% identity	100
NCBI Description	sucrose synthase (EC 2.4.1.13) - rice >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza sativa]

Seq. No.	397362
Seq. ID	LIB3431-001-P1-N1-E3
Method	BLASTN
NCBI GI	g20181
BLAST score	163
E value	2.0e-86
Match length	178
% identity	98
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	397363
Seq. ID	LIB3431-001-P1-N1-E4
Method	BLASTX
NCBI GI	g4539545
BLAST score	392
E value	6.0e-38
Match length	93
% identity	82
NCBI Description	(Y16644) PRCI [Nicotiana tabacum]

Seq. No.	397364
Seq. ID	LIB3431-001-P1-N1-E5
Method	BLASTX
NCBI GI	g4079798
BLAST score	345
E value	2.0e-32
Match length	66
% identity	100
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	397365
Seq. ID	LIB3431-001-P1-N1-E6
Method	BLASTX

NCBI GI g1806283
BLAST score 248
E value 3.0e-21
Match length 67
% identity 78
NCBI Description (Z79637) Histone H4 homologue [Sesbania rostrata]

Seq. No. 397366
Seq. ID LIB3431-001-P1-N1-E8
Method BLASTX
NCBI GI g1835731
BLAST score 282
E value 4.0e-25
Match length 65
% identity 83
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 397367
Seq. ID LIB3431-001-P1-N1-F1
Method BLASTX
NCBI GI g131225
BLAST score 181
E value 3.0e-13
Match length 49
% identity 69
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 397368
Seq. ID LIB3431-001-P1-N1-F11
Method BLASTX
NCBI GI g3184288
BLAST score 214
E value 4.0e-17
Match length 62
% identity 60
NCBI Description (AC004136) unknown protein [Arabidopsis thaliana]

Seq. No. 397369
Seq. ID LIB3431-001-P1-N1-F2
Method BLASTX
NCBI GI g487006
BLAST score 204
E value 4.0e-16
Match length 52
% identity 75
NCBI Description protoporphyrin IX magnesium chelatase - garden snapdragon >gi_312129_emb_CAA51664_ (X73144) protoporphyrin IX:Mg Chelatase [Antirrhinum majus]

Seq. No. 397370
Seq. ID LIB3431-001-P1-N1-F4
Method BLASTX
NCBI GI g132105
BLAST score 173

E value	2.0e-12
Match length	33
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397371
Seq. ID	LIB3431-001-P1-N1-F7
Method	BLASTN
NCBI GI	g218180
BLAST score	244
E value	1.0e-135
Match length	281
% identity	96
NCBI Description	Rice mRNA for oryzain alpha (EC 3.4.22)

Seq. No.	397372
Seq. ID	LIB3431-001-P1-N1-F9
Method	BLASTX
NCBI GI	g517500
BLAST score	223
E value	2.0e-18
Match length	64
% identity	73
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	397373
Seq. ID	LIB3431-001-P1-N1-G1
Method	BLASTX
NCBI GI	g517500
BLAST score	273
E value	3.0e-24
Match length	70
% identity	81
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	397374
Seq. ID	LIB3431-001-P1-N1-G10
Method	BLASTN
NCBI GI	g1519250
BLAST score	282
E value	1.0e-157
Match length	318
% identity	97
NCBI Description	Oryza sativa GF14-c protein mRNA, complete cds

Seq. No.	397375
Seq. ID	LIB3431-001-P1-N1-G4
Method	BLASTX
NCBI GI	g671737
BLAST score	248
E value	5.0e-21
Match length	56
% identity	88
NCBI Description	(X74731) Chloropyll a/b binding protein [Amaranthus hypochondriacus]

Seq. No.	397376
Seq. ID	LIB3431-001-P1-N1-H11
Method	BLASTX
NCBI GI	g1835731
BLAST score	197
E value	3.0e-15
Match length	49
% identity	80
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	397377
Seq. ID	LIB3431-001-P1-N1-H2
Method	BLASTN
NCBI GI	g1835730
BLAST score	225
E value	1.0e-123
Match length	293
% identity	94
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No.	397378
Seq. ID	LIB3431-001-P1-N1-H8
Method	BLASTN
NCBI GI	g5441872
BLAST score	146
E value	2.0e-76
Match length	250
% identity	90
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig a)

Seq. No.	397379
Seq. ID	LIB3431-002-P1-K1-A1
Method	BLASTX
NCBI GI	g2072555
BLAST score	170
E value	4.0e-12
Match length	59
% identity	54
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397380
Seq. ID	LIB3431-002-P1-K1-A11

Method	BLASTX
NCBI GI	g6063542
BLAST score	233
E value	2.0e-19
Match length	99
% identity	59
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No.	397381
Seq. ID	LIB3431-002-P1-K1-A2
Method	BLASTX
NCBI GI	g118104
BLAST score	212
E value	4.0e-17
Match length	86
% identity	55
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) - maize >gi_168461 (M55021) cyclophilin [Zea mays] >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No.	397382
Seq. ID	LIB3431-002-P1-K1-A3
Method	BLASTX
NCBI GI	g3063524
BLAST score	282
E value	4.0e-25
Match length	131
% identity	29
NCBI Description	(AF052305) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	397383
Seq. ID	LIB3431-002-P1-K1-B2
Method	BLASTX
NCBI GI	g3885886
BLAST score	342
E value	3.0e-32
Match length	114
% identity	64
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.	397384
Seq. ID	LIB3431-002-P1-K1-B5
Method	BLASTX
NCBI GI	g2827002
BLAST score	338
E value	9.0e-32
Match length	112
% identity	65
NCBI Description	(AF005993) HSP70 [Triticum aestivum]

Seq. No.	397385
Seq. ID	LIB3431-002-P1-K1-B6

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Method	BLASTX
NCBI GI	g1519251
BLAST score	191
E value	6.0e-15
Match length	63
% identity	68
NCBI Description	(U65957) GF14-c protein [Oryza sativa]

Seq. No.	397386
Seq. ID	LIB3431-002-P1-K1-C11
Method	BLASTX
NCBI GI	g4079798
BLAST score	203
E value	5.0e-16
Match length	93
% identity	47
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	397387
Seq. ID	LIB3431-002-P1-K1-C4
Method	BLASTX
NCBI GI	g3063524
BLAST score	252
E value	1.0e-21
Match length	76
% identity	67
NCBI Description	(AF052305) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	397388
Seq. ID	LIB3431-002-P1-K1-C5
Method	BLASTN
NCBI GI	g6006355
BLAST score	71
E value	2.0e-31
Match length	263
% identity	82
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	397389
Seq. ID	LIB3431-002-P1-K1-C6
Method	BLASTX
NCBI GI	g2500380
BLAST score	240
E value	3.0e-20
Match length	95
% identity	51
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No.	397390
Seq. ID	LIB3431-002-P1-K1-C8
Method	BLASTX

NCBI GI	g2493494
BLAST score	163
E value	3.0e-19
Match length	82
% identity	57
NCBI Description	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase II-2 [Hordeum vulgare]

Seq. No.	397391
Seq. ID	LIB3431-002-P1-K1-C9
Method	BLASTX
NCBI GI	g4574135
BLAST score	145
E value	2.0e-09
Match length	38
% identity	71
NCBI Description	(AF073695) cysteine synthase [Oryza sativa]

Seq. No.	397392
Seq. ID	LIB3431-002-P1-K1-D7
Method	BLASTX
NCBI GI	g548603
BLAST score	355
E value	1.0e-33
Match length	105
% identity	70
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	397393
Seq. ID	LIB3431-002-P1-K1-E7
Method	BLASTN
NCBI GI	g20262
BLAST score	41
E value	1.0e-13
Match length	53
% identity	94
NCBI Description	O.sativa light-induced mRNA

Seq. No.	397394
Seq. ID	LIB3431-002-P1-K1-E9
Method	BLASTX
NCBI GI	g2072555
BLAST score	213
E value	4.0e-17
Match length	62
% identity	68
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 397395

Seq. ID LIB3431-002-P1-K1-F3
Method BLASTX
NCBI GI g548605
BLAST score 399
E value 6.0e-39
Match length 109
% identity 76
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 397396
Seq. ID LIB3431-002-P1-K1-G3
Method BLASTX
NCBI GI g3126854
BLAST score 256
E value 3.0e-22
Match length 73
% identity 71
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 397397
Seq. ID LIB3431-002-P1-K1-G7
Method BLASTX
NCBI GI g4079798
BLAST score 275
E value 6.0e-28
Match length 107
% identity 69
NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 397398
Seq. ID LIB3431-002-P1-K1-H11
Method BLASTX
NCBI GI g2262105
BLAST score 145
E value 4.0e-09
Match length 88
% identity 40
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 397399
Seq. ID LIB3431-002-P1-K1-H2
Method BLASTX
NCBI GI g4959710
BLAST score 154
E value 3.0e-10
Match length 56
% identity 57
NCBI Description (AF135596) Skp1 [Medicago sativa]

Seq. No. 397400
Seq. ID LIB3431-002-P1-K1-H5
Method BLASTN

NCBI GI	g1747293
BLAST score	35
E value	2.0e-10
Match length	79
% identity	86
NCBI Description	Oryza sativa mRNA for vacuolar H+-pyrophosphatase, complete cds

Seq. No.	397401
Seq. ID	LIB3431-002-P1-K1-H6
Method	BLASTX
NCBI GI	g131225
BLAST score	271
E value	5.0e-24
Match length	85
% identity	65
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	397402
Seq. ID	LIB3431-002-P1-N1-A1
Method	BLASTN
NCBI GI	g2072554
BLAST score	241
E value	1.0e-133
Match length	245
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397403
Seq. ID	LIB3431-002-P1-N1-A11
Method	BLASTN
NCBI GI	g6063530
BLAST score	225
E value	1.0e-123
Match length	258
% identity	96
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	397404
Seq. ID	LIB3431-002-P1-N1-A2
Method	BLASTN
NCBI GI	g600766
BLAST score	319
E value	1.0e-179
Match length	335
% identity	99
NCBI Description	Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds

Seq. No.	397405
Seq. ID	LIB3431-002-P1-N1-A3
Method	BLASTX
NCBI GI	g347451
BLAST score	312

E value	1.0e-28
Match length	61
% identity	95
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	397406
Seq. ID	LIB3431-002-P1-N1-B5
Method	BLASTX
NCBI GI	g3962377
BLAST score	200
E value	1.0e-31
Match length	114
% identity	70
NCBI Description	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No.	397407
Seq. ID	LIB3431-002-P1-N1-B6
Method	BLASTN
NCBI GI	g1519250
BLAST score	75
E value	5.0e-34
Match length	121
% identity	90
NCBI Description	Oryza sativa GF14-c protein mRNA, complete cds

Seq. No.	397408
Seq. ID	LIB3431-002-P1-N1-C3
Method	BLASTX
NCBI GI	g115793
BLAST score	164
E value	2.0e-23
Match length	63
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]

Seq. No.	397409
Seq. ID	LIB3431-002-P1-N1-C4
Method	BLASTN
NCBI GI	g218207
BLAST score	275
E value	1.0e-153
Match length	283
% identity	99
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397410
Seq. ID	LIB3431-002-P1-N1-D1
Method	BLASTN
NCBI GI	g20262
BLAST score	218

E value	1.0e-119
Match length	323
% identity	91
NCBI Description	O.sativa light-induced mRNA

Seq. No.	397411
Seq. ID	LIB3431-002-P1-N1-D11
Method	BLASTX
NCBI GI	g461812
BLAST score	161
E value	5.0e-11
Match length	52
% identity	56
NCBI Description	CYTOCHROME P450 72A1 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	397412
Seq. ID	LIB3431-002-P1-N1-D12
Method	BLASTX
NCBI GI	g114332
BLAST score	260
E value	2.0e-22
Match length	116
% identity	53
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_482389_pir__A45506 H+-transporting ATPase (EC 3.6.1.35) LHA1 - tomato >gi_170464 (M60166) H+-ATPase [Lycopersicon esculentum] >gi_228405_prf__1803518A H ATPase [Lycopersicon esculentum]

Seq. No.	397413
Seq. ID	LIB3431-002-P1-N1-D4
Method	BLASTN
NCBI GI	g20262
BLAST score	327
E value	0.0e+00
Match length	333
% identity	99
NCBI Description	O.sativa light-induced mRNA

Seq. No.	397414
Seq. ID	LIB3431-002-P1-N1-D7
Method	BLASTX
NCBI GI	g548603
BLAST score	230
E value	3.0e-19
Match length	48
% identity	94
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	397415

Seq. ID	LIB3431-002-P1-N1-E12
Method	BLASTN
NCBI GI	g347450
BLAST score	36
E value	1.0e-10
Match length	68
% identity	88
NCBI Description	Oryza sativum mitochondrial ribulose bisphosphate carboxylase/oxygenase (rbcS) mRNA, complete cds

Seq. No.	397416
Seq. ID	LIB3431-002-P1-N1-E3
Method	BLASTN
NCBI GI	g6016845
BLAST score	36
E value	8.0e-11
Match length	44
% identity	95
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	397417
Seq. ID	LIB3431-002-P1-N1-E6
Method	BLASTX
NCBI GI	g1168537
BLAST score	202
E value	7.0e-16
Match length	41
% identity	90
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732 aspartic proteinase (EC 3.4.23.-) - rice >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase [Oryza sativa]

Seq. No.	397418
Seq. ID	LIB3431-002-P1-N1-E9
Method	BLASTN
NCBI GI	g2072554
BLAST score	97
E value	3.0e-47
Match length	189
% identity	87
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397419
Seq. ID	LIB3431-002-P1-N1-F10
Method	BLASTX
NCBI GI	g2407279
BLAST score	151
E value	6.0e-10
Match length	31
% identity	97
NCBI Description	(AF017362) aldolase [Oryza sativa]

Seq. No.	397420
Seq. ID	LIB3431-002-P1-N1-F3
Method	BLASTX

NCBI GI	g548605
BLAST score	273
E value	4.0e-24
Match length	66
% identity	83
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	397421
Seq. ID	LIB3431-002-P1-N1-F4
Method	BLASTN
NCBI GI	g4138289
BLAST score	279
E value	1.0e-155
Match length	314
% identity	97
NCBI Description	Oryza sativa mRNA for thioredoxin M

Seq. No.	397422
Seq. ID	LIB3431-002-P1-N1-F5
Method	BLASTX
NCBI GI	g3789954
BLAST score	214
E value	3.0e-17
Match length	41
% identity	95
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	397423
Seq. ID	LIB3431-002-P1-N1-G10
Method	BLASTN
NCBI GI	g416266
BLAST score	127
E value	4.0e-65
Match length	279
% identity	86
NCBI Description	Rice mRNA for oxygen-evolving protein, partial sequence

Seq. No.	397424
Seq. ID	LIB3431-002-P1-N1-G11
Method	BLASTX
NCBI GI	g517500
BLAST score	144
E value	4.0e-09
Match length	61
% identity	57
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	397425
Seq. ID	LIB3431-002-P1-N1-H2
Method	BLASTX

NCBI GI	g3719211
BLAST score	177
E value	6.0e-13
Match length	52
% identity	71
NCBI Description	(U97021) UIP2 [Arabidopsis thaliana]

Seq. No.	397426
Seq. ID	LIB3431-003-P1-K1-A10
Method	BLASTX
NCBI GI	g5732060
BLAST score	308
E value	3.0e-28
Match length	105
% identity	60
NCBI Description	(AF147263) contains similarity to Pfam families PF00106 (short chain dehydrogenase; score=151.7, E=1.3e-41, N=1) and PF00678 (Short chain dehydrogenase/reductase C-terminus; score=48.9, E=1.1e-10, N=1) [Arabidopsis t

Seq. No.	397427
Seq. ID	LIB3431-003-P1-K1-A11
Method	BLASTX
NCBI GI	g2662343
BLAST score	211
E value	8.0e-17
Match length	41
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	397428
Seq. ID	LIB3431-003-P1-K1-A12
Method	BLASTX
NCBI GI	g1835731
BLAST score	573
E value	3.0e-59
Match length	109
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	397429
Seq. ID	LIB3431-003-P1-K1-A2
Method	BLASTX
NCBI GI	g4469021
BLAST score	166
E value	2.0e-11
Match length	39
% identity	82
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397430
Seq. ID	LIB3431-003-P1-K1-A4
Method	BLASTX
NCBI GI	g585241
BLAST score	165
E value	1.0e-11
Match length	45

% identity	71
NCBI Description	HISTONE H1 >gi_629668_pir__S45662 histone H1 - tomato >gi_424100 (U03391) histone H1 [Lycopersicon esculentum]

Seq. No.	397431
Seq. ID	LIB3431-003-P1-K1-A5
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	397432
Seq. ID	LIB3431-003-P1-K1-A6
Method	BLASTX
NCBI GI	g6063542
BLAST score	648
E value	5.0e-68
Match length	131
% identity	98
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No.	397433
Seq. ID	LIB3431-003-P1-K1-A9
Method	BLASTX
NCBI GI	g462195
BLAST score	230
E value	3.0e-19
Match length	51
% identity	86
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	397434
Seq. ID	LIB3431-003-P1-K1-B10
Method	BLASTN
NCBI GI	g20255
BLAST score	106
E value	6.0e-53
Match length	106
% identity	100
NCBI Description	O.sativa gene for heat shock protein 82 HSP82

Seq. No.	397435
Seq. ID	LIB3431-003-P1-K1-B12
Method	BLASTN
NCBI GI	g218207
BLAST score	41
E value	1.0e-14
Match length	48

% identity	98
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397436
Seq. ID	LIB3431-003-P1-K1-B3
Method	BLASTX
NCBI GI	g4325041
BLAST score	244
E value	5.0e-26
Match length	80
% identity	78
NCBI Description	(AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No.	397437
Seq. ID	LIB3431-003-P1-K1-B4
Method	BLASTX
NCBI GI	g5002516
BLAST score	228
E value	9.0e-19
Match length	94
% identity	51
NCBI Description	(AL078606) putative protein [Arabidopsis thaliana]

Seq. No.	397438
Seq. ID	LIB3431-003-P1-K1-B5
Method	BLASTX
NCBI GI	g729668
BLAST score	256
E value	5.0e-22
Match length	73
% identity	63
NCBI Description	HISTONE H1 >gi_2147479_pir__S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No.	397439
Seq. ID	LIB3431-003-P1-K1-B6
Method	BLASTX
NCBI GI	g1076725
BLAST score	315
E value	3.0e-29
Match length	98
% identity	70
NCBI Description	NADPH dehydrogenase (EC 1.6.99.1) - barley >gi_683476_emb_CAA59228_ (X84738) NADPH dehydrogenase [Hordeum vulgare]

Seq. No.	397440
Seq. ID	LIB3431-003-P1-K1-B8
Method	BLASTX
NCBI GI	g548603
BLAST score	355
E value	1.0e-33
Match length	110

% identity	67
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	397441
Seq. ID	LIB3431-003-P1-K1-B9
Method	BLASTX
NCBI GI	g733454
BLAST score	453
E value	3.0e-45
Match length	108
% identity	81
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	397442
Seq. ID	LIB3431-003-P1-K1-C11
Method	BLASTX
NCBI GI	g633110
BLAST score	595
E value	8.0e-62
Match length	135
% identity	87
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	397443
Seq. ID	LIB3431-003-P1-K1-C12
Method	BLASTX
NCBI GI	g1168408
BLAST score	347
E value	9.0e-33
Match length	84
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	397444
Seq. ID	LIB3431-003-P1-K1-C4
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397445
Seq. ID	LIB3431-003-P1-K1-C7
Method	BLASTX
NCBI GI	g1361982
BLAST score	190

E value	1.0e-14
Match length	45
% identity	80
NCBI Description	4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase [Arabidopsis thaliana] >gi_5702184_gb_AAD47191.1_AF106084_1 (AF106084) 4-coumarate:CoA ligase 1 [Arabidopsis thaliana]

Seq. No.	397446
Seq. ID	LIB3431-003-P1-K1-C9
Method	BLASTN
NCBI GI	g3075487
BLAST score	128
E value	5.0e-66
Match length	136
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	397447
Seq. ID	LIB3431-003-P1-K1-D10
Method	BLASTX
NCBI GI	g4336610
BLAST score	396
E value	2.0e-38
Match length	94
% identity	81
NCBI Description	(AF099112) sigma factor; Sig3 [Zea mays]

Seq. No.	397448
Seq. ID	LIB3431-003-P1-K1-D11
Method	BLASTX
NCBI GI	g3126854
BLAST score	641
E value	3.0e-67
Match length	120
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	397449
Seq. ID	LIB3431-003-P1-K1-D12
Method	BLASTN
NCBI GI	g3885887
BLAST score	175
E value	1.0e-93
Match length	210
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	397450
Seq. ID	LIB3431-003-P1-K1-D2
Method	BLASTN
NCBI GI	g3075487
BLAST score	300
E value	1.0e-168
Match length	304

% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	397451
Seq. ID	LIB3431-003-P1-K1-D3
Method	BLASTX
NCBI GI	g132105
BLAST score	660
E value	2.0e-69
Match length	122
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397452
Seq. ID	LIB3431-003-P1-K1-D6
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397453
Seq. ID	LIB3431-003-P1-K1-D8
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	47
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	397454
Seq. ID	LIB3431-003-P1-K1-D9
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	7.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397455

Seq. ID	LIB3431-003-P1-K1-E1
Method	BLASTX
NCBI GI	g417260
BLAST score	406
E value	1.0e-39
Match length	125
% identity	66
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	397456
Seq. ID	LIB3431-003-P1-K1-E10
Method	BLASTX
NCBI GI	g3126854
BLAST score	209
E value	5.0e-22
Match length	74
% identity	78
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	397457
Seq. ID	LIB3431-003-P1-K1-E12
Method	BLASTX
NCBI GI	g4185511
BLAST score	405
E value	2.0e-39
Match length	111
% identity	70
NCBI Description	(AF102822) actin depolymerizing factor 4 [Arabidopsis thaliana]

Seq. No.	397458
Seq. ID	LIB3431-003-P1-K1-E2
Method	BLASTX
NCBI GI	g3777600
BLAST score	422
E value	2.0e-41
Match length	134
% identity	68
NCBI Description	(AF095708) 50S ribosomal protein L5 [Oryza sativa]

Seq. No.	397459
Seq. ID	LIB3431-003-P1-K1-E3
Method	BLASTX
NCBI GI	g2407281
BLAST score	644
E value	1.0e-67
Match length	125
% identity	94
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	397460
Seq. ID	LIB3431-003-P1-K1-E4
Method	BLASTX
NCBI GI	g2072555

BLAST score	237
E value	7.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397461
Seq. ID	LIB3431-003-P1-K1-E5
Method	BLASTX
NCBI GI	g4165550
BLAST score	655
E value	8.0e-69
Match length	136
% identity	90
NCBI Description	(AJ004915) apgm [Malus domestica]

Seq. No.	397462
Seq. ID	LIB3431-003-P1-K1-E6
Method	BLASTX
NCBI GI	g4972075
BLAST score	385
E value	3.0e-37
Match length	137
% identity	52
NCBI Description	(AL078467) proton pump interactor [Arabidopsis thaliana]

Seq. No.	397463
Seq. ID	LIB3431-003-P1-K1-E7
Method	BLASTX
NCBI GI	g3511285
BLAST score	204
E value	6.0e-16
Match length	98
% identity	41
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	397464
Seq. ID	LIB3431-003-P1-K1-E8
Method	BLASTX
NCBI GI	g537403
BLAST score	300
E value	3.0e-27
Match length	57
% identity	96
NCBI Description	(D26538) WSI724 protein induced by water stress [Oryza sativa]

Seq. No.	397465
Seq. ID	LIB3431-003-P1-K1-F11
Method	BLASTX
NCBI GI	g115787
BLAST score	523
E value	3.0e-53
Match length	120

% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	397466
Seq. ID	LIB3431-003-P1-K1-F3
Method	BLASTX
NCBI GI	g6103011
BLAST score	313
E value	1.0e-28
Match length	72
% identity	50
NCBI Description	(X84225) precursor of photosystem II subunit (22KDa) [Nicotiana tabacum]

Seq. No.	397467
Seq. ID	LIB3431-003-P1-K1-F4
Method	BLASTX
NCBI GI	g2306981
BLAST score	424
E value	1.0e-43
Match length	101
% identity	88
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No.	397468
Seq. ID	LIB3431-003-P1-K1-F6
Method	BLASTX
NCBI GI	g2407281
BLAST score	604
E value	7.0e-63
Match length	121
% identity	93
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	397469
Seq. ID	LIB3431-003-P1-K1-F8
Method	BLASTX
NCBI GI	g2191138
BLAST score	201
E value	1.0e-15
Match length	78
% identity	54
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No.	397470
Seq. ID	LIB3431-003-P1-K1-G10
Method	BLASTX
NCBI GI	g1076746
BLAST score	621
E value	7.0e-65
Match length	135

% identity	92
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]
Seq. No.	397471
Seq. ID	LIB3431-003-P1-K1-G12
Method	BLASTX
NCBI GI	g2501190
BLAST score	420
E value	2.0e-41
Match length	89
% identity	91
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]
Seq. No.	397472
Seq. ID	LIB3431-003-P1-K1-G2
Method	BLASTX
NCBI GI	g548603
BLAST score	307
E value	5.0e-28
Match length	99
% identity	65
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.	397473
Seq. ID	LIB3431-003-P1-K1-G3
Method	BLASTX
NCBI GI	g4455208
BLAST score	466
E value	1.0e-46
Match length	130
% identity	72
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	397474
Seq. ID	LIB3431-003-P1-K1-G5
Method	BLASTX
NCBI GI	g6091757
BLAST score	506
E value	2.0e-51
Match length	137
% identity	67
NCBI Description	(AC009327) hypothetical protein [Arabidopsis thaliana]
Seq. No.	397475
Seq. ID	LIB3431-003-P1-K1-G6
Method	BLASTX
NCBI GI	g2829927
BLAST score	219
E value	1.0e-17

Match length	107
% identity	50
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	397476
Seq. ID	LIB3431-003-P1-K1-G7
Method	BLASTX
NCBI GI	g3885892
BLAST score	595
E value	7.0e-62
Match length	129
% identity	89
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	397477
Seq. ID	LIB3431-003-P1-K1-G8
Method	BLASTN
NCBI GI	g3777597
BLAST score	36
E value	7.0e-11
Match length	40
% identity	97
NCBI Description	Oryza sativa clone LS273 30S ribosomal protein S17 (rps17) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	397478
Seq. ID	LIB3431-003-P1-K1-G9
Method	BLASTX
NCBI GI	g3386621
BLAST score	445
E value	3.0e-44
Match length	125
% identity	67
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	397479
Seq. ID	LIB3431-003-P1-K1-H10
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397480
Seq. ID	LIB3431-003-P1-K1-H11
Method	BLASTX
NCBI GI	g1841462
BLAST score	649
E value	4.0e-68
Match length	130
% identity	96
NCBI Description	(Y10991) Elongation factor 2 [Nicotiana tabacum]

Seq. No.	397481
Seq. ID	LIB3431-003-P1-K1-H4
Method	BLASTX
NCBI GI	g4539001
BLAST score	494
E value	5.0e-50
Match length	125
% identity	73
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	397482
Seq. ID	LIB3431-003-P1-K1-H5
Method	BLASTX
NCBI GI	g2088650
BLAST score	344
E value	2.0e-32
Match length	137
% identity	53
NCBI Description	(AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]

Seq. No.	397483
Seq. ID	LIB3431-003-P1-K1-H7
Method	BLASTX
NCBI GI	g4105721
BLAST score	556
E value	3.0e-57
Match length	135
% identity	79
NCBI Description	(AF050129) cell wall invertase Incw1; beta-fructosidase [Zea mays]

Seq. No.	397484
Seq. ID	LIB3431-003-P1-K1-H8
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	397485
Seq. ID	LIB3431-003-P1-N1-A11
Method	BLASTN
NCBI GI	g2662346
BLAST score	185
E value	1.0e-99
Match length	185
% identity	100
NCBI Description	Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No.	397486
Seq. ID	LIB3431-003-P1-N1-A12
Method	BLASTX
NCBI GI	g1835731

BLAST score	269
E value	1.0e-23
Match length	67
% identity	78
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	397487
Seq. ID	LIB3431-003-P1-N1-A6
Method	BLASTN
NCBI GI	g6063530
BLAST score	183
E value	1.0e-98
Match length	207
% identity	96
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	397488
Seq. ID	LIB3431-003-P1-N1-B10
Method	BLASTN
NCBI GI	g20255
BLAST score	102
E value	2.0e-50
Match length	106
% identity	99
NCBI Description	O.sativa gene for heat shock protein 82 HSP82

Seq. No.	397489
Seq. ID	LIB3431-003-P1-N1-B4
Method	BLASTX
NCBI GI	g5002516
BLAST score	148
E value	4.0e-13
Match length	90
% identity	53
NCBI Description	(AL078606) putative protein [Arabidopsis thaliana]

Seq. No.	397490
Seq. ID	LIB3431-003-P1-N1-B8
Method	BLASTN
NCBI GI	g3819189
BLAST score	71
E value	1.0e-31
Match length	87
% identity	95
NCBI Description	Hordeum vulgare partial mRNA; clone cMWG0654

Seq. No.	397491
Seq. ID	LIB3431-003-P1-N1-B9
Method	BLASTX
NCBI GI	g733454
BLAST score	217
E value	2.0e-17
Match length	47
% identity	89
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	397492
Seq. ID	LIB3431-003-P1-N1-C11
Method	BLASTX
NCBI GI	g114332
BLAST score	162
E value	2.0e-11
Match length	33
% identity	100
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_482389_pir__A45506 H+-transporting ATPase (EC 3.6.1.35) LHA1 - tomato >gi_170464 (M60166) H+-ATPase [Lycopersicon esculentum] >gi_228405_prf__1803518A H ATPase [Lycopersicon esculentum]

Seq. No.	397493
Seq. ID	LIB3431-003-P1-N1-C4
Method	BLASTN
NCBI GI	g2072554
BLAST score	217
E value	1.0e-119
Match length	229
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397494
Seq. ID	LIB3431-003-P1-N1-C9
Method	BLASTN
NCBI GI	g3075487
BLAST score	211
E value	1.0e-115
Match length	211
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	397495
Seq. ID	LIB3431-003-P1-N1-D11
Method	BLASTN
NCBI GI	g3126853
BLAST score	179
E value	5.0e-96
Match length	221
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	397496
Seq. ID	LIB3431-003-P1-N1-D12
Method	BLASTN
NCBI GI	g3885887
BLAST score	373
E value	0.0e+00
Match length	373
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No.	397497
Seq. ID	LIB3431-003-P1-N1-D2
Method	BLASTN
NCBI GI	g3075487
BLAST score	243
E value	1.0e-134
Match length	243
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	397498
Seq. ID	LIB3431-003-P1-N1-D6
Method	BLASTN
NCBI GI	g2072554
BLAST score	242
E value	1.0e-134
Match length	246
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397499
Seq. ID	LIB3431-003-P1-N1-D9
Method	BLASTN
NCBI GI	g2072554
BLAST score	279
E value	1.0e-156
Match length	291
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397500
Seq. ID	LIB3431-003-P1-N1-E1
Method	BLASTN
NCBI GI	g5091597
BLAST score	160
E value	8.0e-85
Match length	252
% identity	26
NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No.	397501
Seq. ID	LIB3431-003-P1-N1-E10
Method	BLASTN
NCBI GI	g3126853
BLAST score	81
E value	6.0e-38
Match length	101
% identity	95
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	397502
Seq. ID	LIB3431-003-P1-N1-E2
Method	BLASTN
NCBI GI	g3777599
BLAST score	190
E value	1.0e-103
Match length	219
% identity	98
NCBI Description	Oryza sativa clone LS101 50S ribosomal protein L5 (rpl5) mRNA, nuclear gene encoding chloroplast protein, partial cds

Seq. No.	397503
Seq. ID	LIB3431-003-P1-N1-E4
Method	BLASTN
NCBI GI	g2072554
BLAST score	147
E value	4.0e-77
Match length	227
% identity	91
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397504
Seq. ID	LIB3431-003-P1-N1-E8
Method	BLASTN
NCBI GI	g2913892
BLAST score	216
E value	1.0e-118
Match length	250
% identity	96
NCBI Description	Oryza sativa mRNA for LIP5, complete cds

Seq. No.	397505
Seq. ID	LIB3431-003-P1-N1-F4
Method	BLASTN
NCBI GI	g2306980
BLAST score	86
E value	1.0e-40
Match length	118
% identity	94
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	397506
Seq. ID	LIB3431-003-P1-N1-G5
Method	BLASTX
NCBI GI	g3122291
BLAST score	221
E value	6.0e-18
Match length	82
% identity	49
NCBI Description	INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2624379_emb_CAA04453_ (AJ001000) inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) [Pichia pastoris]

Seq. No.	397507
Seq. ID	LIB3431-003-P1-N1-G7
Method	BLASTN
NCBI GI	g3885891
BLAST score	253
E value	1.0e-140
Match length	267
% identity	99
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	397508
Seq. ID	LIB3431-003-P1-N1-H11
Method	BLASTN
NCBI GI	g2072554
BLAST score	210
E value	1.0e-115
Match length	210
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397509
Seq. ID	LIB3431-003-P1-N1-H2
Method	BLASTX
NCBI GI	g3913633
BLAST score	172
E value	1.0e-12
Match length	41
% identity	83
NCBI Description	HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	397510
Seq. ID	LIB3431-003-P1-N1-H6
Method	BLASTX
NCBI GI	g2088650
BLAST score	202
E value	5.0e-16
Match length	56
% identity	70
NCBI Description	(AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]

Seq. No.	397511
Seq. ID	LIB3431-004-P1-K1-A1
Method	BLASTX
NCBI GI	g1063400
BLAST score	437
E value	2.0e-43
Match length	123
% identity	75
NCBI Description	(X92888) glycolate oxidase [Lycopersicon esculentum]

Seq. No.	397512
Seq. ID	LIB3431-004-P1-K1-A10
Method	BLASTN

NCBI GI	g20181
BLAST score	41
E value	6.0e-14
Match length	57
% identity	93
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	397513
Seq. ID	LIB3431-004-P1-K1-A11
Method	BLASTX
NCBI GI	g1352461
BLAST score	292
E value	2.0e-26
Match length	68
% identity	81
NCBI Description	IN2-2 PROTEIN

Seq. No.	397514
Seq. ID	LIB3431-004-P1-K1-A12
Method	BLASTX
NCBI GI	g132105
BLAST score	630
E value	2.0e-65
Match length	123
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397515
Seq. ID	LIB3431-004-P1-K1-A2
Method	BLASTX
NCBI GI	g3759184
BLAST score	221
E value	1.0e-18
Match length	53
% identity	70
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	397516
Seq. ID	LIB3431-004-P1-K1-A5
Method	BLASTN
NCBI GI	g5091597
BLAST score	160
E value	1.0e-84
Match length	252
% identity	26
NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No. 397517

Seq. ID	LIB3431-004-P1-K1-A6
Method	BLASTX
NCBI GI	g2407281
BLAST score	705
E value	1.0e-74
Match length	132
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	397518
Seq. ID	LIB3431-004-P1-K1-A8
Method	BLASTX
NCBI GI	g2072555
BLAST score	314
E value	3.0e-29
Match length	59
% identity	95
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397519
Seq. ID	LIB3431-004-P1-K1-A9
Method	BLASTX
NCBI GI	g1800227
BLAST score	176
E value	7.0e-13
Match length	41
% identity	63
NCBI Description	(U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]

Seq. No.	397520
Seq. ID	LIB3431-004-P1-K1-B1
Method	BLASTX
NCBI GI	g3249105
BLAST score	159
E value	1.0e-10
Match length	105
% identity	33
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	397521
Seq. ID	LIB3431-004-P1-K1-B10
Method	BLASTX
NCBI GI	g2130089
BLAST score	404
E value	2.0e-39
Match length	80
% identity	90
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]

Seq. No.	397522

Seq. ID	LIB3431-004-P1-K1-B9
Method	BLASTX
NCBI GI	g131166
BLAST score	475
E value	1.0e-47
Match length	94
% identity	94
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_82100_pir__S00449 photosystem I chain II precursor - tomato >gi_170492 (M21344) photosystem I subunit II protein precursor [Lycopersicon esculentum] >gi_226544_prf__1601516A photosystem I reaction center II [Lycopersicon esculentum]

Seq. No.	397523
Seq. ID	LIB3431-004-P1-K1-C12
Method	BLASTX
NCBI GI	g2961176
BLAST score	569
E value	1.0e-58
Match length	146
% identity	78
NCBI Description	(AF050674) ribosomal protein L27 precursor [Oryza sativa]

Seq. No.	397524
Seq. ID	LIB3431-004-P1-K1-C4
Method	BLASTX
NCBI GI	g132105
BLAST score	600
E value	2.0e-62
Match length	129
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397525
Seq. ID	LIB3431-004-P1-K1-C5
Method	BLASTN
NCBI GI	g1808687
BLAST score	61
E value	1.0e-25
Match length	109
% identity	89
NCBI Description	S.stapfianus pSD.13 mRNA

Seq. No.	397526
Seq. ID	LIB3431-004-P1-K1-C7
Method	BLASTN
NCBI GI	g4138289
BLAST score	270

E value	1.0e-150
Match length	277
% identity	100
NCBI Description	Oryza sativa mRNA for thioredoxin M

Seq. No.	397527
Seq. ID	LIB3431-004-P1-K1-C9
Method	BLASTX
NCBI GI	g4836934
BLAST score	196
E value	6.0e-15
Match length	95
% identity	43
NCBI Description	(AC006085) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	397528
Seq. ID	LIB3431-004-P1-K1-D10
Method	BLASTX
NCBI GI	g4239879
BLAST score	303
E value	2.0e-27
Match length	109
% identity	60
NCBI Description	(AB016780) Glutamine:fructose-6-phosphate amidotransferase 2 [Mus musculus]

Seq. No.	397529
Seq. ID	LIB3431-004-P1-K1-D11
Method	BLASTX
NCBI GI	g118564
BLAST score	357
E value	4.0e-34
Match length	79
% identity	81
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No.	397530
Seq. ID	LIB3431-004-P1-K1-D12
Method	BLASTX
NCBI GI	g2072555
BLAST score	279
E value	8.0e-25
Match length	51
% identity	98
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397531
Seq. ID	LIB3431-004-P1-K1-D2
Method	BLASTX

NCBI GI g2565305
BLAST score 316
E value 4.0e-36
Match length 94
% identity 85
NCBI Description (AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No. 397532
Seq. ID LIB3431-004-P1-K1-D3
Method BLASTX
NCBI GI g1835731
BLAST score 559
E value 1.0e-57
Match length 106
% identity 100
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 397533
Seq. ID LIB3431-004-P1-K1-D4
Method BLASTX
NCBI GI g2253092
BLAST score 420
E value 3.0e-41
Match length 106
% identity 78
NCBI Description (Y14198) hypothetical protein [Spinacia oleracea]

Seq. No. 397534
Seq. ID LIB3431-004-P1-K1-D5
Method BLASTX
NCBI GI g3345477
BLAST score 600
E value 2.0e-62
Match length 114
% identity 100
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 397535
Seq. ID LIB3431-004-P1-K1-D6
Method BLASTN
NCBI GI g3821780
BLAST score 33
E value 3.0e-09
Match length 33
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 397536
Seq. ID LIB3431-004-P1-K1-D7
Method BLASTX
NCBI GI g3789952
BLAST score 560
E value 1.0e-57
Match length 112
% identity 98
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No.	397537
Seq. ID	LIB3431-004-P1-K1-D8
Method	BLASTX
NCBI GI	g4585882
BLAST score	548
E value	3.0e-56
Match length	145
% identity	72
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	397538
Seq. ID	LIB3431-004-P1-K1-D9
Method	BLASTX
NCBI GI	g2293480
BLAST score	365
E value	8.0e-36
Match length	83
% identity	96
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	397539
Seq. ID	LIB3431-004-P1-K1-E1
Method	BLASTX
NCBI GI	g3158476
BLAST score	352
E value	1.0e-33
Match length	90
% identity	71
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	397540
Seq. ID	LIB3431-004-P1-K1-E11
Method	BLASTX
NCBI GI	g2570511
BLAST score	543
E value	1.0e-55
Match length	106
% identity	96
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	397541
Seq. ID	LIB3431-004-P1-K1-E2
Method	BLASTX
NCBI GI	g4678311
BLAST score	175
E value	5.0e-13
Match length	61
% identity	62
NCBI Description	(AL049655) aquaporin/MIP-like protein [Arabidopsis thaliana]

Seq. No.	397542
Seq. ID	LIB3431-004-P1-K1-E3
Method	BLASTX

NCBI GI	g417260
BLAST score	329
E value	7.0e-32
Match length	127
% identity	58
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	397543
Seq. ID	LIB3431-004-P1-K1-E4
Method	BLASTN
NCBI GI	g20262
BLAST score	89
E value	1.0e-42
Match length	165
% identity	88
NCBI Description	O.sativa light-induced mRNA

Seq. No.	397544
Seq. ID	LIB3431-004-P1-K1-E6
Method	BLASTX
NCBI GI	g2130073
BLAST score	415
E value	1.0e-40
Match length	116
% identity	72
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No.	397545
Seq. ID	LIB3431-004-P1-K1-E8
Method	BLASTX
NCBI GI	g4586039
BLAST score	409
E value	6.0e-40
Match length	127
% identity	62
NCBI Description	(AC007109) unknown protein [Arabidopsis thaliana]

Seq. No.	397546
Seq. ID	LIB3431-004-P1-K1-E9
Method	BLASTN
NCBI GI	g259136
BLAST score	273
E value	1.0e-152
Match length	273
% identity	100
NCBI Description	oryzacystatin=cysteine protease inhibitor [Oryza=rice, mRNA, 643 nt]

Seq. No.	397547
Seq. ID	LIB3431-004-P1-K1-F10
Method	BLASTX
NCBI GI	g871931

BLAST score	449
E value	1.0e-44
Match length	108
% identity	84
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	397548
Seq. ID	LIB3431-004-P1-K1-F11
Method	BLASTX
NCBI GI	g3808101
BLAST score	552
E value	1.0e-56
Match length	115
% identity	91
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	397549
Seq. ID	LIB3431-004-P1-K1-F2
Method	BLASTN
NCBI GI	g4138289
BLAST score	82
E value	2.0e-38
Match length	118
% identity	92
NCBI Description	Oryza sativa mRNA for thioredoxin M

Seq. No.	397550
Seq. ID	LIB3431-004-P1-K1-F3
Method	BLASTX
NCBI GI	g3643602
BLAST score	207
E value	6.0e-17
Match length	58
% identity	71
NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	397551
Seq. ID	LIB3431-004-P1-K1-F4
Method	BLASTX
NCBI GI	g3702329
BLAST score	187
E value	6.0e-14
Match length	128
% identity	33
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397552
Seq. ID	LIB3431-004-P1-K1-F6
Method	BLASTX
NCBI GI	g132105
BLAST score	300
E value	3.0e-30
Match length	101
% identity	72
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	397553
Seq. ID	LIB3431-004-P1-K1-F9
Method	BLASTX
NCBI GI	g4263696
BLAST score	245
E value	9.0e-21
Match length	94
% identity	54
NCBI Description	(AC006223) hypothetical protein [Arabidopsis thaliana]
Seq. No.	397554
Seq. ID	LIB3431-004-P1-K1-G1
Method	BLASTX
NCBI GI	g5734636
BLAST score	325
E value	4.0e-30
Match length	117
% identity	50
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]
Seq. No.	397555
Seq. ID	LIB3431-004-P1-K1-G6
Method	BLASTX
NCBI GI	g2497746
BLAST score	167
E value	3.0e-12
Match length	41
% identity	78
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2) >gi_951334 (U31766) lipid transfer protein precursor [Oryza sativa]
Seq. No.	397556
Seq. ID	LIB3431-004-P1-K1-G7
Method	BLASTN
NCBI GI	g3618309
BLAST score	53
E value	1.0e-21
Match length	64
% identity	97
NCBI Description	Oryza sativa mRNA for zinc finger protein, complete cds, clone:E10707
Seq. No.	397557
Seq. ID	LIB3431-004-P1-K1-G9
Method	BLASTX
NCBI GI	g1707998
BLAST score	684

E value	4.0e-72
Match length	155
% identity	88
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir__S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No.	397558
Seq. ID	LIB3431-004-P1-K1-H10
Method	BLASTX
NCBI GI	g2072555
BLAST score	340
E value	5.0e-32
Match length	62
% identity	97
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397559
Seq. ID	LIB3431-004-P1-K1-H3
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397560
Seq. ID	LIB3431-004-P1-K1-H5
Method	BLASTX
NCBI GI	g115766
BLAST score	321
E value	5.0e-30
Match length	80
% identity	75
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCI TYPE II CAB) >gi_82243_pir__S00442 chlorophyll a/b-binding protein precursor - garden petunia >gi_169214 (M21317) chlorophyll binding protein precursor [Petunia hybrida] >gi_226259_prf__1503272A chlorophyll binding protein [Petunia sp.]

Seq. No.	397561
Seq. ID	LIB3431-004-P1-K1-H7
Method	BLASTX
NCBI GI	g131225
BLAST score	538
E value	2.0e-55
Match length	132
% identity	86

NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]
Seq. No.	397562
Seq. ID	LIB3431-004-P1-N1-A11
Method	BLASTN
NCBI GI	g5091597
BLAST score	145
E value	7.0e-76
Match length	241
% identity	25
NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.	397563
Seq. ID	LIB3431-004-P1-N1-A3
Method	BLASTN
NCBI GI	g2072554
BLAST score	280
E value	1.0e-156
Match length	284
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds
Seq. No.	397564
Seq. ID	LIB3431-004-P1-N1-B4
Method	BLASTX
NCBI GI	g3063524
BLAST score	262
E value	9.0e-23
Match length	58
% identity	88
NCBI Description	(AF052305) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]
Seq. No.	397565
Seq. ID	LIB3431-004-P1-N1-B5
Method	BLASTX
NCBI GI	g517500
BLAST score	216
E value	1.0e-17
Match length	57
% identity	77
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]
Seq. No.	397566
Seq. ID	LIB3431-004-P1-N1-B6
Method	BLASTX
NCBI GI	g517500
BLAST score	210
E value	6.0e-17
Match length	57
% identity	75

NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	397567
Seq. ID	LIB3431-004-P1-N1-C1
Method	BLASTN
NCBI GI	g3819189
BLAST score	39
E value	1.0e-12
Match length	59
% identity	92
NCBI Description	Hordeum vulgare partial mRNA; clone cMWG0654

Seq. No.	397568
Seq. ID	LIB3431-004-P1-N1-C10
Method	BLASTN
NCBI GI	g218207
BLAST score	207
E value	1.0e-113
Match length	235
% identity	97
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397569
Seq. ID	LIB3431-004-P1-N1-C4
Method	BLASTN
NCBI GI	g4176421
BLAST score	77
E value	1.0e-35
Match length	77
% identity	100
NCBI Description	Oryza sativa rpl12-1 gene for chloroplast ribosomal protein L12, complete cds

Seq. No.	397570
Seq. ID	LIB3431-004-P1-N1-C5
Method	BLASTX
NCBI GI	g4115939
BLAST score	200
E value	1.0e-15
Match length	50
% identity	40
NCBI Description	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No.	397571
Seq. ID	LIB3431-004-P1-N1-C6
Method	BLASTX
NCBI GI	g4115939
BLAST score	167
E value	8.0e-12
Match length	41
% identity	73

NCBI Description	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No.	397572
Seq. ID	LIB3431-004-P1-N1-C7
Method	BLASTN
NCBI GI	g3287498
BLAST score	168
E value	1.0e-89
Match length	180
% identity	98
NCBI Description	Oryza sativa gene for importin alpha, complete cds

Seq. No.	397573
Seq. ID	LIB3431-004-P1-N1-C8
Method	BLASTN
NCBI GI	g416266
BLAST score	133
E value	1.0e-68
Match length	182
% identity	93
NCBI Description	Rice mRNA for oxygen-evolving protein, partial sequence

Seq. No.	397574
Seq. ID	LIB3431-004-P1-N1-D11
Method	BLASTN
NCBI GI	g3345476
BLAST score	146
E value	1.0e-76
Match length	162
% identity	98
NCBI Description	Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No.	397575
Seq. ID	LIB3431-004-P1-N1-D2
Method	BLASTX
NCBI GI	g3789952
BLAST score	161
E value	3.0e-11
Match length	31
% identity	94
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	397576
Seq. ID	LIB3431-004-P1-N1-D4
Method	BLASTN
NCBI GI	g2961175
BLAST score	65
E value	4.0e-28
Match length	69
% identity	99
NCBI Description	Oryza sativa ribosomal protein L27 precursor, mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	397577

Seq. ID	LIB3431-004-P1-N1-D9
Method	BLASTN
NCBI GI	g1835730
BLAST score	121
E value	1.0e-61
Match length	157
% identity	94
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No.	397578
Seq. ID	LIB3431-004-P1-N1-E1
Method	BLASTN
NCBI GI	g2331130
BLAST score	152
E value	5.0e-80
Match length	193
% identity	94
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No.	397579
Seq. ID	LIB3431-004-P1-N1-E4
Method	BLASTN
NCBI GI	g2072554
BLAST score	120
E value	5.0e-61
Match length	190
% identity	92
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397580
Seq. ID	LIB3431-004-P1-N1-E5
Method	BLASTX
NCBI GI	g2570511
BLAST score	163
E value	2.0e-22
Match length	67
% identity	78
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	397581
Seq. ID	LIB3431-004-P1-N1-E6
Method	BLASTX
NCBI GI	g115832
BLAST score	154
E value	2.0e-10
Match length	44
% identity	70
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_81414_pir__JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi_169020 (M23532) major chlorophyll binding protein [Physcomitrella patens]

Seq. No.	397582

Seq. ID	LIB3431-004-P1-N1-G12
Method	BLASTN
NCBI GI	g886692
BLAST score	107
E value	1.0e-53
Match length	123
% identity	97
NCBI Description	O.sativa mRNA for lipid transfer protein, b1

Seq. No.	397583
Seq. ID	LIB3431-004-P1-N1-G2
Method	BLASTN
NCBI GI	g3618309
BLAST score	95
E value	5.0e-46
Match length	234
% identity	93
NCBI Description	Oryza sativa mRNA for zinc finger protein, complete cds, clone:E10707

Seq. No.	397584
Seq. ID	LIB3431-004-P1-N1-G5
Method	BLASTN
NCBI GI	g2073379
BLAST score	178
E value	2.0e-95
Match length	208
% identity	96
NCBI Description	Rice CP26 mRNA, partial sequence

Seq. No.	397585
Seq. ID	LIB3431-004-P1-N1-G6
Method	BLASTN
NCBI GI	g2073379
BLAST score	58
E value	4.0e-24
Match length	72
% identity	94
NCBI Description	Rice CP26 mRNA, partial sequence

Seq. No.	397586
Seq. ID	LIB3431-004-P1-N1-H2
Method	BLASTX
NCBI GI	g131225
BLAST score	167
E value	7.0e-12
Match length	45
% identity	69
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	397587
Seq. ID	LIB3431-004-P1-N1-H5
Method	BLASTN
NCBI GI	g2072554

BLAST score 268
E value 1.0e-149
Match length 268
% identity 100
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 397588
Seq. ID LIB3431-005-P1-K1-A10
Method BLASTX
NCBI GI g218157
BLAST score 678
E value 1.0e-71
Match length 137
% identity 96
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No. 397589
Seq. ID LIB3431-005-P1-K1-A11
Method BLASTX
NCBI GI g606817
BLAST score 192
E value 2.0e-14
Match length 46
% identity 80
NCBI Description (U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]

Seq. No. 397590
Seq. ID LIB3431-005-P1-K1-A12
Method BLASTX
NCBI GI g3345477
BLAST score 387
E value 2.0e-37
Match length 73
% identity 100
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 397591
Seq. ID LIB3431-005-P1-K1-A2
Method BLASTX
NCBI GI g131388
BLAST score 267
E value 2.0e-23
Match length 91
% identity 69
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 397592
Seq. ID LIB3431-005-P1-K1-A3

Method	BLASTX
NCBI GI	g266893
BLAST score	540
E value	2.0e-55
Match length	108
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	397593
Seq. ID	LIB3431-005-P1-K1-A5
Method	BLASTN
NCBI GI	g11957
BLAST score	399
E value	0.0e+00
Match length	435
% identity	43
NCBI Description	Rice complete chloroplast genome

Seq. No.	397594
Seq. ID	LIB3431-005-P1-K1-A8
Method	BLASTX
NCBI GI	g3913018
BLAST score	564
E value	2.0e-58
Match length	113
% identity	100
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	397595
Seq. ID	LIB3431-005-P1-K1-B10
Method	BLASTX
NCBI GI	g4056487
BLAST score	397
E value	8.0e-39
Match length	98
% identity	76
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397596
Seq. ID	LIB3431-005-P1-K1-B11
Method	BLASTX
NCBI GI	g1346764
BLAST score	778
E value	3.0e-83
Match length	147
% identity	95
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 >gi_951336_gb_AAA74625_ (U31773) protein phosphatase 1 [Oryza sativa]

Seq. No.	397597

Seq. ID	LIB3431-005-P1-K1-B12
Method	BLASTX
NCBI GI	g3075488
BLAST score	513
E value	4.0e-52
Match length	116
% identity	84
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	397598
Seq. ID	LIB3431-005-P1-K1-B4
Method	BLASTX
NCBI GI	g136640
BLAST score	721
E value	2.0e-76
Match length	144
% identity	92
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720) ubiquitin carrier protein [Triticum aestivum]

Seq. No.	397599
Seq. ID	LIB3431-005-P1-K1-B6
Method	BLASTX
NCBI GI	g1353352
BLAST score	176
E value	2.0e-14
Match length	83
% identity	60
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	397600
Seq. ID	LIB3431-005-P1-K1-B7
Method	BLASTX
NCBI GI	g132105
BLAST score	707
E value	7.0e-75
Match length	129
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397601
Seq. ID	LIB3431-005-P1-K1-B9
Method	BLASTX
NCBI GI	g2961355
BLAST score	232
E value	2.0e-19
Match length	76

% identity	54
NCBI Description	(AL022140) glucosidase like protein [Arabidopsis thaliana]

Seq. No.	397602
Seq. ID	LIB3431-005-P1-K1-C1
Method	BLASTX
NCBI GI	g115772
BLAST score	589
E value	4.0e-61
Match length	111
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_ (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No.	397603
Seq. ID	LIB3431-005-P1-K1-C12
Method	BLASTX
NCBI GI	g3913193
BLAST score	451
E value	7.0e-45
Match length	150
% identity	55
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_556422 (L36823) cinnamyl-alcohol dehydrogenase [Stylosanthes humilis]

Seq. No.	397604
Seq. ID	LIB3431-005-P1-K1-C4
Method	BLASTN
NCBI GI	g2072554
BLAST score	286
E value	1.0e-160
Match length	286
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397605
Seq. ID	LIB3431-005-P1-K1-C5
Method	BLASTX
NCBI GI	g3334320
BLAST score	519
E value	7.0e-53
Match length	103
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	397606
Seq. ID	LIB3431-005-P1-K1-C7
Method	BLASTX
NCBI GI	g99894
BLAST score	392
E value	3.0e-38
Match length	100

% identity	79
NCBI Description	chlorophyll a/b-binding protein 5 - soybean

Seq. No.	397607
Seq. ID	LIB3431-005-P1-K1-C9
Method	BLASTX
NCBI GI	g2832672
BLAST score	154
E value	5.0e-10
Match length	31
% identity	97
NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No.	397608
Seq. ID	LIB3431-005-P1-K1-D1
Method	BLASTX
NCBI GI	g4559339
BLAST score	481
E value	2.0e-48
Match length	125
% identity	77
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	397609
Seq. ID	LIB3431-005-P1-K1-D11
Method	BLASTX
NCBI GI	g132105
BLAST score	409
E value	6.0e-40
Match length	102
% identity	76
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397610
Seq. ID	LIB3431-005-P1-K1-D2
Method	BLASTX
NCBI GI	g283008
BLAST score	576
E value	9.0e-71
Match length	138
% identity	92
NCBI Description	sucrose synthase (EC 2.4.1.13) - rice >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza sativa]

Seq. No.	397611
Seq. ID	LIB3431-005-P1-K1-D3
Method	BLASTX

NCBI GI	g1168599
BLAST score	205
E value	4.0e-16
Match length	43
% identity	100
NCBI Description	ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III) >gi_1262602_dbj_BAA04320.1_ (D17510) H+-ATPase III subunit [Pinus thunbergii]

Seq. No.	397612
Seq. ID	LIB3431-005-P1-K1-D5
Method	BLASTX
NCBI GI	g129915
BLAST score	674
E value	5.0e-71
Match length	147
% identity	91
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_66912_pir__TVWTGC phosphoglycerate kinase (EC 2.7.2.3) precursor, chloroplast - wheat >gi_21833_emb_CAA33303_ (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum aestivum] >gi_3293043_emb_CAA51931_ (X73528) phosphoglycerate kinase [Triticum aestivum]

Seq. No.	397613
Seq. ID	LIB3431-005-P1-K1-D6
Method	BLASTX
NCBI GI	g3345477
BLAST score	457
E value	1.0e-45
Match length	129
% identity	71
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	397614
Seq. ID	LIB3431-005-P1-K1-D7
Method	BLASTX
NCBI GI	g729478
BLAST score	315
E value	3.0e-29
Match length	69
% identity	86
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	397615
Seq. ID	LIB3431-005-P1-K1-E1
Method	BLASTX
NCBI GI	g3789952
BLAST score	534
E value	8.0e-55
Match length	104
% identity	95

NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	397616
Seq. ID	LIB3431-005-P1-K1-E11
Method	BLASTX
NCBI GI	g4455271
BLAST score	227
E value	1.0e-18
Match length	103
% identity	47
NCBI Description	(AL035527) serine protease-like protein [Arabidopsis thaliana]

Seq. No.	397617
Seq. ID	LIB3431-005-P1-K1-E12
Method	BLASTX
NCBI GI	g4539404
BLAST score	374
E value	8.0e-36
Match length	91
% identity	74
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	397618
Seq. ID	LIB3431-005-P1-K1-E3
Method	BLASTN
NCBI GI	g3789947
BLAST score	124
E value	2.0e-63
Match length	164
% identity	95
NCBI Description	Oryza sativa translation initiation factor 5A (eIF-5A) mRNA, complete cds

Seq. No.	397619
Seq. ID	LIB3431-005-P1-K1-E4
Method	BLASTX
NCBI GI	g3522947
BLAST score	181
E value	7.0e-14
Match length	68
% identity	53
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397620
Seq. ID	LIB3431-005-P1-K1-E5
Method	BLASTX
NCBI GI	g1835731
BLAST score	584
E value	2.0e-60
Match length	124
% identity	91
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	397621
Seq. ID	LIB3431-005-P1-K1-E6

Method	BLASTX
NCBI GI	g132105
BLAST score	340
E value	4.0e-32
Match length	86
% identity	80
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397622
Seq. ID	LIB3431-005-P1-K1-E7
Method	BLASTX
NCBI GI	g125580
BLAST score	394
E value	3.0e-38
Match length	117
% identity	71
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608) phosphoribulokinase [Triticum aestivum]

Seq. No.	397623
Seq. ID	LIB3431-005-P1-K1-E9
Method	BLASTX
NCBI GI	g1055130
BLAST score	241
E value	2.0e-20
Match length	120
% identity	45
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No.	397624
Seq. ID	LIB3431-005-P1-K1-F1
Method	BLASTX
NCBI GI	g1346753
BLAST score	143
E value	2.0e-09
Match length	37
% identity	65
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 2 >gi_2654373_emb_CAA82264_ (Z28632) protein phosphatase 1 [Acetabularia cliftonii]

Seq. No.	397625
Seq. ID	LIB3431-005-P1-K1-F11

Method	BLASTX
NCBI GI	g132105
BLAST score	683
E value	5.0e-72
Match length	132
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397626
Seq. ID	LIB3431-005-P1-K1-F12
Method	BLASTX
NCBI GI	g3063446
BLAST score	198
E value	3.0e-15
Match length	131
% identity	37
NCBI Description	(AC003981) F22O13.8 [Arabidopsis thaliana]

Seq. No.	397627
Seq. ID	LIB3431-005-P1-K1-F2
Method	BLASTN
NCBI GI	g3126853
BLAST score	75
E value	4.0e-34
Match length	217
% identity	85
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	397628
Seq. ID	LIB3431-005-P1-K1-F4
Method	BLASTX
NCBI GI	g671740
BLAST score	453
E value	3.0e-45
Match length	82
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397629
Seq. ID	LIB3431-005-P1-K1-F6
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100

NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397630
Seq. ID	LIB3431-005-P1-K1-F7
Method	BLASTX
NCBI GI	g1362009
BLAST score	462
E value	3.0e-46
Match length	95
% identity	54
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	397631
Seq. ID	LIB3431-005-P1-K1-F8
Method	BLASTX
NCBI GI	g5922625
BLAST score	630
E value	5.0e-66
Match length	115
% identity	99
NCBI Description	(AP000492) ESTs AU065732(E51179),AU030519(E51179) correspond to a region of the predicted gene.; similar to epoxide hydrolases; coded for by A. thaliana cDNA T04215. (AF069298) [Oryza sativa] >gi_6016858_dbj_BAA85201.1_ (AP000570) ESTs AU065732(E51179),AU030519(E51179) correspond to a region of the predicted gene.; Similar to epoxide hydrolases; coded for by A. thaliana cDNA T04215. (AF069298) [Oryza sativa]

Seq. No.	397632
Seq. ID	LIB3431-005-P1-K1-F9
Method	BLASTX
NCBI GI	g1778095
BLAST score	443
E value	5.0e-44
Match length	121
% identity	68
NCBI Description	(U64903) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	397633
Seq. ID	LIB3431-005-P1-K1-G1
Method	BLASTX
NCBI GI	g285317
BLAST score	562
E value	7.0e-58
Match length	140
% identity	76
NCBI Description	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea

Seq. No.	397634
Seq. ID	LIB3431-005-P1-K1-G10
Method	BLASTN
NCBI GI	g4138289

BLAST score	224
E value	1.0e-123
Match length	240
% identity	98
NCBI Description	Oryza sativa mRNA for thioredoxin M

Seq. No.	397635
Seq. ID	LIB3431-005-P1-K1-G2
Method	BLASTX
NCBI GI	g2130069
BLAST score	712
E value	1.0e-75
Match length	129
% identity	98
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No.	397636
Seq. ID	LIB3431-005-P1-K1-G3
Method	BLASTX
NCBI GI	g2429290
BLAST score	235
E value	8.0e-20
Match length	47
% identity	96
NCBI Description	(AF014469) peroxidase [Oryza sativa]

Seq. No.	397637
Seq. ID	LIB3431-005-P1-K1-G4
Method	BLASTX
NCBI GI	g5918016
BLAST score	211
E value	7.0e-17
Match length	137
% identity	36
NCBI Description	(AL035525) myosin-like protein [Arabidopsis thaliana]

Seq. No.	397638
Seq. ID	LIB3431-005-P1-K1-G6
Method	BLASTX
NCBI GI	g543867
BLAST score	561
E value	1.0e-57
Match length	150
% identity	73
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit [Ipomoea batatas]

Seq. No.	397639
Seq. ID	LIB3431-005-P1-K1-G7
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	2.0e-11

Match length	48
% identity	66
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	397640
Seq. ID	LIB3431-005-P1-K1-G8
Method	BLASTN
NCBI GI	g1245938
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	397641
Seq. ID	LIB3431-005-P1-K1-G9
Method	BLASTX
NCBI GI	g4239845
BLAST score	201
E value	1.0e-15
Match length	122
% identity	39
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	397642
Seq. ID	LIB3431-005-P1-K1-H1
Method	BLASTX
NCBI GI	g133748
BLAST score	211
E value	4.0e-17
Match length	43
% identity	98
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_70961_pir__R3RZ12 ribosomal protein S12 - rice chloroplast >gi_1213603_emb_CAA33929_ (X15901) ribosomal protein S12 [Oryza sativa] >gi_226658_prf__1603356CJ ribosomal protein S12 [Oryza sativa]

Seq. No.	397643
Seq. ID	LIB3431-005-P1-K1-H10
Method	BLASTX
NCBI GI	g4454799
BLAST score	644
E value	2.0e-67
Match length	146
% identity	88
NCBI Description	(AF079782) translation initiation factor 4A2 [Zea mays]

Seq. No.	397644
Seq. ID	LIB3431-005-P1-K1-H12
Method	BLASTX
NCBI GI	g132105
BLAST score	551
E value	1.0e-56
Match length	122
% identity	85

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	397645
Seq. ID	LIB3431-005-P1-K1-H2
Method	BLASTN
NCBI GI	g5852170
BLAST score	56
E value	1.0e-22
Match length	68
% identity	96
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804
Seq. No.	397646
Seq. ID	LIB3431-005-P1-K1-H5
Method	BLASTX
NCBI GI	g1747294
BLAST score	468
E value	3.0e-51
Match length	145
% identity	80
NCBI Description	(D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.	397647
Seq. ID	LIB3431-005-P1-K1-H7
Method	BLASTX
NCBI GI	g133748
BLAST score	429
E value	3.0e-42
Match length	86
% identity	99
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_70961_pir__R3RZ12 ribosomal protein S12 - rice chloroplast >gi_1213603_emb_CAA33929_ (X15901) ribosomal protein S12 [Oryza sativa] >gi_226658_prf__1603356CJ ribosomal protein S12 [Oryza sativa]
Seq. No.	397648
Seq. ID	LIB3431-005-P1-K1-H8
Method	BLASTX
NCBI GI	g1346698
BLAST score	622
E value	6.0e-65
Match length	136
% identity	91
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_21272_emb_CAA48479_ (X68430) phosphoglycerate kinase [Spinacia oleracea]

Seq. No.	397649
Seq. ID	LIB3431-005-P1-N1-A10
Method	BLASTX
NCBI GI	g113622
BLAST score	277
E value	1.0e-24
Match length	55
% identity	98
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68197_pir__ADRZY fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - rice >gi_20204_emb_CAA37290_ (X53130) fructose-diphosphate aldolase (AA 1-358) [Oryza sativa]

Seq. No.	397650
Seq. ID	LIB3431-005-P1-N1-A11
Method	BLASTX
NCBI GI	g3345477
BLAST score	191
E value	2.0e-14
Match length	40
% identity	90
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	397651
Seq. ID	LIB3431-005-P1-N1-A12
Method	BLASTN
NCBI GI	g606816
BLAST score	279
E value	1.0e-156
Match length	287
% identity	99
NCBI Description	Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds

Seq. No.	397652
Seq. ID	LIB3431-005-P1-N1-A2
Method	BLASTN
NCBI GI	g416266
BLAST score	102
E value	2.0e-50
Match length	164
% identity	90
NCBI Description	Rice mRNA for oxygen-evolving protein, partial sequence

Seq. No.	397653
Seq. ID	LIB3431-005-P1-N1-A3
Method	BLASTX
NCBI GI	g167097
BLAST score	175
E value	4.0e-25
Match length	71
% identity	85
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	397654

Seq. ID	LIB3431-005-P1-N1-A5
Method	BLASTX
NCBI GI	g82532
BLAST score	295
E value	1.0e-26
Match length	56
% identity	100
NCBI Description	hypothetical 6K protein (rps15-trnL intergenic region) - rice chloroplast >gi_12046_emb_CAA33949_ (X15901) ORF56; 5' portion of ORF393 [Oryza sativa] >gi_226666_prf__1603356CT ORF 393 N term [Oryza sativa]

Seq. No.	397655
Seq. ID	LIB3431-005-P1-N1-A8
Method	BLASTN
NCBI GI	g218154
BLAST score	80
E value	5.0e-37
Match length	140
% identity	100
NCBI Description	Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No.	397656
Seq. ID	LIB3431-005-P1-N1-B10
Method	BLASTX
NCBI GI	g4056487
BLAST score	152
E value	4.0e-10
Match length	40
% identity	70
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397657
Seq. ID	LIB3431-005-P1-N1-B12
Method	BLASTX
NCBI GI	g2326947
BLAST score	216
E value	2.0e-17
Match length	42
% identity	98
NCBI Description	(Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays]

Seq. No.	397658
Seq. ID	LIB3431-005-P1-N1-B4
Method	BLASTN
NCBI GI	g170784
BLAST score	42
E value	2.0e-14
Match length	78
% identity	88
NCBI Description	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds

Seq. No.	397659
Seq. ID	LIB3431-005-P1-N1-B7
Method	BLASTN

NCBI GI	g218207
BLAST score	272
E value	1.0e-151
Match length	300
% identity	98
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397660
Seq. ID	LIB3431-005-P1-N1-C1
Method	BLASTX
NCBI GI	g2804572
BLAST score	167
E value	1.0e-11
Match length	46
% identity	76
NCBI Description	(AB006081) chlorophyll a/b-binding protein [Fagus crenata]

Seq. No.	397661
Seq. ID	LIB3431-005-P1-N1-C12
Method	BLASTX
NCBI GI	g558511
BLAST score	150
E value	9.0e-10
Match length	32
% identity	91
NCBI Description	(D16624) cinnamyl alcohol dehydrogenase [Eucalyptus botryoides]

Seq. No.	397662
Seq. ID	LIB3431-005-P1-N1-C3
Method	BLASTN
NCBI GI	g20191
BLAST score	380
E value	0.0e+00
Match length	411
% identity	98
NCBI Description	O.sativa mRNA for catalase

Seq. No.	397663
Seq. ID	LIB3431-005-P1-N1-C4
Method	BLASTN
NCBI GI	g2072554
BLAST score	267
E value	1.0e-148
Match length	279
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397664
Seq. ID	LIB3431-005-P1-N1-C8
Method	BLASTX
NCBI GI	g1168587
BLAST score	217
E value	1.0e-17

Match length	52
% identity	83
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_1084467_pir__S43728 H+-transporting ATP synthase (EC 3.6.1.34) - sorghum >gi_311231_emb_CAA46803_ (X66004) H(+)-transporting ATP synthase [Sorghum bicolor]

Seq. No.	397665
Seq. ID	LIB3431-005-P1-N1-D10
Method	BLASTX
NCBI GI	g223582
BLAST score	168
E value	7.0e-24
Match length	77
% identity	90
NCBI Description	histone H4 [Homo sapiens]

Seq. No.	397666
Seq. ID	LIB3431-005-P1-N1-D2
Method	BLASTN
NCBI GI	g20365
BLAST score	173
E value	9.0e-93
Match length	177
% identity	99
NCBI Description	O.sativa RSs1 gene for sucrose synthase

Seq. No.	397667
Seq. ID	LIB3431-005-P1-N1-D3
Method	BLASTN
NCBI GI	g11957
BLAST score	330
E value	0.0e+00
Match length	374
% identity	97
NCBI Description	Rice complete chloroplast genome

Seq. No.	397668
Seq. ID	LIB3431-005-P1-N1-D6
Method	BLASTX
NCBI GI	g3345477
BLAST score	171
E value	6.0e-12
Match length	34
% identity	94
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	397669
Seq. ID	LIB3431-005-P1-N1-D7
Method	BLASTX
NCBI GI	g729478
BLAST score	371
E value	1.0e-35
Match length	84
% identity	85
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+

reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	397670
Seq. ID	LIB3431-005-P1-N1-E1
Method	BLASTN
NCBI GI	g3789951
BLAST score	190
E value	1.0e-102
Match length	247
% identity	98
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	397671
Seq. ID	LIB3431-005-P1-N1-E11
Method	BLASTX
NCBI GI	g2695937
BLAST score	197
E value	3.0e-15
Match length	61
% identity	49
NCBI Description	(AJ222782) subtilisin-like protease [Hordeum vulgare]

Seq. No.	397672
Seq. ID	LIB3431-005-P1-N1-E3
Method	BLASTN
NCBI GI	g3789947
BLAST score	287
E value	1.0e-160
Match length	291
% identity	100
NCBI Description	Oryza sativa translation initiation factor 5A (eIF-5A) mRNA, complete cds

Seq. No.	397673
Seq. ID	LIB3431-005-P1-N1-E5
Method	BLASTX
NCBI GI	g1835731
BLAST score	202
E value	2.0e-18
Match length	66
% identity	79
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	397674
Seq. ID	LIB3431-005-P1-N1-E6
Method	BLASTX
NCBI GI	g347451
BLAST score	248
E value	4.0e-21
Match length	48
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza

sativa]

Seq. No.	397675
Seq. ID	LIB3431-005-P1-N1-F3
Method	BLASTN
NCBI GI	g5091597
BLAST score	149
E value	4.0e-78
Match length	229
% identity	29
NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No.	397676
Seq. ID	LIB3431-005-P1-N1-F4
Method	BLASTX
NCBI GI	g671740
BLAST score	150
E value	9.0e-10
Match length	28
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397677
Seq. ID	LIB3431-005-P1-N1-F5
Method	BLASTN
NCBI GI	g21838
BLAST score	56
E value	1.0e-22
Match length	209
% identity	83
NCBI Description	T.aestivum PRK gene for ribulose-5-phosphate kinase

Seq. No.	397678
Seq. ID	LIB3431-005-P1-N1-F6
Method	BLASTN
NCBI GI	g2072554
BLAST score	246
E value	1.0e-136
Match length	262
% identity	98
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397679
Seq. ID	LIB3431-005-P1-N1-F7
Method	BLASTX
NCBI GI	g1362009
BLAST score	259
E value	2.0e-22
Match length	55
% identity	47
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	397680
Seq. ID	LIB3431-005-P1-N1-F8
Method	BLASTX

NCBI GI	g5922625
BLAST score	412
E value	2.0e-40
Match length	75
% identity	100
NCBI Description	(AP000492) ESTs AU065732(E51179),AU030519(E51179) correspond to a region of the predicted gene.; similar to epoxide hydrolases; coded for by A. thaliana cDNA T04215. (AF069298) [Oryza sativa] >gi_6016858_dbj_BAA85201.1_ (AP000570) ESTs AU065732(E51179),AU030519(E51179) correspond to a region of the predicted gene.; Similar to epoxide hydrolases; coded for by A. thaliana cDNA T04215. (AF069298) [Oryza sativa]

Seq. No.	397681
Seq. ID	LIB3431-005-P1-N1-G10
Method	BLASTX
NCBI GI	g4138290
BLAST score	309
E value	3.0e-28
Match length	61
% identity	98
NCBI Description	(AJ005841) thioredoxin M [Oryza sativa]

Seq. No.	397682
Seq. ID	LIB3431-005-P1-N1-G2
Method	BLASTN
NCBI GI	g20191
BLAST score	391
E value	0.0e+00
Match length	406
% identity	100
NCBI Description	O.sativa mRNA for catalase

Seq. No.	397683
Seq. ID	LIB3431-005-P1-N1-G3
Method	BLASTN
NCBI GI	g2429289
BLAST score	152
E value	6.0e-80
Match length	184
% identity	96
NCBI Description	Oryza sativa peroxidase (POX5.1) mRNA, complete cds

Seq. No.	397684
Seq. ID	LIB3431-005-P1-N1-H10
Method	BLASTX
NCBI GI	g547712
BLAST score	298
E value	7.0e-27
Match length	57
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No.	397685
Seq. ID	LIB3431-005-P1-N1-H12
Method	BLASTX
NCBI GI	g671740
BLAST score	458
E value	6.0e-46
Match length	83
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397686
Seq. ID	LIB3431-005-P1-N1-H2
Method	BLASTX
NCBI GI	g3776573
BLAST score	225
E value	2.0e-18
Match length	56
% identity	68
NCBI Description	(AC005388) Similar to nodulins and lipase homolog F14J9.5 gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis thaliana]

Seq. No.	397687
Seq. ID	LIB3431-005-P1-N1-H5
Method	BLASTN
NCBI GI	g3298473
BLAST score	108
E value	6.0e-54
Match length	197
% identity	88
NCBI Description	Oryza sativa gene for ovp1, complete cds

Seq. No.	397688
Seq. ID	LIB3431-005-P1-N1-H7
Method	BLASTX
NCBI GI	g1173275
BLAST score	337
E value	1.0e-31
Match length	84
% identity	83
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_2119068_pir__S58630 ribosomal protein S7 - maize chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563) ribosomal protein S7 [Zea mays]

Seq. No.	397689
Seq. ID	LIB3431-006-P1-K1-A1
Method	BLASTX
NCBI GI	g3345477
BLAST score	476
E value	6.0e-48
Match length	89
% identity	99
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	397690
Seq. ID	LIB3431-006-P1-K1-A10
Method	BLASTX
NCBI GI	g3128186
BLAST score	250
E value	2.0e-21
Match length	131
% identity	44
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397691
Seq. ID	LIB3431-006-P1-K1-A11
Method	BLASTX
NCBI GI	g4996602
BLAST score	268
E value	2.0e-23
Match length	71
% identity	75
NCBI Description	(AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana tabacum]

Seq. No.	397692
Seq. ID	LIB3431-006-P1-K1-A12
Method	BLASTX
NCBI GI	g5257277
BLAST score	503
E value	6.0e-51
Match length	109
% identity	91
NCBI Description	(AP000364) ESTs C98431(E0144),C71728(E0144) correspond to a region of the predicted gene.; Similar to Medicago sativa S-adenosyl-L-methionine. (U20736) [Oryza sativa]

Seq. No.	397693
Seq. ID	LIB3431-006-P1-K1-A3
Method	BLASTX
NCBI GI	g133748
BLAST score	634
E value	3.0e-66
Match length	124
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_70961_pir__R3RZ12 ribosomal protein S12 - rice chloroplast >gi_1213603_emb_CAA33929_ (X15901) ribosomal protein S12 [Oryza sativa] >gi_226658_prf__1603356CJ ribosomal protein S12 [Oryza sativa]

Seq. No.	397694
Seq. ID	LIB3431-006-P1-K1-A4
Method	BLASTX
NCBI GI	g2570511
BLAST score	633
E value	3.0e-66
Match length	123
% identity	98
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	397695
Seq. ID	LIB3431-006-P1-K1-A6
Method	BLASTX
NCBI GI	g3126854
BLAST score	418
E value	7.0e-43
Match length	127
% identity	74
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	397696
Seq. ID	LIB3431-006-P1-K1-A7
Method	BLASTX
NCBI GI	g4588906
BLAST score	447
E value	1.0e-44
Match length	98
% identity	90
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	397697
Seq. ID	LIB3431-006-P1-K1-A9
Method	BLASTX
NCBI GI	g4914452
BLAST score	444
E value	4.0e-44
Match length	132
% identity	64
NCBI Description	(AL050398) putative protein [Arabidopsis thaliana]

Seq. No.	397698
Seq. ID	LIB3431-006-P1-K1-B1
Method	BLASTX
NCBI GI	g115787
BLAST score	681
E value	8.0e-72
Match length	152
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	397699
Seq. ID	LIB3431-006-P1-K1-B10
Method	BLASTX
NCBI GI	g3789952
BLAST score	484
E value	1.0e-48
Match length	104
% identity	91
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	397700

Seq. ID	LIB3431-006-P1-K1-B11
Method	BLASTX
NCBI GI	g4926827
BLAST score	401
E value	6.0e-39
Match length	97
% identity	77
NCBI Description	(AC004135) T17H7.12 [Arabidopsis thaliana]

Seq. No.	397701
Seq. ID	LIB3431-006-P1-K1-B12
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	1.0e-19
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397702
Seq. ID	LIB3431-006-P1-K1-B4
Method	BLASTX
NCBI GI	g3345477
BLAST score	745
E value	3.0e-79
Match length	156
% identity	91
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	397703
Seq. ID	LIB3431-006-P1-K1-B5
Method	BLASTX
NCBI GI	g129231
BLAST score	771
E value	2.0e-82
Match length	146
% identity	97
NCBI Description	ORYZAIN ALPHA CHAIN PRECURSOR >gi_67644_pir__KHRZOA oryzain (EC 3.4.22.-) alpha precursor - rice >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor [Oryza sativa]

Seq. No.	397704
Seq. ID	LIB3431-006-P1-K1-B7
Method	BLASTN
NCBI GI	g2570516
BLAST score	331
E value	0.0e+00
Match length	370
% identity	98
NCBI Description	Oryza sativa thioredoxin F isoform mRNA, complete cds

Seq. No.	397705
Seq. ID	LIB3431-006-P1-K1-B8
Method	BLASTX

NCBI GI	g2827078
BLAST score	185
E value	6.0e-14
Match length	92
% identity	46
NCBI Description	(AF020270) malate dehydrogenase precursor [Medicago sativa]

Seq. No.	397706
Seq. ID	LIB3431-006-P1-K1-C1
Method	BLASTX
NCBI GI	g4019275
BLAST score	158
E value	1.0e-10
Match length	130
% identity	4
NCBI Description	(AF083424) orf 48 [Ateline herpesvirus 3]

Seq. No.	397707
Seq. ID	LIB3431-006-P1-K1-C10
Method	BLASTX
NCBI GI	g1173027
BLAST score	166
E value	2.0e-11
Match length	36
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	397708
Seq. ID	LIB3431-006-P1-K1-C11
Method	BLASTX
NCBI GI	g3047124
BLAST score	188
E value	5.0e-14
Match length	57
% identity	61
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	397709
Seq. ID	LIB3431-006-P1-K1-C12
Method	BLASTX
NCBI GI	g132105
BLAST score	547
E value	3.0e-56
Match length	119
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397710

Seq. ID	LIB3431-006-P1-K1-C4
Method	BLASTX
NCBI GI	g1052960
BLAST score	768
E value	5.0e-82
Match length	147
% identity	93
NCBI Description	(U37437) PNIL34 [Ipomoea nil]

Seq. No.	397711
Seq. ID	LIB3431-006-P1-K1-C5
Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	397712
Seq. ID	LIB3431-006-P1-K1-C6
Method	BLASTX
NCBI GI	g548605
BLAST score	230
E value	6.0e-19
Match length	64
% identity	73
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	397713
Seq. ID	LIB3431-006-P1-K1-C7
Method	BLASTX
NCBI GI	g4325041
BLAST score	241
E value	9.0e-38
Match length	138
% identity	68
NCBI Description	(AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No.	397714
Seq. ID	LIB3431-006-P1-K1-C8
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	7.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397715

Seq. ID	LIB3431-006-P1-K1-C9
Method	BLASTX
NCBI GI	g2493318
BLAST score	219
E value	1.0e-17
Match length	88
% identity	48
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	397716
Seq. ID	LIB3431-006-P1-K1-D1
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	3.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	397717
Seq. ID	LIB3431-006-P1-K1-D10
Method	BLASTX
NCBI GI	g2398853
BLAST score	295
E value	2.0e-26
Match length	151
% identity	40
NCBI Description	(AB004822) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana]

Seq. No.	397718
Seq. ID	LIB3431-006-P1-K1-D11
Method	BLASTX
NCBI GI	g1617197
BLAST score	180
E value	1.0e-21
Match length	73
% identity	77
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	397719
Seq. ID	LIB3431-006-P1-K1-D2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397720
Seq. ID	LIB3431-006-P1-K1-D3
Method	BLASTX

NCBI GI	g4960024
BLAST score	664
E value	8.0e-70
Match length	158
% identity	80
NCBI Description	(AF144079) S-adenosyl-L-methionine:L-methionine S-methyltransferase [Zea mays]

Seq. No.	397721
Seq. ID	LIB3431-006-P1-K1-D4
Method	BLASTX
NCBI GI	g131271
BLAST score	562
E value	8.0e-58
Match length	116
% identity	91
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72705_pir__QJRZ6A photosystem II chlorophyll a-binding protein psbB - rice chloroplast >gi_12013_emb_CAA33973_ (X15901) PSII 47kDa protein [Oryza sativa] >gi_226634_prf__1603356BH photosystem II 47kD protein [Oryza sativa]

Seq. No.	397722
Seq. ID	LIB3431-006-P1-K1-D6
Method	BLASTX
NCBI GI	g4585882
BLAST score	355
E value	1.0e-33
Match length	88
% identity	75
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	397723
Seq. ID	LIB3431-006-P1-K1-D7
Method	BLASTX
NCBI GI	g4996602
BLAST score	173
E value	2.0e-12
Match length	85
% identity	47
NCBI Description	(AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana tabacum]

Seq. No.	397724
Seq. ID	LIB3431-006-P1-K1-E1
Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	397725
Seq. ID	LIB3431-006-P1-K1-E10

Method	BLASTX
NCBI GI	g320618
BLAST score	699
E value	7.0e-74
Match length	151
% identity	89
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	397726
Seq. ID	LIB3431-006-P1-K1-E12
Method	BLASTX
NCBI GI	g320618
BLAST score	432
E value	1.0e-42
Match length	103
% identity	81
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	397727
Seq. ID	LIB3431-006-P1-K1-E4
Method	BLASTX
NCBI GI	g115787
BLAST score	452
E value	6.0e-45
Match length	117
% identity	79
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	397728
Seq. ID	LIB3431-006-P1-K1-E6
Method	BLASTN
NCBI GI	g4079797
BLAST score	61
E value	8.0e-26
Match length	158
% identity	90
NCBI Description	Oryza sativa 23 kDa polypeptide of photosystem II mRNA, complete cds

Seq. No.	397729
Seq. ID	LIB3431-006-P1-K1-E7
Method	BLASTX
NCBI GI	g1651865
BLAST score	160
E value	1.0e-10

Match length 81
% identity 47
NCBI Description (D90900) hypothetical protein [Synechocystis sp.]

Seq. No. 397730
Seq. ID LIB3431-006-P1-K1-E8
Method BLASTX
NCBI GI g3283057
BLAST score 223
E value 3.0e-18
Match length 62
% identity 74
NCBI Description (AF054617) one helix protein [Arabidopsis thaliana]

Seq. No. 397731
Seq. ID LIB3431-006-P1-K1-E9
Method BLASTX
NCBI GI g3036951
BLAST score 712
E value 2.0e-75
Match length 143
% identity 95
NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 397732
Seq. ID LIB3431-006-P1-K1-F1
Method BLASTX
NCBI GI g3126854
BLAST score 692
E value 4.0e-73
Match length 143
% identity 92
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 397733
Seq. ID LIB3431-006-P1-K1-F11
Method BLASTN
NCBI GI g1245217
BLAST score 303
E value 1.0e-170
Match length 324
% identity 98
NCBI Description Oryza sativa subsp. indica large ribosomal RNA gene, chloroplast gene encoding chloroplast rRNA, partial sequence

Seq. No. 397734
Seq. ID LIB3431-006-P1-K1-F12
Method BLASTX
NCBI GI g4206210
BLAST score 310
E value 3.0e-28
Match length 125
% identity 49
NCBI Description (AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium

channel [Arabidopsis thaliana]

Seq. No.	397735
Seq. ID	LIB3431-006-P1-K1-F5
Method	BLASTX
NCBI GI	g4758520
BLAST score	158
E value	2.0e-10
Match length	96
% identity	33
NCBI Description	hect domain and RLD 2 >gi_4079809_gb_AAD08657.1_ (AF071172) HERC2 [Homo sapiens]

Seq. No.	397736
Seq. ID	LIB3431-006-P1-K1-F6
Method	BLASTX
NCBI GI	g115787
BLAST score	576
E value	2.0e-59
Match length	134
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	397737
Seq. ID	LIB3431-006-P1-K1-F7
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	7.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397738
Seq. ID	LIB3431-006-P1-K1-F8
Method	BLASTX
NCBI GI	g131225
BLAST score	549
E value	2.0e-56
Match length	118
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	397739
Seq. ID	LIB3431-006-P1-K1-G10
Method	BLASTN
NCBI GI	g11957
BLAST score	365

E value	0.0e+00
Match length	376
% identity	50
NCBI Description	Rice complete chloroplast genome

Seq. No.	397740
Seq. ID	LIB3431-006-P1-K1-G11
Method	BLASTX
NCBI GI	g3927827
BLAST score	210
E value	1.0e-16
Match length	115
% identity	43
NCBI Description	(AC005727) osmotin-like protein precursor [Arabidopsis thaliana]

Seq. No.	397741
Seq. ID	LIB3431-006-P1-K1-G12
Method	BLASTX
NCBI GI	g4585882
BLAST score	252
E value	1.0e-21
Match length	70
% identity	66
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	397742
Seq. ID	LIB3431-006-P1-K1-G2
Method	BLASTX
NCBI GI	g132105
BLAST score	578
E value	9.0e-60
Match length	127
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397743
Seq. ID	LIB3431-006-P1-K1-G5
Method	BLASTX
NCBI GI	g3789954
BLAST score	797
E value	2.0e-85
Match length	147
% identity	99
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	397744

Seq. ID	LIB3431-006-P1-K1-G6
Method	BLASTX
NCBI GI	g122106
BLAST score	360
E value	2.0e-34
Match length	98
% identity	78
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	397745
Seq. ID	LIB3431-006-P1-K1-G7
Method	BLASTX
NCBI GI	g6006360
BLAST score	636
E value	2.0e-66
Match length	115
% identity	100
NCBI Description	(AP000559) Similar to 1-aminocyclopropane-1-carboxylate synthase (U35779) [Oryza sativa]

Seq. No.	397746
Seq. ID	LIB3431-006-P1-K1-G8
Method	BLASTX
NCBI GI	g2130089
BLAST score	150
E value	2.0e-17
Match length	105
% identity	62
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]

Seq. No.	397747
Seq. ID	LIB3431-006-P1-K1-H1
Method	BLASTX
NCBI GI	g3695005
BLAST score	626
E value	2.0e-65
Match length	138
% identity	88
NCBI Description	(AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2

[Zea mays]

Seq. No.	397748
Seq. ID	LIB3431-006-P1-K1-H10
Method	BLASTX
NCBI GI	g3913804
BLAST score	227
E value	1.0e-18
Match length	80
% identity	61
NCBI Description	HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone [Zea mays]

Seq. No.	397749
Seq. ID	LIB3431-006-P1-K1-H12
Method	BLASTX
NCBI GI	g320618
BLAST score	350
E value	4.0e-33
Match length	76
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	397750
Seq. ID	LIB3431-006-P1-K1-H4
Method	BLASTX
NCBI GI	g2811029
BLAST score	523
E value	3.0e-53
Match length	139
% identity	72
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]

Seq. No.	397751
Seq. ID	LIB3431-006-P1-K1-H5
Method	BLASTX
NCBI GI	g2244847
BLAST score	217
E value	2.0e-17
Match length	96
% identity	46
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	397752
Seq. ID	LIB3431-006-P1-K1-H6
Method	BLASTX
NCBI GI	g4894963
BLAST score	163
E value	2.0e-11

Match length	88
% identity	52
NCBI Description	(AF140553) DNA-binding protein WRKY3 [Avena sativa]

Seq. No.	397753
Seq. ID	LIB3431-006-P1-K1-H7
Method	BLASTX
NCBI GI	g4887618
BLAST score	470
E value	3.0e-47
Match length	86
% identity	100
NCBI Description	(AB007628) homeobox gene [Oryza sativa]

Seq. No.	397754
Seq. ID	LIB3431-006-P1-K1-H8
Method	BLASTX
NCBI GI	g115787
BLAST score	529
E value	5.0e-54
Match length	121
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	397755
Seq. ID	LIB3431-006-P1-K1-H9
Method	BLASTX
NCBI GI	g4105561
BLAST score	436
E value	3.0e-43
Match length	108
% identity	83
NCBI Description	(AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No.	397756
Seq. ID	LIB3431-007-P1-K1-A1
Method	BLASTN
NCBI GI	g487321
BLAST score	128
E value	7.0e-66
Match length	188
% identity	93
NCBI Description	Rice mRNA EN77, partial sequence

Seq. No.	397757
Seq. ID	LIB3431-007-P1-K1-A11
Method	BLASTX
NCBI GI	g4972118
BLAST score	238
E value	7.0e-20
Match length	139
% identity	41
NCBI Description	(AL078579) putative protein [Arabidopsis thaliana]

Seq. No.	397758
Seq. ID	LIB3431-007-P1-K1-A5
Method	BLASTX
NCBI GI	g2244818
BLAST score	314
E value	4.0e-29
Match length	91
% identity	63
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397759
Seq. ID	LIB3431-007-P1-K1-A8
Method	BLASTX
NCBI GI	g4538992
BLAST score	163
E value	4.0e-11
Match length	50
% identity	58
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	397760
Seq. ID	LIB3431-007-P1-K1-B1
Method	BLASTN
NCBI GI	g218160
BLAST score	251
E value	1.0e-139
Match length	251
% identity	100
NCBI Description	Oryza sativa mRNA for elongation factor 1 beta'

Seq. No.	397761
Seq. ID	LIB3431-007-P1-K1-B11
Method	BLASTX
NCBI GI	g132105
BLAST score	600
E value	2.0e-62
Match length	129
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397762
Seq. ID	LIB3431-007-P1-K1-B4
Method	BLASTX
NCBI GI	g1168195
BLAST score	209
E value	6.0e-17
Match length	65
% identity	63

NCBI Description	14-3-3-LIKE PROTEIN >gi_478595_pir__S20580 protein kinase C inhibitor homolog - Hooker's evening primrose >gi_20062_emb_CAA44642_ (X62838) protein kinase C inhibitor homologue [Oenothera elata subsp. hookeri]
Seq. No.	397763
Seq. ID	LIB3431-007-P1-K1-B6
Method	BLASTX
NCBI GI	g132105
BLAST score	638
E value	9.0e-67
Match length	139
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	397764
Seq. ID	LIB3431-007-P1-K1-B7
Method	BLASTX
NCBI GI	g4587615
BLAST score	201
E value	1.0e-15
Match length	52
% identity	71
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]
Seq. No.	397765
Seq. ID	LIB3431-007-P1-K1-B8
Method	BLASTX
NCBI GI	g3789952
BLAST score	557
E value	3.0e-57
Match length	106
% identity	96
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]
Seq. No.	397766
Seq. ID	LIB3431-007-P1-K1-B9
Method	BLASTX
NCBI GI	g3023947
BLAST score	350
E value	2.0e-33
Match length	92
% identity	64
NCBI Description	PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi_2665840 (AF035815) putative histone deacetylase RPD3 [Zea mays]

Seq. No.	397767
Seq. ID	LIB3431-007-P1-K1-C11
Method	BLASTX
NCBI GI	g4580470
BLAST score	159
E value	1.0e-10
Match length	40
% identity	70
NCBI Description	(AC006081) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397768
Seq. ID	LIB3431-007-P1-K1-C12
Method	BLASTX
NCBI GI	g4966352
BLAST score	249
E value	1.0e-21
Match length	73
% identity	67
NCBI Description	(AC006341) >F3O9.11 [Arabidopsis thaliana]

Seq. No.	397769
Seq. ID	LIB3431-007-P1-K1-C4
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	7.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397770
Seq. ID	LIB3431-007-P1-K1-C7
Method	BLASTX
NCBI GI	g3914470
BLAST score	448
E value	1.0e-44
Match length	122
% identity	70
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_1321868_emb_CAA66373_ (X97771) 10kD PSII protein [Hordeum vulgare]

Seq. No.	397771
Seq. ID	LIB3431-007-P1-K1-C8
Method	BLASTN
NCBI GI	g3075487
BLAST score	190
E value	1.0e-103
Match length	194
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	397772
Seq. ID	LIB3431-007-P1-K1-D1

Method	BLASTX
NCBI GI	g3126854
BLAST score	512
E value	1.0e-62
Match length	123
% identity	98
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	397773
Seq. ID	LIB3431-007-P1-K1-D11
Method	BLASTX
NCBI GI	g6015059
BLAST score	825
E value	1.0e-88
Match length	156
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096 (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	397774
Seq. ID	LIB3431-007-P1-K1-D3
Method	BLASTX
NCBI GI	g22240
BLAST score	727
E value	3.0e-77
Match length	145
% identity	97
NCBI Description	(X07157) GADPH (383 AA) [Zea mays]

Seq. No.	397775
Seq. ID	LIB3431-007-P1-K1-D4
Method	BLASTN
NCBI GI	g2570516
BLAST score	383
E value	0.0e+00
Match length	430
% identity	97
NCBI Description	Oryza sativa thioredoxin F isoform mRNA, complete cds

Seq. No.	397776
Seq. ID	LIB3431-007-P1-K1-D6
Method	BLASTX
NCBI GI	g3885888
BLAST score	282
E value	5.0e-25
Match length	100
% identity	63
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	397777
Seq. ID	LIB3431-007-P1-K1-D8
Method	BLASTX
NCBI GI	g3668080
BLAST score	498
E value	2.0e-50
Match length	135

% identity	66
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	397778
Seq. ID	LIB3431-007-P1-K1-D9
Method	BLASTX
NCBI GI	g3789954
BLAST score	672
E value	9.0e-71
Match length	124
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	397779
Seq. ID	LIB3431-007-P1-K1-E1
Method	BLASTX
NCBI GI	g4582468
BLAST score	525
E value	2.0e-53
Match length	115
% identity	92
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	397780
Seq. ID	LIB3431-007-P1-K1-E10
Method	BLASTX
NCBI GI	g132105
BLAST score	503
E value	4.0e-51
Match length	124
% identity	79
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397781
Seq. ID	LIB3431-007-P1-K1-E11
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397782
Seq. ID	LIB3431-007-P1-K1-E12

Method	BLASTX
NCBI GI	g3643608
BLAST score	205
E value	5.0e-16
Match length	81
% identity	47
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana] >gi_4874312_gb_AAD31374.1_AC006053_16 (AC006053) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397783
Seq. ID	LIB3431-007-P1-K1-E3
Method	BLASTX
NCBI GI	g134595
BLAST score	475
E value	1.0e-47
Match length	89
% identity	99
NCBI Description	SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir__S22508 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic copper/zinc-superoxide dismutase [Oryza sativa] >gi_1096504_prf__2111424A Cu/Zn superoxide dismutase [Oryza sativa]

Seq. No.	397784
Seq. ID	LIB3431-007-P1-K1-E7
Method	BLASTN
NCBI GI	g20262
BLAST score	65
E value	2.0e-28
Match length	117
% identity	89
NCBI Description	O.sativa light-induced mRNA

Seq. No.	397785
Seq. ID	LIB3431-007-P1-K1-E8
Method	BLASTX
NCBI GI	g3345477
BLAST score	500
E value	1.0e-50
Match length	142
% identity	70
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	397786
Seq. ID	LIB3431-007-P1-K1-E9
Method	BLASTX
NCBI GI	g3413700
BLAST score	367
E value	4.0e-35
Match length	114
% identity	68
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No. 397787

Seq. ID	LIB3431-007-P1-K1-F1
Method	BLASTX
NCBI GI	g2346966
BLAST score	153
E value	7.0e-10
Match length	57
% identity	54
NCBI Description	(AB004871) CPC [Arabidopsis thaliana] >gi_4559383_gb_AAD23043.1_AC006526_8 (AC006526) putative DNA binding protein CPC [Arabidopsis thaliana]

Seq. No.	397788
Seq. ID	LIB3431-007-P1-K1-F10
Method	BLASTX
NCBI GI	g870794
BLAST score	159
E value	1.0e-20
Match length	79
% identity	14
NCBI Description	(L05917) polyubiquitin [Arabidopsis thaliana]

Seq. No.	397789
Seq. ID	LIB3431-007-P1-K1-F12
Method	BLASTX
NCBI GI	g4585979
BLAST score	156
E value	2.0e-10
Match length	68
% identity	49
NCBI Description	(AC005287) Similar to ABC-transporter atp-binding protein [Arabidopsis thaliana]

Seq. No.	397790
Seq. ID	LIB3431-007-P1-K1-F2
Method	BLASTX
NCBI GI	g1617036
BLAST score	414
E value	1.0e-40
Match length	101
% identity	74
NCBI Description	(Y08624) Ted2 [Vigna unguiculata]

Seq. No.	397791
Seq. ID	LIB3431-007-P1-K1-F7
Method	BLASTX
NCBI GI	g5733882
BLAST score	269
E value	2.0e-23
Match length	109
% identity	53
NCBI Description	(AC007932) Similar to gb_Y12465 serine/threonine kinase from Sorghum bicolor and contains a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No.	397792
Seq. ID	LIB3431-007-P1-K1-F8
Method	BLASTX

NCBI GI	g3608137
BLAST score	176
E value	1.0e-12
Match length	90
% identity	42
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	397793
Seq. ID	LIB3431-007-P1-K1-G1
Method	BLASTX
NCBI GI	g2407281
BLAST score	495
E value	3.0e-50
Match length	89
% identity	100
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	397794
Seq. ID	LIB3431-007-P1-K1-G10
Method	BLASTX
NCBI GI	g6063542
BLAST score	685
E value	3.0e-72
Match length	155
% identity	88
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No.	397795
Seq. ID	LIB3431-007-P1-K1-G11
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	4.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397796
Seq. ID	LIB3431-007-P1-K1-G12
Method	BLASTX
NCBI GI	g1352200
BLAST score	473
E value	1.0e-47
Match length	105
% identity	82
NCBI Description	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, CHLOROPLAST PRECURSOR (CTPT) >gi_480909_pir__S37497 triose phosphate/3-phosphoglycerate/phosphate translocator - maize >gi_405635_emb_CAA81349_ (Z26595) triose phosphate/phosphate translocator [Zea mays]

Seq. No.	397797

Seq. ID	LIB3431-007-P1-K1-G4
Method	BLASTN
NCBI GI	g169818
BLAST score	103
E value	3.0e-51
Match length	114
% identity	98
NCBI Description	Rice 25S ribosomal RNA gene

Seq. No.	397798
Seq. ID	LIB3431-007-P1-K1-G5
Method	BLASTX
NCBI GI	g733454
BLAST score	251
E value	6.0e-22
Match length	67
% identity	75
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	397799
Seq. ID	LIB3431-007-P1-K1-G6
Method	BLASTX
NCBI GI	g2624326
BLAST score	431
E value	1.0e-42
Match length	87
% identity	98
NCBI Description	(AJ002893) OsGRP1 [Oryza sativa]

Seq. No.	397800
Seq. ID	LIB3431-007-P1-K1-G8
Method	BLASTX
NCBI GI	g1076660
BLAST score	334
E value	4.0e-31
Match length	123
% identity	60
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	397801
Seq. ID	LIB3431-007-P1-K1-H1
Method	BLASTX
NCBI GI	g417260
BLAST score	280
E value	7.0e-25
Match length	73
% identity	70
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	397802
Seq. ID	LIB3431-007-P1-K1-H2

Method	BLASTX
NCBI GI	g132105
BLAST score	462
E value	2.0e-51
Match length	125
% identity	83
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397803
Seq. ID	LIB3431-007-P1-K1-H4
Method	BLASTX
NCBI GI	g132105
BLAST score	606
E value	4.0e-63
Match length	110
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397804
Seq. ID	LIB3431-007-P1-K1-H7
Method	BLASTN
NCBI GI	g3075487
BLAST score	96
E value	2.0e-46
Match length	116
% identity	96
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	397805
Seq. ID	LIB3431-007-P1-N1-A7
Method	BLASTN
NCBI GI	g14352
BLAST score	37
E value	2.0e-11
Match length	73
% identity	88
NCBI Description	N.plumbaginifolia chloroplast 16SrDNA, trnV and trnI genes for 16S ribosomal RNA, transfer RNA-Val and transfer RNA-Ile (5'exon)

Seq. No.	397806
Seq. ID	LIB3431-007-P1-N1-B1
Method	BLASTN
NCBI GI	g218160
BLAST score	239
E value	1.0e-132
Match length	251
% identity	99
NCBI Description	Oryza sativa mRNA for elongation factor 1 beta'

Seq. No.	397807
Seq. ID	LIB3431-007-P1-N1-B12
Method	BLASTN
NCBI GI	g218207
BLAST score	187
E value	1.0e-101
Match length	223
% identity	96
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397808
Seq. ID	LIB3431-007-P1-N1-B2
Method	BLASTN
NCBI GI	g19086
BLAST score	47
E value	2.0e-17
Match length	79
% identity	90
NCBI Description	Hordeum vulgare pot. psaE mRNA

Seq. No.	397809
Seq. ID	LIB3431-007-P1-N1-B6
Method	BLASTN
NCBI GI	g218207
BLAST score	294
E value	1.0e-164
Match length	302
% identity	99
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397810
Seq. ID	LIB3431-007-P1-N1-B8
Method	BLASTN
NCBI GI	g3789951
BLAST score	186
E value	1.0e-100
Match length	247
% identity	98
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	397811

Seq. ID	LIB3431-007-P1-N1-C3
Method	BLASTN
NCBI GI	g2072554
BLAST score	203
E value	1.0e-110
Match length	203
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397812
Seq. ID	LIB3431-007-P1-N1-C4
Method	BLASTN
NCBI GI	g2072554
BLAST score	268
E value	1.0e-149
Match length	268
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397813
Seq. ID	LIB3431-007-P1-N1-C6
Method	BLASTX
NCBI GI	g729478
BLAST score	170
E value	3.0e-12
Match length	45
% identity	67
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	397814
Seq. ID	LIB3431-007-P1-N1-C8
Method	BLASTX
NCBI GI	g3075488
BLAST score	164
E value	2.0e-11
Match length	32
% identity	94
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	397815
Seq. ID	LIB3431-007-P1-N1-D12
Method	BLASTX
NCBI GI	g6015059
BLAST score	268
E value	1.0e-23
Match length	52
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096 (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	397816
Seq. ID	LIB3431-007-P1-N1-D2
Method	BLASTN
NCBI GI	g2306980
BLAST score	218
E value	1.0e-119
Match length	259
% identity	96
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	397817
Seq. ID	LIB3431-007-P1-N1-D4
Method	BLASTX
NCBI GI	g267120
BLAST score	262
E value	5.0e-23
Match length	63
% identity	83
NCBI Description	THIOREDOXIN F-TYPE, CHLOROPLAST PRECURSOR (TRX-F) >gi_100070_pir__S20929 thioredoxin f precursor - garden pea >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum sativum] >gi_1388086 (U35830) thioredoxin f [Pisum sativum]

Seq. No.	397818
Seq. ID	LIB3431-007-P1-N1-D6
Method	BLASTN
NCBI GI	g3885887
BLAST score	318
E value	1.0e-179
Match length	330
% identity	99
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	397819
Seq. ID	LIB3431-007-P1-N1-D9
Method	BLASTN
NCBI GI	g3789953
BLAST score	284
E value	1.0e-158
Match length	296
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	397820
Seq. ID	LIB3431-007-P1-N1-E10
Method	BLASTN
NCBI GI	g218207
BLAST score	299
E value	1.0e-167
Match length	307
% identity	99
NCBI Description	Oryza sativa mRNA for the small subunit of

	ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139
Seq. No.	397821
Seq. ID	LIB3431-007-P1-N1-E12
Method	BLASTN
NCBI GI	g2072554
BLAST score	292
E value	1.0e-163
Match length	304
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds
Seq. No.	397822
Seq. ID	LIB3431-007-P1-N1-E3
Method	BLASTN
NCBI GI	g685241
BLAST score	259
E value	1.0e-144
Match length	309
% identity	97
NCBI Description	Oryza sativa cytosolic copper/zinc-superoxide dismutase (SodCc1) gene, complete cds
Seq. No.	397823
Seq. ID	LIB3431-007-P1-N1-E7
Method	BLASTN
NCBI GI	g20262
BLAST score	240
E value	1.0e-132
Match length	252
% identity	99
NCBI Description	O.sativa light-induced mRNA
Seq. No.	397824
Seq. ID	LIB3431-007-P1-N1-E8
Method	BLASTX
NCBI GI	g517500
BLAST score	152
E value	3.0e-10
Match length	54
% identity	61
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]
Seq. No.	397825
Seq. ID	LIB3431-007-P1-N1-F1
Method	BLASTX
NCBI GI	g2191152
BLAST score	253
E value	1.0e-21
Match length	76
% identity	61
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	397826
Seq. ID	LIB3431-007-P1-N1-F3
Method	BLASTX
NCBI GI	g132105
BLAST score	160
E value	5.0e-15
Match length	47
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397827
Seq. ID	LIB3431-007-P1-N1-G1
Method	BLASTX
NCBI GI	g671740
BLAST score	294
E value	8.0e-27
Match length	56
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397828
Seq. ID	LIB3431-007-P1-N1-G10
Method	BLASTX
NCBI GI	g6063542
BLAST score	224
E value	2.0e-18
Match length	40
% identity	100
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No.	397829
Seq. ID	LIB3431-007-P1-N1-G11
Method	BLASTN
NCBI GI	g405634
BLAST score	44
E value	2.0e-15
Match length	64
% identity	92
NCBI Description	Z.mays zmcpt mRNA triose phosphate/phosphate translocator

Seq. No.	397830
Seq. ID	LIB3431-007-P1-N1-G12
Method	BLASTN
NCBI GI	g2072554
BLAST score	150

E value	7.0e-79
Match length	230
% identity	91
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397831
Seq. ID	LIB3431-007-P1-N1-G2
Method	BLASTN
NCBI GI	g600766
BLAST score	145
E value	7.0e-76
Match length	273
% identity	88
NCBI Description	Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds

Seq. No.	397832
Seq. ID	LIB3431-007-P1-N1-G5
Method	BLASTX
NCBI GI	g733454
BLAST score	326
E value	3.0e-30
Match length	69
% identity	93
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	397833
Seq. ID	LIB3431-007-P1-N1-G6
Method	BLASTN
NCBI GI	g2624325
BLAST score	248
E value	1.0e-137
Match length	270
% identity	99
NCBI Description	Oryza sativa mRNA for glycine-rich RNA-binding protein (OsGRP1)

Seq. No.	397834
Seq. ID	LIB3431-007-P1-N1-H1
Method	BLASTN
NCBI GI	g20262
BLAST score	343
E value	0.0e+00
Match length	343
% identity	100
NCBI Description	O.sativa light-induced mRNA

Seq. No.	397835
Seq. ID	LIB3431-007-P1-N1-H2
Method	BLASTX
NCBI GI	g347451
BLAST score	202
E value	8.0e-16
Match length	38
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza

09604805.1-050705

	sativa]
Seq. No.	397836
Seq. ID	LIB3431-007-P1-N1-H6
Method	BLASTN
NCBI GI	g6006355
BLAST score	316
E value	1.0e-177
Match length	319
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.	397837
Seq. ID	LIB3431-007-P1-N1-H7
Method	BLASTN
NCBI GI	g3885889
BLAST score	242
E value	1.0e-133
Match length	314
% identity	94
NCBI Description	Oryza sativa histone H3 mRNA, complete cds
Seq. No.	397838
Seq. ID	LIB3431-008-P1-K1-A10
Method	BLASTX
NCBI GI	g115794
BLAST score	363
E value	5.0e-35
Match length	76
% identity	92
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]
Seq. No.	397839
Seq. ID	LIB3431-008-P1-K1-A12
Method	BLASTX
NCBI GI	g5230785
BLAST score	185
E value	7.0e-14
Match length	51
% identity	67
NCBI Description	(AF107024) histone H1 WH1B.1 [Triticum aestivum]
Seq. No.	397840
Seq. ID	LIB3431-008-P1-K1-A2
Method	BLASTX
NCBI GI	g1881585
BLAST score	217
E value	2.0e-17
Match length	114
% identity	47
NCBI Description	(U72489) remorin [Solanum tuberosum]
Seq. No.	397841

Seq. ID	LIB3431-008-P1-K1-A3
Method	BLASTX
NCBI GI	g3885882
BLAST score	585
E value	1.0e-60
Match length	134
% identity	84
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No.	397842
Seq. ID	LIB3431-008-P1-K1-A4
Method	BLASTX
NCBI GI	g5478530
BLAST score	605
E value	7.0e-63
Match length	153
% identity	17
NCBI Description	(AF130441) UVB-resistance protein UVR8 [Arabidopsis thaliana]

Seq. No.	397843
Seq. ID	LIB3431-008-P1-K1-A8
Method	BLASTX
NCBI GI	g3036949
BLAST score	331
E value	4.0e-31
Match length	63
% identity	100
NCBI Description	(AB012638) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	397844
Seq. ID	LIB3431-008-P1-K1-B11
Method	BLASTX
NCBI GI	g3063524
BLAST score	172
E value	1.0e-12
Match length	54
% identity	65
NCBI Description	(AF052305) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	397845
Seq. ID	LIB3431-008-P1-K1-B12
Method	BLASTX
NCBI GI	g115794
BLAST score	658
E value	4.0e-69
Match length	142
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No.	397846

Seq. ID	LIB3431-008-P1-K1-B2
Method	BLASTX
NCBI GI	g4588906
BLAST score	525
E value	2.0e-53
Match length	121
% identity	90
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	397847
Seq. ID	LIB3431-008-P1-K1-B4
Method	BLASTX
NCBI GI	g132096
BLAST score	205
E value	1.0e-16
Match length	45
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_ (D00644) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa]

Seq. No.	397848
Seq. ID	LIB3431-008-P1-K1-B7
Method	BLASTX
NCBI GI	g2924785
BLAST score	158
E value	2.0e-10
Match length	93
% identity	38
NCBI Description	(AC002334) similar to disease resistance protein [Arabidopsis thaliana]

Seq. No.	397849
Seq. ID	LIB3431-008-P1-K1-B8
Method	BLASTX
NCBI GI	g132105
BLAST score	268
E value	1.0e-23
Match length	76
% identity	74
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397850
Seq. ID	LIB3431-008-P1-K1-C10
Method	BLASTX
NCBI GI	g3885886

BLAST score	532
E value	2.0e-54
Match length	104
% identity	99
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.	397851
Seq. ID	LIB3431-008-P1-K1-C12
Method	BLASTX
NCBI GI	g4585882
BLAST score	533
E value	2.0e-54
Match length	143
% identity	72
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	397852
Seq. ID	LIB3431-008-P1-K1-C2
Method	BLASTX
NCBI GI	g2598049
BLAST score	425
E value	8.0e-42
Match length	110
% identity	74
NCBI Description	(Y15269) chloroplast drought-induced stress protein, 34 kD) [Solanum tuberosum]

Seq. No.	397853
Seq. ID	LIB3431-008-P1-K1-C4
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397854
Seq. ID	LIB3431-008-P1-K1-C5
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	2.0e-10
Match length	35
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	397855
Seq. ID	LIB3431-008-P1-K1-C7
Method	BLASTX
NCBI GI	g132105
BLAST score	759
E value	6.0e-81
Match length	139

% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	397856
Seq. ID	LIB3431-008-P1-K1-C8
Method	BLASTX
NCBI GI	g833835
BLAST score	184
E value	3.0e-14
Match length	58
% identity	57
NCBI Description	(U26025) amygdalin hydrolase isoform AH I precursor [Prunus serotina]
Seq. No.	397857
Seq. ID	LIB3431-008-P1-K1-D1
Method	BLASTX
NCBI GI	g3461848
BLAST score	621
E value	8.0e-65
Match length	147
% identity	79
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]
Seq. No.	397858
Seq. ID	LIB3431-008-P1-K1-D10
Method	BLASTX
NCBI GI	g2832661
BLAST score	176
E value	5.0e-13
Match length	78
% identity	54
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]
Seq. No.	397859
Seq. ID	LIB3431-008-P1-K1-D11
Method	BLASTX
NCBI GI	g729668
BLAST score	249
E value	3.0e-21
Match length	79
% identity	58
NCBI Description	HISTONE H1 >gi_2147479_pir__S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.	397860
Seq. ID	LIB3431-008-P1-K1-D2

Method	BLASTN
NCBI GI	g11957
BLAST score	106
E value	8.0e-53
Match length	110
% identity	99
NCBI Description	Rice complete chloroplast genome

Seq. No.	397861
Seq. ID	LIB3431-008-P1-K1-D3
Method	BLASTN
NCBI GI	g3618309
BLAST score	73
E value	9.0e-33
Match length	73
% identity	100
NCBI Description	Oryza sativa mRNA for zinc finger protein, complete cds, clone:E10707

Seq. No.	397862
Seq. ID	LIB3431-008-P1-K1-D4
Method	BLASTN
NCBI GI	g20262
BLAST score	72
E value	1.0e-32
Match length	87
% identity	95
NCBI Description	O.sativa light-induced mRNA

Seq. No.	397863
Seq. ID	LIB3431-008-P1-K1-D5
Method	BLASTX
NCBI GI	g3914535
BLAST score	270
E value	6.0e-24
Match length	59
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_ (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No.	397864
Seq. ID	LIB3431-008-P1-K1-D6
Method	BLASTX
NCBI GI	g132105
BLAST score	448
E value	1.0e-44
Match length	100
% identity	82
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397865
Seq. ID	LIB3431-008-P1-K1-E1
Method	BLASTX
NCBI GI	g267196
BLAST score	265
E value	1.0e-23
Match length	69
% identity	72
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_66574_pir__YUPOY ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - potato >gi_21471_emb_CAA41359_ (X58453) glycogen (starch) synthase [Solanum tuberosum]

Seq. No.	397866
Seq. ID	LIB3431-008-P1-K1-E10
Method	BLASTN
NCBI GI	g2570512
BLAST score	94
E value	1.0e-45
Match length	106
% identity	97
NCBI Description	Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No.	397867
Seq. ID	LIB3431-008-P1-K1-E11
Method	BLASTX
NCBI GI	g3789948
BLAST score	225
E value	8.0e-19
Match length	45
% identity	93
NCBI Description	(AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No.	397868
Seq. ID	LIB3431-008-P1-K1-E2
Method	BLASTX
NCBI GI	g2407281
BLAST score	711
E value	2.0e-75
Match length	135
% identity	98
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	397869
Seq. ID	LIB3431-008-P1-K1-E6
Method	BLASTX
NCBI GI	g2459417
BLAST score	304
E value	1.0e-27
Match length	79
% identity	70
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	397870
Seq. ID	LIB3431-008-P1-K1-E7
Method	BLASTX
NCBI GI	g671740
BLAST score	547
E value	4.0e-56
Match length	101
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397871
Seq. ID	LIB3431-008-P1-K1-E8
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	1.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	397872
Seq. ID	LIB3431-008-P1-K1-E9
Method	BLASTX
NCBI GI	g3550982
BLAST score	158
E value	1.0e-10
Match length	71
% identity	51
NCBI Description	(AB010690) mutM homologue-1 [Arabidopsis thaliana] >gi_5903053_gb_AAD55612.1_AC008016_22 (AC008016) Identical to gb_AB010690 mutM homologue-1 (formamidopyrimidine-DNA glycosylase 1) from Arabidopsis thaliana. EST gb_Z18192 comes from this gene

Seq. No.	397873
Seq. ID	LIB3431-008-P1-K1-F1
Method	BLASTN
NCBI GI	g20181
BLAST score	81
E value	1.0e-37
Match length	173
% identity	87
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	397874
Seq. ID	LIB3431-008-P1-K1-F10
Method	BLASTN
NCBI GI	g3789949
BLAST score	40
E value	2.0e-13
Match length	64
% identity	91
NCBI Description	Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No.	397875
Seq. ID	LIB3431-008-P1-K1-F11
Method	BLASTX
NCBI GI	g4544408
BLAST score	366
E value	5.0e-35
Match length	89
% identity	74
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	397876
Seq. ID	LIB3431-008-P1-K1-F12
Method	BLASTX
NCBI GI	g3885894
BLAST score	483
E value	8.0e-49
Match length	135
% identity	76
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No.	397877
Seq. ID	LIB3431-008-P1-K1-F2
Method	BLASTX
NCBI GI	g2570515
BLAST score	535
E value	1.0e-54
Match length	120
% identity	88
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	397878
Seq. ID	LIB3431-008-P1-K1-F3
Method	BLASTX
NCBI GI	g3023816
BLAST score	435
E value	4.0e-43
Match length	112
% identity	79
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	397879
Seq. ID	LIB3431-008-P1-K1-F4
Method	BLASTX
NCBI GI	g462013
BLAST score	156
E value	1.0e-10
Match length	40
% identity	78
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	397880
Seq. ID	LIB3431-008-P1-K1-F6

Method	BLASTX
NCBI GI	g2129472
BLAST score	147
E value	7.0e-10
Match length	42
% identity	67
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi_1100225 (L32561) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No.	397881
Seq. ID	LIB3431-008-P1-K1-G12
Method	BLASTX
NCBI GI	g2444271
BLAST score	506
E value	3.0e-51
Match length	153
% identity	60
NCBI Description	(AF019637) putative amino acid or GABA permease [Arabidopsis thaliana]

Seq. No.	397882
Seq. ID	LIB3431-008-P1-K1-G2
Method	BLASTX
NCBI GI	g2072555
BLAST score	208
E value	2.0e-16
Match length	39
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397883
Seq. ID	LIB3431-008-P1-K1-G4
Method	BLASTX
NCBI GI	g115787
BLAST score	276
E value	1.0e-24
Match length	73
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	397884
Seq. ID	LIB3431-008-P1-K1-G6
Method	BLASTX
NCBI GI	g2660669
BLAST score	174
E value	2.0e-12
Match length	76
% identity	53
NCBI Description	(AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]

Seq. No.	397885
Seq. ID	LIB3431-008-P1-K1-G8
Method	BLASTN
NCBI GI	g6015437
BLAST score	38
E value	8.0e-13
Match length	48
% identity	66
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	397886
Seq. ID	LIB3431-008-P1-K1-G9
Method	BLASTX
NCBI GI	g2570511
BLAST score	305
E value	3.0e-28
Match length	63
% identity	92
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	397887
Seq. ID	LIB3431-008-P1-K1-H10
Method	BLASTN
NCBI GI	g1184775
BLAST score	42
E value	3.0e-14
Match length	70
% identity	90
NCBI Description	Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4 (gpc4) mRNA, complete cds

Seq. No.	397888
Seq. ID	LIB3431-008-P1-K1-H11
Method	BLASTX
NCBI GI	g2570511
BLAST score	653
E value	3.0e-68
Match length	135
% identity	96
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	397889
Seq. ID	LIB3431-008-P1-K1-H12
Method	BLASTN
NCBI GI	g3868757
BLAST score	44
E value	2.0e-15
Match length	52
% identity	96
NCBI Description	Oryza sativa mRNA for elongation factor 1B gamma, complete cds

Seq. No.	397890
Seq. ID	LIB3431-008-P1-K1-H2
Method	BLASTN
NCBI GI	g1245938

BLAST score	35
E value	2.0e-10
Match length	35
% identity	100
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	397891
Seq. ID	LIB3431-008-P1-K1-H3
Method	BLASTX
NCBI GI	g3789952
BLAST score	638
E value	9.0e-67
Match length	128
% identity	97
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	397892
Seq. ID	LIB3431-008-P1-K1-H4
Method	BLASTX
NCBI GI	g4322327
BLAST score	270
E value	1.0e-23
Match length	92
% identity	53
NCBI Description	(AF080545) peptide transporter [Nepenthes alata]

Seq. No.	397893
Seq. ID	LIB3431-008-P1-K1-H5
Method	BLASTN
NCBI GI	g5748493
BLAST score	37
E value	2.0e-11
Match length	49
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSA project)

Seq. No.	397894
Seq. ID	LIB3431-008-P1-K1-H6
Method	BLASTX
NCBI GI	g3868758
BLAST score	457
E value	4.0e-54
Match length	123
% identity	90
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	397895
Seq. ID	LIB3431-008-P1-K1-H8
Method	BLASTX
NCBI GI	g548605
BLAST score	519
E value	7.0e-53
Match length	114
% identity	90

NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]
Seq. No.	397896
Seq. ID	LIB3431-008-P1-K1-H9
Method	BLASTX
NCBI GI	g4567263
BLAST score	275
E value	3.0e-24
Match length	124
% identity	52
NCBI Description	(AC006841) putative cell division inhibitor [Arabidopsis thaliana]
Seq. No.	397897
Seq. ID	LIB3431-008-P1-N1-A10
Method	BLASTN
NCBI GI	g2570510
BLAST score	265
E value	1.0e-147
Match length	285
% identity	99
NCBI Description	Oryza sativa chlorophyll a-b binding protein mRNA, complete cds
Seq. No.	397898
Seq. ID	LIB3431-008-P1-N1-A11
Method	BLASTN
NCBI GI	g218209
BLAST score	233
E value	1.0e-128
Match length	333
% identity	93
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106
Seq. No.	397899
Seq. ID	LIB3431-008-P1-N1-A3
Method	BLASTN
NCBI GI	g3885881
BLAST score	233
E value	1.0e-128
Match length	273
% identity	96
NCBI Description	Oryza sativa inorganic pyrophosphatase (IPP) mRNA, complete cds
Seq. No.	397900
Seq. ID	LIB3431-008-P1-N1-A5
Method	BLASTN
NCBI GI	g2331130
BLAST score	134
E value	2.0e-69

Match length	174
% identity	94
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No.	397901
Seq. ID	LIB3431-008-P1-N1-A9
Method	BLASTX
NCBI GI	g671740
BLAST score	175
E value	5.0e-13
Match length	38
% identity	87
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397902
Seq. ID	LIB3431-008-P1-N1-B1
Method	BLASTX
NCBI GI	g1350821
BLAST score	221
E value	5.0e-18
Match length	55
% identity	75
NCBI Description	31 KD RIBONUCLEOPROTEIN, CHLOROPLAST PRECURSOR >gi_280403_pir__S26204 RNA-binding protein 31 - curled-leaved tobacco >gi_19710_emb_CAA46233_ (X65117) RNA binding protein 31 [Nicotiana plumbaginifolia]

Seq. No.	397903
Seq. ID	LIB3431-008-P1-N1-B11
Method	BLASTX
NCBI GI	g132105
BLAST score	169
E value	6.0e-12
Match length	32
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397904
Seq. ID	LIB3431-008-P1-N1-B12
Method	BLASTX
NCBI GI	g4689380
BLAST score	236
E value	6.0e-20
Match length	55
% identity	84
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]

Seq. No.	397905
Seq. ID	LIB3431-008-P1-N1-B2
Method	BLASTX
NCBI GI	g4588906
BLAST score	278
E value	1.0e-24
Match length	67
% identity	76
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	397906
Seq. ID	LIB3431-008-P1-N1-B4
Method	BLASTX
NCBI GI	g347451
BLAST score	380
E value	8.0e-37
Match length	69
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	397907
Seq. ID	LIB3431-008-P1-N1-B5
Method	BLASTX
NCBI GI	g4996602
BLAST score	268
E value	2.0e-23
Match length	71
% identity	75
NCBI Description	(AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana tabacum]

Seq. No.	397908
Seq. ID	LIB3431-008-P1-N1-B6
Method	BLASTX
NCBI GI	g4220517
BLAST score	227
E value	8.0e-19
Match length	68
% identity	59
NCBI Description	(AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No.	397909
Seq. ID	LIB3431-008-P1-N1-B8
Method	BLASTN
NCBI GI	g218207
BLAST score	326
E value	0.0e+00
Match length	333
% identity	100
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397910
Seq. ID	LIB3431-008-P1-N1-B9

Method	BLASTX
NCBI GI	g2864617
BLAST score	240
E value	4.0e-20
Match length	75
% identity	67
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1_ (AJ245574) ATP synthase beta chain precursor (subunit II) [Arabidopsis thaliana]

Seq. No.	397911
Seq. ID	LIB3431-008-P1-N1-C10
Method	BLASTN
NCBI GI	g3885885
BLAST score	171
E value	2.0e-91
Match length	186
% identity	98
NCBI Description	Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA, complete cds

Seq. No.	397912
Seq. ID	LIB3431-008-P1-N1-C2
Method	BLASTX
NCBI GI	g2598049
BLAST score	276
E value	2.0e-24
Match length	79
% identity	66
NCBI Description	(Y15269) chloroplast drought-induced stress protein, 34 kD) [Solanum tuberosum]

Seq. No.	397913
Seq. ID	LIB3431-008-P1-N1-C4
Method	BLASTN
NCBI GI	g2072554
BLAST score	284
E value	1.0e-158
Match length	284
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397914
Seq. ID	LIB3431-008-P1-N1-C6
Method	BLASTX
NCBI GI	g3914685
BLAST score	219
E value	1.0e-17
Match length	58
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal protein L17 [Zea mays]

Seq. No.	397915
Seq. ID	LIB3431-008-P1-N1-C7

Method	BLASTX
NCBI GI	g671740
BLAST score	248
E value	4.0e-21
Match length	50
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397916
Seq. ID	LIB3431-008-P1-N1-D2
Method	BLASTN
NCBI GI	g11957
BLAST score	321
E value	0.0e+00
Match length	329
% identity	99
NCBI Description	Rice complete chloroplast genome

Seq. No.	397917
Seq. ID	LIB3431-008-P1-N1-D3
Method	BLASTN
NCBI GI	g3618309
BLAST score	306
E value	1.0e-172
Match length	306
% identity	100
NCBI Description	Oryza sativa mRNA for zinc finger protein, complete cds, clone:E10707

Seq. No.	397918
Seq. ID	LIB3431-008-P1-N1-D4
Method	BLASTN
NCBI GI	g20262
BLAST score	343
E value	0.0e+00
Match length	355
% identity	99
NCBI Description	O.sativa light-induced mRNA

Seq. No.	397919
Seq. ID	LIB3431-008-P1-N1-D6
Method	BLASTX
NCBI GI	g671740
BLAST score	159
E value	8.0e-11
Match length	30
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397920
Seq. ID	LIB3431-008-P1-N1-D8
Method	BLASTN
NCBI GI	g218207
BLAST score	37
E value	1.0e-11

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Match length	93
% identity	85
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397921
Seq. ID	LIB3431-008-P1-N1-E1
Method	BLASTX
NCBI GI	g3688123
BLAST score	226
E value	2.0e-18
Match length	55
% identity	73
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	397922
Seq. ID	LIB3431-008-P1-N1-E10
Method	BLASTX
NCBI GI	g3126854
BLAST score	263
E value	5.0e-23
Match length	51
% identity	96
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	397923
Seq. ID	LIB3431-008-P1-N1-E11
Method	BLASTX
NCBI GI	g3789948
BLAST score	160
E value	8.0e-11
Match length	34
% identity	94
NCBI Description	(AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No.	397924
Seq. ID	LIB3431-008-P1-N1-E2
Method	BLASTX
NCBI GI	g671740
BLAST score	393
E value	3.0e-38
Match length	71
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	397925
Seq. ID	LIB3431-008-P1-N1-E5
Method	BLASTX
NCBI GI	g5823570
BLAST score	395
E value	3.0e-38
Match length	108
% identity	74
NCBI Description	(AL049730) putative protein [Arabidopsis thaliana]

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Seq. No.	397926
Seq. ID	LIB3431-008-P1-N1-E6
Method	BLASTN
NCBI GI	g809513
BLAST score	356
E value	0.0e+00
Match length	356
% identity	100
NCBI Description	Rice mRNA for ferredoxin-nitrite reductase, complete cds

Seq. No.	397927
Seq. ID	LIB3431-008-P1-N1-E7
Method	BLASTX
NCBI GI	g132105
BLAST score	522
E value	3.0e-53
Match length	94
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	397928
Seq. ID	LIB3431-008-P1-N1-F1
Method	BLASTN
NCBI GI	g20181
BLAST score	41
E value	7.0e-14
Match length	77
% identity	88
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	397929
Seq. ID	LIB3431-008-P1-N1-F10
Method	BLASTX
NCBI GI	g3024657
BLAST score	180
E value	3.0e-13
Match length	50
% identity	72
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_2668740 (AF034944) translation initiation factor; GOS2 [Zea mays]

Seq. No.	397930
Seq. ID	LIB3431-008-P1-N1-F12
Method	BLASTX
NCBI GI	g3885894
BLAST score	162

E value	2.0e-11
Match length	31
% identity	100
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No.	397931
Seq. ID	LIB3431-008-P1-N1-F2
Method	BLASTN
NCBI GI	g2570514
BLAST score	244
E value	1.0e-135
Match length	260
% identity	98
NCBI Description	Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	397932
Seq. ID	LIB3431-008-P1-N1-F4
Method	BLASTN
NCBI GI	g22651
BLAST score	50
E value	5.0e-19
Match length	98
% identity	88
NCBI Description	H.vulgare mRNA for GRP94 homologue

Seq. No.	397933
Seq. ID	LIB3431-008-P1-N1-F5
Method	BLASTX
NCBI GI	g3914470
BLAST score	407
E value	9.0e-40
Match length	94
% identity	79
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_1321868_emb_CAA66373_ (X97771) 10kD PSII protein [Hordeum vulgare]

Seq. No.	397934
Seq. ID	LIB3431-008-P1-N1-F6
Method	BLASTX
NCBI GI	g4835756
BLAST score	307
E value	5.0e-28
Match length	71
% identity	83
NCBI Description	(AC007202) Is a member of the PF_00044 glyceraldehyde 3-phosphate dehydrogenase family. ESTs gb_T43985, gb_N38667, gb_N65037, gb_AA713069 and gb_AI099548 come from this gene. [Arabidopsis thaliana]

Seq. No.	397935
Seq. ID	LIB3431-008-P1-N1-F8
Method	BLASTX
NCBI GI	g3808101
BLAST score	217
E value	1.0e-17
Match length	50

% identity	88
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	397936
Seq. ID	LIB3431-008-P1-N1-F9
Method	BLASTX
NCBI GI	g2864617
BLAST score	173
E value	2.0e-12
Match length	53
% identity	66
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1_ (AJ245574) ATP synthase beta chain precursor (subunit II) [Arabidopsis thaliana]

Seq. No.	397937
Seq. ID	LIB3431-008-P1-N1-G10
Method	BLASTX
NCBI GI	g1351303
BLAST score	204
E value	6.0e-16
Match length	56
% identity	71
NCBI Description	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS) >gi_619732 (U18770) indole-3-glycerol phosphate synthase [Arabidopsis thaliana]

Seq. No.	397938
Seq. ID	LIB3431-008-P1-N1-G2
Method	BLASTN
NCBI GI	g2072554
BLAST score	372
E value	0.0e+00
Match length	388
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397939
Seq. ID	LIB3431-008-P1-N1-G4
Method	BLASTN
NCBI GI	g20181
BLAST score	105
E value	6.0e-52
Match length	173
% identity	91
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	397940
Seq. ID	LIB3431-008-P1-N1-G5
Method	BLASTX
NCBI GI	g4689108
BLAST score	168
E value	1.0e-11
Match length	48

% identity	60
NCBI Description	(AF077030) hypothetical 43.2 kDa protein [Homo sapiens] >gi_4929577_gb_AAD34049.1_AF151812_1 (AF151812) CGI-54 protein [Homo sapiens]

Seq. No.	397941
Seq. ID	LIB3431-008-P1-N1-G6
Method	BLASTN
NCBI GI	g2570516
BLAST score	76
E value	1.0e-34
Match length	120
% identity	91
NCBI Description	Oryza sativa thioredoxin F isoform mRNA, complete cds

Seq. No.	397942
Seq. ID	LIB3431-008-P1-N1-G8
Method	BLASTN
NCBI GI	g2062705
BLAST score	39
E value	2.0e-13
Match length	39
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	397943
Seq. ID	LIB3431-008-P1-N1-H11
Method	BLASTN
NCBI GI	g2570510
BLAST score	205
E value	1.0e-111
Match length	224
% identity	98
NCBI Description	Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No.	397944
Seq. ID	LIB3431-008-P1-N1-H3
Method	BLASTN
NCBI GI	g3789951
BLAST score	178
E value	2.0e-95
Match length	363
% identity	95
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	397945
Seq. ID	LIB3431-008-P1-N1-H6
Method	BLASTN
NCBI GI	g3868757
BLAST score	42
E value	2.0e-14
Match length	210
% identity	81
NCBI Description	Oryza sativa mRNA for elongation factor 1B gamma, complete

cds

Seq. No.	397946
Seq. ID	LIB3431-008-P1-N1-H8
Method	BLASTX
NCBI GI	g548605
BLAST score	378
E value	2.0e-36
Match length	79
% identity	94
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	397947
Seq. ID	LIB3431-008-P1-N1-H9
Method	BLASTX
NCBI GI	g4567263
BLAST score	236
E value	1.0e-19
Match length	58
% identity	76
NCBI Description	(AC006841) putative cell division inhibitor [Arabidopsis thaliana]

Seq. No.	397948
Seq. ID	LIB3431-009-P1-K1-A1
Method	BLASTN
NCBI GI	g2072554
BLAST score	394
E value	0.0e+00
Match length	394
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	397949
Seq. ID	LIB3431-009-P1-K1-A10
Method	BLASTX
NCBI GI	g5001458
BLAST score	457
E value	1.0e-45
Match length	145
% identity	60
NCBI Description	(AC006225) putative multidrug resistance protein [Arabidopsis thaliana]

Seq. No.	397950
Seq. ID	LIB3431-009-P1-K1-A12
Method	BLASTX
NCBI GI	g2583127
BLAST score	292
E value	1.0e-26
Match length	70
% identity	80

NCBI Description	(AC002387) putative sialoglycoprotease [Arabidopsis thaliana]

Seq. No.	397951
Seq. ID	LIB3431-009-P1-K1-A3
Method	BLASTX
NCBI GI	g5816996
BLAST score	477
E value	6.0e-48
Match length	125
% identity	74
NCBI Description	(AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No.	397952
Seq. ID	LIB3431-009-P1-K1-A4
Method	BLASTX
NCBI GI	g4455169
BLAST score	368
E value	4.0e-35
Match length	117
% identity	56
NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	397953
Seq. ID	LIB3431-009-P1-K1-A6
Method	BLASTN
NCBI GI	g4079797
BLAST score	60
E value	7.0e-25
Match length	100
% identity	90
NCBI Description	Oryza sativa 23 kDa polypeptide of photosystem II mRNA, complete cds

Seq. No.	397954
Seq. ID	LIB3431-009-P1-K1-A7
Method	BLASTX
NCBI GI	g3288821
BLAST score	323
E value	9.0e-35
Match length	112
% identity	66
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	397955
Seq. ID	LIB3431-009-P1-K1-B12
Method	BLASTX
NCBI GI	g228403
BLAST score	633
E value	3.0e-66
Match length	144
% identity	85

NCBI Description	glycolate oxidase [Lens culinaris]
Seq. No.	397956
Seq. ID	LIB3431-009-P1-K1-B2
Method	BLASTN
NCBI GI	g4959460
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.	397957
Seq. ID	LIB3431-009-P1-K1-B3
Method	BLASTX
NCBI GI	g2130069
BLAST score	261
E value	1.0e-22
Match length	120
% identity	48
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.	397958
Seq. ID	LIB3431-009-P1-K1-B4
Method	BLASTX
NCBI GI	g2130069
BLAST score	358
E value	3.0e-34
Match length	90
% identity	76
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.	397959
Seq. ID	LIB3431-009-P1-K1-B6
Method	BLASTX
NCBI GI	g132105
BLAST score	271
E value	3.0e-24
Match length	63
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	397960
Seq. ID	LIB3431-009-P1-K1-B8
Method	BLASTX
NCBI GI	g1730512
BLAST score	186

E value	2.0e-14
Match length	48
% identity	79
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST >gi_2129669_pir__S71368 phosphoglycerate kinase - Arabidopsis thaliana (fragment) >gi_1022805_gb_AAB60303.1_ (U37701) phosphoglycerate kinase [Arabidopsis thaliana]

Seq. No.	397961
Seq. ID	LIB3431-009-P1-K1-C10
Method	BLASTX
NCBI GI	g347451
BLAST score	154
E value	1.0e-10
Match length	38
% identity	82
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	397962
Seq. ID	LIB3431-009-P1-K1-C11
Method	BLASTN
NCBI GI	g1184773
BLAST score	67
E value	1.0e-29
Match length	115
% identity	90
NCBI Description	Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3 (gpc3) mRNA, complete cds

Seq. No.	397963
Seq. ID	LIB3431-009-P1-K1-C12
Method	BLASTX
NCBI GI	g4006818
BLAST score	442
E value	8.0e-44
Match length	138
% identity	62
NCBI Description	(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]

Seq. No.	397964
Seq. ID	LIB3431-009-P1-K1-C3
Method	BLASTX
NCBI GI	g733454
BLAST score	535
E value	1.0e-54
Match length	123
% identity	82
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	397965
Seq. ID	LIB3431-009-P1-K1-D1
Method	BLASTX
NCBI GI	g320618
BLAST score	466

E value	1.0e-46
Match length	105
% identity	84
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	397966
Seq. ID	LIB3431-009-P1-K1-D11
Method	BLASTX
NCBI GI	g115787
BLAST score	249
E value	2.0e-21
Match length	70
% identity	79
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	397967
Seq. ID	LIB3431-009-P1-K1-D12
Method	BLASTX
NCBI GI	g226263
BLAST score	342
E value	4.0e-32
Match length	70
% identity	93
NCBI Description	chlorophyll a/b binding protein [Glycine max]

Seq. No.	397968
Seq. ID	LIB3431-009-P1-K1-D3
Method	BLASTX
NCBI GI	g115787
BLAST score	379
E value	2.0e-36
Match length	95
% identity	82
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	397969
Seq. ID	LIB3431-009-P1-K1-D6
Method	BLASTX
NCBI GI	g320618
BLAST score	619
E value	2.0e-73
Match length	144
% identity	97
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	397970
Seq. ID	LIB3431-009-P1-K1-D7
Method	BLASTX
NCBI GI	g2196772
BLAST score	170
E value	4.0e-12
Match length	74
% identity	50
NCBI Description	(AF003128) chlorophyll a/b-binding protein [Mesembryanthemum crystallinum]

Seq. No.	397971
Seq. ID	LIB3431-009-P1-K1-E1
Method	BLASTX
NCBI GI	g118170
BLAST score	429
E value	3.0e-42
Match length	102
% identity	85
NCBI Description	CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I) >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784 (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259) oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967) oryzacystatin=cysteine protease inhibitor [Oryza=rice, Peptide, 102 aa] [Oryza] >gi_1280613 (U54702) oryzacystatin [Oryza sativa]

Seq. No.	397972
Seq. ID	LIB3431-009-P1-K1-E10
Method	BLASTN
NCBI GI	g218207
BLAST score	215
E value	1.0e-117
Match length	239
% identity	97
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	397973
Seq. ID	LIB3431-009-P1-K1-E11
Method	BLASTX
NCBI GI	g4210330
BLAST score	245
E value	2.0e-21
Match length	57
% identity	79
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	397974
Seq. ID	LIB3431-009-P1-K1-E12
Method	BLASTX

NCBI GI	g417260
BLAST score	421
E value	2.0e-41
Match length	128
% identity	66
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	397975
Seq. ID	LIB3431-009-P1-K1-E4
Method	BLASTN
NCBI GI	g2306980
BLAST score	75
E value	2.0e-34
Match length	119
% identity	91
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	397976
Seq. ID	LIB3431-009-P1-K1-E5
Method	BLASTX
NCBI GI	g2077957
BLAST score	384
E value	4.0e-37
Match length	132
% identity	64
NCBI Description	(Y12780) ATPase [Arabidopsis thaliana]

Seq. No.	397977
Seq. ID	LIB3431-009-P1-K1-F1
Method	BLASTX
NCBI GI	g3334150
BLAST score	657
E value	5.0e-69
Match length	144
% identity	90
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir__JC4312 chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase subunit (46 kD) [Glycine max]

Seq. No.	397978
Seq. ID	LIB3431-009-P1-K1-F12
Method	BLASTX
NCBI GI	g2306981
BLAST score	328
E value	7.0e-32
Match length	95
% identity	75
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No.	397979
Seq. ID	LIB3431-009-P1-K1-F3
Method	BLASTX

NCBI GI	g3789952
BLAST score	584
E value	2.0e-60
Match length	119
% identity	97
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	397980
Seq. ID	LIB3431-009-P1-K1-F5
Method	BLASTX
NCBI GI	g3914603
BLAST score	684
E value	3.0e-72
Match length	130
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	397981
Seq. ID	LIB3431-009-P1-K1-F6
Method	BLASTX
NCBI GI	g3914603
BLAST score	236
E value	6.0e-20
Match length	89
% identity	60
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	397982
Seq. ID	LIB3431-009-P1-K1-F7
Method	BLASTX
NCBI GI	g3334150
BLAST score	571
E value	6.0e-59
Match length	129
% identity	88
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir__JC4312 chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase subunit (46 kD) [Glycine max]

Seq. No.	397983
Seq. ID	LIB3431-009-P1-K1-G10
Method	BLASTX
NCBI GI	g2129538
BLAST score	190
E value	1.0e-24
Match length	89
% identity	72
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)

AT103 [Arabidopsis thaliana]

Seq. No.	397984
Seq. ID	LIB3431-009-P1-K1-G12
Method	BLASTX
NCBI GI	g3885888
BLAST score	227
E value	1.0e-18
Match length	52
% identity	88
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	397985
Seq. ID	LIB3431-009-P1-K1-G2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	397986
Seq. ID	LIB3431-009-P1-K1-G3
Method	BLASTX
NCBI GI	g3152559
BLAST score	274
E value	5.0e-30
Match length	124
% identity	63
NCBI Description	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No.	397987
Seq. ID	LIB3431-009-P1-K1-G4
Method	BLASTX
NCBI GI	g3914603
BLAST score	419
E value	3.0e-41
Match length	86
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	397988
Seq. ID	LIB3431-009-P1-K1-G5
Method	BLASTX
NCBI GI	g167097
BLAST score	288
E value	2.0e-36
Match length	110
% identity	75

NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	397989
Seq. ID	LIB3431-009-P1-K1-G7
Method	BLASTN
NCBI GI	g218209
BLAST score	55
E value	3.0e-22
Match length	154
% identity	84
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	397990
Seq. ID	LIB3431-009-P1-K1-G9
Method	BLASTX
NCBI GI	g3775999
BLAST score	159
E value	3.0e-11
Match length	74
% identity	49
NCBI Description	(AJ010463) RNA helicase [Arabidopsis thaliana]

Seq. No.	397991
Seq. ID	LIB3431-009-P1-K1-H11
Method	BLASTX
NCBI GI	g1617197
BLAST score	244
E value	1.0e-20
Match length	50
% identity	90
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	397992
Seq. ID	LIB3431-009-P1-K1-H2
Method	BLASTX
NCBI GI	g417260
BLAST score	410
E value	5.0e-40
Match length	128
% identity	66
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	397993
Seq. ID	LIB3431-009-P1-K1-H8
Method	BLASTX
NCBI GI	g2959781
BLAST score	639
E value	6.0e-67
Match length	136
% identity	85
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	397994
Seq. ID	LIB3431-009-P1-K1-H9
Method	BLASTX
NCBI GI	g3885892
BLAST score	532
E value	2.0e-54
Match length	110
% identity	94
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	397995
Seq. ID	LIB3431-009-P1-N1-A10
Method	BLASTX
NCBI GI	g5001458
BLAST score	177
E value	8.0e-13
Match length	59
% identity	58
NCBI Description	(AC006225) putative multidrug resistance protein [Arabidopsis thaliana]

Seq. No.	397996
Seq. ID	LIB3431-009-P1-N1-A3
Method	BLASTX
NCBI GI	g5816996
BLAST score	224
E value	2.0e-18
Match length	49
% identity	90
NCBI Description	(AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No.	397997
Seq. ID	LIB3431-009-P1-N1-B1
Method	BLASTN
NCBI GI	g902200
BLAST score	105
E value	6.0e-52
Match length	105
% identity	50
NCBI Description	Z.mays complete chloroplast genome

Seq. No.	397998
Seq. ID	LIB3431-009-P1-N1-B2
Method	BLASTX
NCBI GI	g451193
BLAST score	158
E value	1.0e-10
Match length	48
% identity	65
NCBI Description	(L28008) wali7 [Triticum aestivum] >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]

Seq. No.	397999
Seq. ID	LIB3431-009-P1-N1-B3
Method	BLASTN
NCBI GI	g20191

BLAST score	427
E value	0.0e+00
Match length	446
% identity	99
NCBI Description	O.sativa mRNA for catalase

Seq. No.	398000
Seq. ID	LIB3431-009-P1-N1-B4
Method	BLASTN
NCBI GI	g169133
BLAST score	43
E value	6.0e-15
Match length	143
% identity	83
NCBI Description	Zea mays precursor of the oxygen evolving complex 17 kDa protein mRNA, complete cds

Seq. No.	398001
Seq. ID	LIB3431-009-P1-N1-B6
Method	BLASTN
NCBI GI	g218207
BLAST score	114
E value	1.0e-57
Match length	118
% identity	99
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398002
Seq. ID	LIB3431-009-P1-N1-B8
Method	BLASTX
NCBI GI	g3738261
BLAST score	248
E value	4.0e-21
Match length	57
% identity	91
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	398003
Seq. ID	LIB3431-009-P1-N1-C10
Method	BLASTX
NCBI GI	g671740
BLAST score	197
E value	3.0e-15
Match length	37
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	398004
Seq. ID	LIB3431-009-P1-N1-C11
Method	BLASTX
NCBI GI	g120668
BLAST score	223
E value	3.0e-18

Match length	45
% identity	91
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82399_pir__A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment) >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var. distichum]

Seq. No.	398005
Seq. ID	LIB3431-009-P1-N1-C3
Method	BLASTN
NCBI GI	g2073379
BLAST score	158
E value	1.0e-83
Match length	173
% identity	98
NCBI Description	Rice CP26 mRNA, partial sequence

Seq. No.	398006
Seq. ID	LIB3431-009-P1-N1-C4
Method	BLASTN
NCBI GI	g20177
BLAST score	359
E value	0.0e+00
Match length	389
% identity	99
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398007
Seq. ID	LIB3431-009-P1-N1-C9
Method	BLASTX
NCBI GI	g2952326
BLAST score	223
E value	3.0e-18
Match length	42
% identity	100
NCBI Description	(AF049888) 1-aminocyclopropane-1-carboxylate oxidase [Oryza sativa]

Seq. No.	398008
Seq. ID	LIB3431-009-P1-N1-D1
Method	BLASTN
NCBI GI	g20177
BLAST score	144
E value	2.0e-75
Match length	151
% identity	99
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398009
Seq. ID	LIB3431-009-P1-N1-D10
Method	BLASTN
NCBI GI	g310316

BLAST score	36
E value	7.0e-11
Match length	48
% identity	94
NCBI Description	Rice beta-tubulin (RTUB-1) mRNA, complete cds

Seq. No.	398010
Seq. ID	LIB3431-009-P1-N1-D11
Method	BLASTN
NCBI GI	g20181
BLAST score	170
E value	1.0e-90
Match length	177
% identity	99
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398011
Seq. ID	LIB3431-009-P1-N1-D12
Method	BLASTN
NCBI GI	g20181
BLAST score	80
E value	4.0e-37
Match length	108
% identity	94
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398012
Seq. ID	LIB3431-009-P1-N1-D3
Method	BLASTX
NCBI GI	g421916
BLAST score	231
E value	4.0e-19
Match length	45
% identity	96
NCBI Description	chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No.	398013
Seq. ID	LIB3431-009-P1-N1-D4
Method	BLASTX
NCBI GI	g548603
BLAST score	234
E value	1.0e-19
Match length	50
% identity	90
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	398014
Seq. ID	LIB3431-009-P1-N1-D6
Method	BLASTN
NCBI GI	g20181

BLAST score	98
E value	7.0e-48
Match length	108
% identity	97
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398015
Seq. ID	LIB3431-009-P1-N1-D9
Method	BLASTX
NCBI GI	g4836907
BLAST score	188
E value	4.0e-14
Match length	45
% identity	84
NCBI Description	(AC007153) Highly similar to putative callose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	398016
Seq. ID	LIB3431-009-P1-N1-E1
Method	BLASTN
NCBI GI	g259136
BLAST score	282
E value	1.0e-157
Match length	282
% identity	100
NCBI Description	oryzacystatin=cysteine protease inhibitor [Oryza=rice, mRNA, 643 nt]

Seq. No.	398017
Seq. ID	LIB3431-009-P1-N1-E10
Method	BLASTN
NCBI GI	g218207
BLAST score	296
E value	1.0e-166
Match length	296
% identity	100
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398018
Seq. ID	LIB3431-009-P1-N1-E12
Method	BLASTN
NCBI GI	g5091597
BLAST score	106
E value	1.0e-52
Match length	170
% identity	31
NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No.	398019
Seq. ID	LIB3431-009-P1-N1-E2
Method	BLASTN
NCBI GI	g310322
BLAST score	52
E value	4.0e-20

Match length	241
% identity	82
NCBI Description	Oryza sativa triosephosphate isomerase (Rictipi2) gene, exons 1-9

Seq. No.	398020
Seq. ID	LIB3431-009-P1-N1-E4
Method	BLASTN
NCBI GI	g2306980
BLAST score	235
E value	1.0e-129
Match length	260
% identity	98
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	398021
Seq. ID	LIB3431-009-P1-N1-E5
Method	BLASTX
NCBI GI	g5734790
BLAST score	241
E value	2.0e-20
Match length	53
% identity	89
NCBI Description	(AC007980) ATP-dependent metalloprotease [Arabidopsis thaliana]

Seq. No.	398022
Seq. ID	LIB3431-009-P1-N1-E6
Method	BLASTN
NCBI GI	g473602
BLAST score	35
E value	3.0e-10
Match length	116
% identity	83
NCBI Description	Zea mays W-22 histone H2A mRNA, complete cds

Seq. No.	398023
Seq. ID	LIB3431-009-P1-N1-E8
Method	BLASTX
NCBI GI	g1617197
BLAST score	160
E value	7.0e-11
Match length	31
% identity	90
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	398024
Seq. ID	LIB3431-009-P1-N1-E9
Method	BLASTN
NCBI GI	g3075487
BLAST score	224
E value	1.0e-123
Match length	240
% identity	98
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	398025
Seq. ID	LIB3431-009-P1-N1-F1
Method	BLASTX
NCBI GI	g3334150
BLAST score	209
E value	3.0e-21
Match length	62
% identity	90
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir__JC4312 chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase subunit (46 kD) [Glycine max]

Seq. No.	398026
Seq. ID	LIB3431-009-P1-N1-F10
Method	BLASTX
NCBI GI	g6091740
BLAST score	287
E value	1.0e-25
Match length	78
% identity	74
NCBI Description	(AC010797) putative aspartate kinase [Arabidopsis thaliana]

Seq. No.	398027
Seq. ID	LIB3431-009-P1-N1-F3
Method	BLASTN
NCBI GI	g3789951
BLAST score	149
E value	3.0e-78
Match length	288
% identity	98
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398028
Seq. ID	LIB3431-009-P1-N1-F4
Method	BLASTN
NCBI GI	g218207
BLAST score	47
E value	2.0e-17
Match length	87
% identity	89
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398029
Seq. ID	LIB3431-009-P1-N1-F5
Method	BLASTX
NCBI GI	g132166
BLAST score	160
E value	7.0e-11
Match length	31
% identity	87

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	398030
Seq. ID	LIB3431-009-P1-N1-F7
Method	BLASTN
NCBI GI	g20177
BLAST score	322
E value	0.0e+00
Match length	344
% identity	99
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398031
Seq. ID	LIB3431-009-P1-N1-G12
Method	BLASTN
NCBI GI	g3885887
BLAST score	267
E value	1.0e-148
Match length	267
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	398032
Seq. ID	LIB3431-009-P1-N1-G2
Method	BLASTN
NCBI GI	g2072554
BLAST score	257
E value	1.0e-142
Match length	257
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398033
Seq. ID	LIB3431-009-P1-N1-G4
Method	BLASTX
NCBI GI	g132166
BLAST score	160
E value	6.0e-11
Match length	31
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	398034
Seq. ID	LIB3431-009-P1-N1-G5

Method	BLASTX
NCBI GI	g4105561
BLAST score	226
E value	1.0e-18
Match length	47
% identity	96
NCBI Description	(AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No.	398035
Seq. ID	LIB3431-009-P1-N1-G7
Method	BLASTN
NCBI GI	g218209
BLAST score	152
E value	4.0e-80
Match length	200
% identity	95
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	398036
Seq. ID	LIB3431-009-P1-N1-H11
Method	BLASTX
NCBI GI	g1617197
BLAST score	228
E value	1.0e-18
Match length	49
% identity	84
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	398037
Seq. ID	LIB3431-009-P1-N1-H2
Method	BLASTN
NCBI GI	g20262
BLAST score	160
E value	7.0e-85
Match length	200
% identity	95
NCBI Description	O.sativa light-induced mRNA

Seq. No.	398038
Seq. ID	LIB3431-009-P1-N1-H7
Method	BLASTN
NCBI GI	g4138289
BLAST score	324
E value	0.0e+00
Match length	324
% identity	100
NCBI Description	Oryza sativa mRNA for thioredoxin M

Seq. No.	398039
Seq. ID	LIB3431-009-P1-N1-H8
Method	BLASTX
NCBI GI	g2149640
BLAST score	215
E value	3.0e-17
Match length	60

% identity	73
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana] >gi_5733867_gb_AAD49755.1_AC007932_3 (AC007932) Identical to gb_U91995 Argonaute protein from Arabidopsis thaliana. ESTs gb_H76075, gb_AA720232, gb_N65911 and gb_AA651494 come from this gene

Seq. No.	398040
Seq. ID	LIB3431-009-P1-N1-H9
Method	BLASTN
NCBI GI	g3885891
BLAST score	196
E value	1.0e-106
Match length	324
% identity	90
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	398041
Seq. ID	LIB3431-010-P1-K1-A11
Method	BLASTX
NCBI GI	g132105
BLAST score	609
E value	2.0e-63
Match length	131
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398042
Seq. ID	LIB3431-010-P1-K1-A2
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	2.0e-10
Match length	35
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	398043
Seq. ID	LIB3431-010-P1-K1-A3
Method	BLASTX
NCBI GI	g2407281
BLAST score	700
E value	5.0e-74
Match length	133
% identity	98
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398044
Seq. ID	LIB3431-010-P1-K1-A8
Method	BLASTX
NCBI GI	g2262116
BLAST score	297
E value	9.0e-27
Match length	124
% identity	46
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.	398045
Seq. ID	LIB3431-010-P1-K1-A9
Method	BLASTX
NCBI GI	g548603
BLAST score	647
E value	7.0e-68
Match length	131
% identity	95
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	398046
Seq. ID	LIB3431-010-P1-K1-B1
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398047
Seq. ID	LIB3431-010-P1-K1-B12
Method	BLASTX
NCBI GI	g6103623
BLAST score	649
E value	4.0e-68
Match length	145
% identity	89
NCBI Description	(AF172094) actin [Picea rubens]

Seq. No.	398048
Seq. ID	LIB3431-010-P1-K1-B2
Method	BLASTX
NCBI GI	g5802955
BLAST score	155
E value	4.0e-10
Match length	66
% identity	44
NCBI Description	(AF178990) stress related protein [Vitis riparia]

Seq. No.	398049
Seq. ID	LIB3431-010-P1-K1-B5

Method	BLASTX
NCBI GI	g82080
BLAST score	409
E value	5.0e-40
Match length	119
% identity	67
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	398050
Seq. ID	LIB3431-010-P1-K1-B6
Method	BLASTN
NCBI GI	g20181
BLAST score	69
E value	9.0e-31
Match length	128
% identity	88
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398051
Seq. ID	LIB3431-010-P1-K1-B7
Method	BLASTX
NCBI GI	g131225
BLAST score	440
E value	9.0e-44
Match length	109
% identity	80
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	398052
Seq. ID	LIB3431-010-P1-K1-C1
Method	BLASTX
NCBI GI	g1353352
BLAST score	226
E value	2.0e-18
Match length	60
% identity	73
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	398053
Seq. ID	LIB3431-010-P1-K1-C10
Method	BLASTN
NCBI GI	g1661161
BLAST score	82
E value	4.0e-38
Match length	102
% identity	95
NCBI Description	Oryza sativa water stress inducible protein (KCDL917) mRNA, complete cds

Seq. No.	398054

Seq. ID	LIB3431-010-P1-K1-C2
Method	BLASTX
NCBI GI	g3885888
BLAST score	287
E value	1.0e-25
Match length	101
% identity	63
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	398055
Seq. ID	LIB3431-010-P1-K1-C3
Method	BLASTX
NCBI GI	g2196672
BLAST score	420
E value	3.0e-41
Match length	90
% identity	87
NCBI Description	(Y08807) HMGd1 [Zea mays]

Seq. No.	398056
Seq. ID	LIB3431-010-P1-K1-C7
Method	BLASTX
NCBI GI	g82080
BLAST score	331
E value	5.0e-31
Match length	96
% identity	69
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	398057
Seq. ID	LIB3431-010-P1-K1-D11
Method	BLASTX
NCBI GI	g417103
BLAST score	612
E value	1.0e-63
Match length	122
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

	(AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to histone H3 (AB015760) [Oryza sativa]
Seq. No.	398058
Seq. ID	LIB3431-010-P1-K1-D2
Method	BLASTX
NCBI GI	g5923670
BLAST score	247
E value	6.0e-21
Match length	78
% identity	59
NCBI Description	(AC009326) unknown protein [Arabidopsis thaliana]
Seq. No.	398059
Seq. ID	LIB3431-010-P1-K1-D3
Method	BLASTX
NCBI GI	g3860247
BLAST score	425
E value	6.0e-42
Match length	102
% identity	78
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.	398060
Seq. ID	LIB3431-010-P1-K1-D4
Method	BLASTN
NCBI GI	g11957
BLAST score	202
E value	1.0e-110
Match length	246
% identity	48
NCBI Description	Rice complete chloroplast genome
Seq. No.	398061
Seq. ID	LIB3431-010-P1-K1-D5
Method	BLASTN
NCBI GI	g20262
BLAST score	55
E value	3.0e-22
Match length	63
% identity	97
NCBI Description	O.sativa light-induced mRNA
Seq. No.	398062
Seq. ID	LIB3431-010-P1-K1-D7
Method	BLASTX
NCBI GI	g115772
BLAST score	186
E value	2.0e-14
Match length	41
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_ (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)

[Oryza sativa]

Seq. No.	398063
Seq. ID	LIB3431-010-P1-K1-D8
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398064
Seq. ID	LIB3431-010-P1-K1-E10
Method	BLASTX
NCBI GI	g1174778
BLAST score	440
E value	6.0e-44
Match length	90
% identity	96
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 1 (ORANGE PERICARP 1) >gi_320136_pir__PQ0449 tryptophan synthase (EC 4.2.1.20) beta-1 chain - maize (fragment) >gi_168572 (M76684) tryptophan synthase beta-subunit [Zea mays]

Seq. No.	398065
Seq. ID	LIB3431-010-P1-K1-E2
Method	BLASTN
NCBI GI	g20181
BLAST score	111
E value	7.0e-56
Match length	127
% identity	97
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398066
Seq. ID	LIB3431-010-P1-K1-E3
Method	BLASTX
NCBI GI	g132105
BLAST score	609
E value	2.0e-63
Match length	131
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398067
Seq. ID	LIB3431-010-P1-K1-E4
Method	BLASTN

NCBI GI	g11957
BLAST score	170
E value	7.0e-91
Match length	190
% identity	49
NCBI Description	Rice complete chloroplast genome

Seq. No.	398068
Seq. ID	LIB3431-010-P1-K1-F10
Method	BLASTX
NCBI GI	g3892708
BLAST score	297
E value	6.0e-27
Match length	104
% identity	52
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]

Seq. No.	398069
Seq. ID	LIB3431-010-P1-K1-F11
Method	BLASTX
NCBI GI	g167097
BLAST score	372
E value	1.0e-35
Match length	86
% identity	81
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	398070
Seq. ID	LIB3431-010-P1-K1-F2
Method	BLASTX
NCBI GI	g464705
BLAST score	416
E value	6.0e-41
Match length	87
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_419802_pir__S30146 ribosomal protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]

Seq. No.	398071
Seq. ID	LIB3431-010-P1-K1-F3
Method	BLASTX
NCBI GI	g2495180
BLAST score	442
E value	6.0e-44
Match length	116
% identity	71
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi_421882_pir__S35873 hydroxymethylbilane synthase (EC 4.3.1.8) - garden pea >gi_541971_pir__JQ2278 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - garden pea chloroplast >gi_313724_emb_CAA51820_ (X73418) hydroxymethylbilane synthase [Pisum sativum]

Seq. No.	398072

Seq. ID	LIB3431-010-P1-K1-F8
Method	BLASTX
NCBI GI	g687677
BLAST score	222
E value	1.0e-18
Match length	53
% identity	83
NCBI Description	(U19925) unknown [Arabidopsis thaliana]

Seq. No.	398073
Seq. ID	LIB3431-010-P1-K1-F9
Method	BLASTX
NCBI GI	g1835731
BLAST score	581
E value	4.0e-60
Match length	111
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	398074
Seq. ID	LIB3431-010-P1-K1-G10
Method	BLASTX
NCBI GI	g3913018
BLAST score	626
E value	2.0e-65
Match length	128
% identity	99
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	398075
Seq. ID	LIB3431-010-P1-K1-G11
Method	BLASTX
NCBI GI	g6015059
BLAST score	406
E value	1.0e-39
Match length	80
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096 (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	398076
Seq. ID	LIB3431-010-P1-K1-G2
Method	BLASTX
NCBI GI	g4502881
BLAST score	165
E value	3.0e-11
Match length	141
% identity	34
NCBI Description	chloride intracellular channel 1 >gi_3121852_sp_O00299_CLI1_HUMAN CHLORIDE INTRACELLULAR CHANNEL PROTEIN 1 (NUCLEAR CHLORIDE ION CHANNEL 27) (P64 CLCP) >gi_2073569 (U93205) nuclear chloride ion channel protein [Homo sapiens] >gi_4588526_gb_AAD26137.1_AF109197_1 (AF109197) nuclear chloride channel [Homo sapiens]

Seq. No.	398077
Seq. ID	LIB3431-010-P1-K1-G3
Method	BLASTX
NCBI GI	g3345477
BLAST score	502
E value	8.0e-51
Match length	142
% identity	70
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	398078
Seq. ID	LIB3431-010-P1-K1-G4
Method	BLASTX
NCBI GI	g548603
BLAST score	210
E value	8.0e-17
Match length	82
% identity	57
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	398079
Seq. ID	LIB3431-010-P1-K1-G5
Method	BLASTX
NCBI GI	g2501190
BLAST score	214
E value	5.0e-17
Match length	63
% identity	71
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	398080
Seq. ID	LIB3431-010-P1-K1-G6
Method	BLASTX
NCBI GI	g548605
BLAST score	306
E value	1.0e-51
Match length	132
% identity	84
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398081
Seq. ID	LIB3431-010-P1-K1-G7
Method	BLASTX
NCBI GI	g132105
BLAST score	567
E value	2.0e-58

Match length	122
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398082
Seq. ID	LIB3431-010-P1-K1-G8
Method	BLASTX
NCBI GI	g115796
BLAST score	737
E value	2.0e-78
Match length	148
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398083
Seq. ID	LIB3431-010-P1-K1-G9
Method	BLASTX
NCBI GI	g2737973
BLAST score	742
E value	5.0e-79
Match length	145
% identity	96
NCBI Description	(U83625) protein kinase ZmMEK1 [Zea mays]

Seq. No.	398084
Seq. ID	LIB3431-010-P1-K1-H10
Method	BLASTX
NCBI GI	g3551523
BLAST score	247
E value	6.0e-21
Match length	156
% identity	37
NCBI Description	(AB017026) oxysterol-binding protein [Mus musculus]

Seq. No.	398085
Seq. ID	LIB3431-010-P1-K1-H11
Method	BLASTX
NCBI GI	g231610
BLAST score	257
E value	4.0e-22
Match length	74
% identity	76
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No.	398086
Seq. ID	LIB3431-010-P1-K1-H5
Method	BLASTX
NCBI GI	g4206112
BLAST score	639
E value	5.0e-67
Match length	127
% identity	94
NCBI Description	(AF097662) alpha tubulin [Mesembryanthemum crystallinum]

Seq. No.	398087
Seq. ID	LIB3431-010-P1-K1-H9
Method	BLASTX
NCBI GI	g3876874
BLAST score	211
E value	9.0e-17
Match length	88
% identity	43
NCBI Description	(Z81535) Similarity to Human signal recognition particle receptor alpha subunit (SW:P08240) [Caenorhabditis elegans]

Seq. No.	398088
Seq. ID	LIB3431-010-P1-N1-A10
Method	BLASTX
NCBI GI	g2911886
BLAST score	154
E value	6.0e-12
Match length	56
% identity	70
NCBI Description	(AF047663) Contains similarity to Pfam domain: PF00448 (SRP54), Score=14.7, E-value=2.7e-12, N=1 [Caenorhabditis elegans]

Seq. No.	398089
Seq. ID	LIB3431-010-P1-N1-A11
Method	BLASTN
NCBI GI	g218207
BLAST score	187
E value	1.0e-101
Match length	323
% identity	89
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398090
Seq. ID	LIB3431-010-P1-N1-A3
Method	BLASTN
NCBI GI	g218209
BLAST score	124
E value	3.0e-63
Match length	248
% identity	98
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS2106

Seq. No.	398091
Seq. ID	LIB3431-010-P1-N1-A5
Method	BLASTX
NCBI GI	g3367536
BLAST score	233
E value	2.0e-19
Match length	48
% identity	92
NCBI Description	(AC004392) Contains similarity to symbiosis-related like protein F1N20.80 gi_2961343 from A. thaliana BAC gb_AL022140. EST gb_T04695 comes from this gene. [Arabidopsis thaliana]

Seq. No.	398092
Seq. ID	LIB3431-010-P1-N1-A9
Method	BLASTX
NCBI GI	g417544
BLAST score	206
E value	2.0e-16
Match length	43
% identity	86
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5) >gi_320209_pir__A60695 photosystem I chain II precursor - cucumber >gi_625966_pir__JQ2132 photosystem I complex 20K protein precursor - cucumber >gi_227772_prf__1710320A photosystem I 20kD protein [Cucumis sativus]

Seq. No.	398093
Seq. ID	LIB3431-010-P1-N1-B1
Method	BLASTN
NCBI GI	g2072554
BLAST score	185
E value	1.0e-100
Match length	185
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398094
Seq. ID	LIB3431-010-P1-N1-B11
Method	BLASTX
NCBI GI	g6093830
BLAST score	157
E value	1.0e-10
Match length	50
% identity	44
NCBI Description	PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

Seq. No.	398095
Seq. ID	LIB3431-010-P1-N1-B4
Method	BLASTN

NCBI GI	g20262
BLAST score	315
E value	1.0e-177
Match length	327
% identity	99
NCBI Description	O.sativa light-induced mRNA

Seq. No.	398096
Seq. ID	LIB3431-010-P1-N1-B5
Method	BLASTN
NCBI GI	g1835730
BLAST score	65
E value	3.0e-28
Match length	109
% identity	90
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No.	398097
Seq. ID	LIB3431-010-P1-N1-B6
Method	BLASTX
NCBI GI	g115813
BLAST score	152
E value	6.0e-10
Match length	33
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398098
Seq. ID	LIB3431-010-P1-N1-C10
Method	BLASTX
NCBI GI	g2244734
BLAST score	275
E value	2.0e-24
Match length	60
% identity	88
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No.	398099
Seq. ID	LIB3431-010-P1-N1-C11
Method	BLASTN
NCBI GI	g6006355
BLAST score	307
E value	1.0e-172
Match length	331
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	398100
Seq. ID	LIB3431-010-P1-N1-C12
Method	BLASTN
NCBI GI	g2072726
BLAST score	283
E value	1.0e-158
Match length	322

% identity	97
NCBI Description	O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No.	398101
Seq. ID	LIB3431-010-P1-N1-C2
Method	BLASTN
NCBI GI	g3885887
BLAST score	359
E value	0.0e+00
Match length	366
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	398102
Seq. ID	LIB3431-010-P1-N1-C4
Method	BLASTN
NCBI GI	g20181
BLAST score	45
E value	3.0e-16
Match length	92
% identity	89
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398103
Seq. ID	LIB3431-010-P1-N1-C7
Method	BLASTX
NCBI GI	g115813
BLAST score	210
E value	1.0e-16
Match length	48
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398104
Seq. ID	LIB3431-010-P1-N1-D12
Method	BLASTN
NCBI GI	g218134
BLAST score	349
E value	0.0e+00
Match length	403
% identity	97
NCBI Description	Rice mRNA for Histone H3

Seq. No.	398105
Seq. ID	LIB3431-010-P1-N1-D2
Method	BLASTX
NCBI GI	g5923670
BLAST score	179
E value	4.0e-13
Match length	72
% identity	50
NCBI Description	(AC009326) unknown protein [Arabidopsis thaliana]

Seq. No.	398106
Seq. ID	LIB3431-010-P1-N1-D6
Method	BLASTN
NCBI GI	g20262
BLAST score	337
E value	0.0e+00
Match length	345
% identity	99
NCBI Description	O.sativa light-induced mRNA

Seq. No.	398107
Seq. ID	LIB3431-010-P1-N1-D7
Method	BLASTX
NCBI GI	g289920
BLAST score	225
E value	1.0e-18
Match length	42
% identity	100
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	398108
Seq. ID	LIB3431-010-P1-N1-D8
Method	BLASTN
NCBI GI	g218207
BLAST score	152
E value	5.0e-80
Match length	168
% identity	98
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398109
Seq. ID	LIB3431-010-P1-N1-E2
Method	BLASTX
NCBI GI	g120661
BLAST score	154
E value	3.0e-10
Match length	29
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	398110
Seq. ID	LIB3431-010-P1-N1-E4
Method	BLASTX
NCBI GI	g231610
BLAST score	346
E value	6.0e-33
Match length	87
% identity	77
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No.	398111
Seq. ID	LIB3431-010-P1-N1-E5
Method	BLASTN
NCBI GI	g11957
BLAST score	133
E value	1.0e-68
Match length	169
% identity	47
NCBI Description	Rice complete chloroplast genome

Seq. No.	398112
Seq. ID	LIB3431-010-P1-N1-E9
Method	BLASTN
NCBI GI	g20181
BLAST score	160
E value	1.0e-84
Match length	179
% identity	98
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398113
Seq. ID	LIB3431-010-P1-N1-F1
Method	BLASTN
NCBI GI	g218207
BLAST score	217
E value	1.0e-119
Match length	221
% identity	100
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398114
Seq. ID	LIB3431-010-P1-N1-F11
Method	BLASTN
NCBI GI	g6016845
BLAST score	204
E value	1.0e-111
Match length	240
% identity	96
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	398115
Seq. ID	LIB3431-010-P1-N1-F12
Method	BLASTX
NCBI GI	g266893
BLAST score	637
E value	8.0e-67
Match length	123
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674)

rubisco activase [Cucumis sativus]

Seq. No.	398116
Seq. ID	LIB3431-010-P1-N1-F3
Method	BLASTN
NCBI GI	g288058
BLAST score	53
E value	6.0e-21
Match length	73
% identity	93
NCBI Description	Z.mays S13 mRNA for cytoplasmic ribosomal protein S13

Seq. No.	398117
Seq. ID	LIB3431-010-P1-N1-G1
Method	BLASTN
NCBI GI	g2661765
BLAST score	50
E value	4.0e-19
Match length	82
% identity	90
NCBI Description	Zea mays mRNA for putative porphobilinogen deaminase

Seq. No.	398118
Seq. ID	LIB3431-010-P1-N1-G11
Method	BLASTN
NCBI GI	g218154
BLAST score	80
E value	6.0e-37
Match length	145
% identity	100
NCBI Description	Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No.	398119
Seq. ID	LIB3431-010-P1-N1-G12
Method	BLASTN
NCBI GI	g2662340
BLAST score	269
E value	1.0e-150
Match length	316
% identity	96
NCBI Description	Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No.	398120
Seq. ID	LIB3431-010-P1-N1-G2
Method	BLASTX
NCBI GI	g125606
BLAST score	250
E value	2.0e-21
Match length	59
% identity	86
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]

Seq. No.	398121

Seq. ID	LIB3431-010-P1-N1-G5
Method	BLASTX
NCBI GI	g548603
BLAST score	225
E value	2.0e-18
Match length	56
% identity	80
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	398122
Seq. ID	LIB3431-010-P1-N1-G7
Method	BLASTX
NCBI GI	g1835731
BLAST score	297
E value	5.0e-27
Match length	67
% identity	85
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	398123
Seq. ID	LIB3431-010-P1-N1-G8
Method	BLASTX
NCBI GI	g132096
BLAST score	154
E value	3.0e-10
Match length	29
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_ (D00644) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa]

Seq. No.	398124
Seq. ID	LIB3431-010-P1-N1-G9
Method	BLASTX
NCBI GI	g3126854
BLAST score	300
E value	2.0e-27
Match length	57
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398125
Seq. ID	LIB3431-010-P1-N1-H1
Method	BLASTX
NCBI GI	g606817
BLAST score	154
E value	4.0e-10
Match length	28
% identity	100
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic

anhydrase 3 [Oryza sativa]

Seq. No.	398126
Seq. ID	LIB3431-010-P1-N1-H2
Method	BLASTN
NCBI GI	g19086
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Hordeum vulgare pot. psaE mRNA

Seq. No.	398127
Seq. ID	LIB3431-010-P1-N1-H4
Method	BLASTX
NCBI GI	g548605
BLAST score	239
E value	1.0e-28
Match length	80
% identity	89
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398128
Seq. ID	LIB3431-010-P1-N1-H6
Method	BLASTN
NCBI GI	g1136121
BLAST score	321
E value	0.0e+00
Match length	324
% identity	100
NCBI Description	O.sativa mRNA for alpha-tubulin (clone OSTA-136)

Seq. No.	398129
Seq. ID	LIB3431-010-P1-N1-H7
Method	BLASTN
NCBI GI	g2737972
BLAST score	38
E value	6.0e-12
Match length	74
% identity	88
NCBI Description	Zea mays protein kinase ZmMEK1 mRNA, complete cds

Seq. No.	398130
Seq. ID	LIB3431-011-P1-K1-A10
Method	BLASTX
NCBI GI	g1742187
BLAST score	170
E value	6.0e-12
Match length	121
% identity	35
NCBI Description	(D90771) ORF_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_ (D90772) ORF_ID:o260#14; similar to [SwissProt Accession

Number P11666] [Escherichia coli] >gi_1787591 (AE000231) orf, hypothetical protein [Escherichia coli]

Seq. No.	398131
Seq. ID	LIB3431-011-P1-K1-A3
Method	BLASTX
NCBI GI	g129233
BLAST score	461
E value	4.0e-46
Match length	120
% identity	79
NCBI Description	ORYZAIN GAMMA CHAIN PRECURSOR >gi_67646_pir__KHRZOG oryzain (EC 3.4.22.-) gamma precursor - rice >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor [Oryza sativa]

Seq. No.	398132
Seq. ID	LIB3431-011-P1-K1-A4
Method	BLASTX
NCBI GI	g416869
BLAST score	320
E value	1.0e-29
Match length	113
% identity	58
NCBI Description	CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_303902_dbj_BAA03542_ (D14722) cysteine synthase [Spinacia oleracea]

Seq. No.	398133
Seq. ID	LIB3431-011-P1-K1-A5
Method	BLASTX
NCBI GI	g3582333
BLAST score	209
E value	1.0e-16
Match length	88
% identity	44
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	398134
Seq. ID	LIB3431-011-P1-K1-A9
Method	BLASTX
NCBI GI	g2708331
BLAST score	376
E value	3.0e-36
Match length	119
% identity	61
NCBI Description	(AF038557) ligand gated channel-like protein [Arabidopsis thaliana]

Seq. No.	398135
Seq. ID	LIB3431-011-P1-K1-B1
Method	BLASTX
NCBI GI	g4755193
BLAST score	445
E value	3.0e-44
Match length	101

% identity	83
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	398136
Seq. ID	LIB3431-011-P1-K1-B12
Method	BLASTX
NCBI GI	g131225
BLAST score	301
E value	3.0e-27
Match length	93
% identity	61
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	398137
Seq. ID	LIB3431-011-P1-K1-B2
Method	BLASTX
NCBI GI	g1621477
BLAST score	378
E value	2.0e-36
Match length	81
% identity	85
NCBI Description	(D85868) reverse transcriptase [Oryza sativa]

Seq. No.	398138
Seq. ID	LIB3431-011-P1-K1-B4
Method	BLASTX
NCBI GI	g5880709
BLAST score	205
E value	3.0e-16
Match length	43
% identity	100
NCBI Description	(AF137379) CF0 subunit III of ATP synthase [Nephroselmis olivacea]

Seq. No.	398139
Seq. ID	LIB3431-011-P1-K1-B5
Method	BLASTX
NCBI GI	g3850566
BLAST score	263
E value	7.0e-23
Match length	134
% identity	43
NCBI Description	(AC005278) F15K9.3 [Arabidopsis thaliana]

Seq. No.	398140
Seq. ID	LIB3431-011-P1-K1-B6
Method	BLASTN
NCBI GI	g218207
BLAST score	294
E value	1.0e-164
Match length	298
% identity	100
NCBI Description	Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398141
Seq. ID	LIB3431-011-P1-K1-B9
Method	BLASTX
NCBI GI	g5734779
BLAST score	156
E value	8.0e-11
Match length	48
% identity	58
NCBI Description	(AC007980) 78688 [Arabidopsis thaliana]

Seq. No.	398142
Seq. ID	LIB3431-011-P1-K1-C1
Method	BLASTX
NCBI GI	g1843440
BLAST score	231
E value	5.0e-19
Match length	125
% identity	41
NCBI Description	(Z70521) unknown [Cucumis melo]

Seq. No.	398143
Seq. ID	LIB3431-011-P1-K1-C10
Method	BLASTX
NCBI GI	g3868756
BLAST score	469
E value	3.0e-47
Match length	94
% identity	96
NCBI Description	(D86611) catalase [Oryza sativa]

Seq. No.	398144
Seq. ID	LIB3431-011-P1-K1-C5
Method	BLASTX
NCBI GI	g320618
BLAST score	485
E value	5.0e-49
Match length	101
% identity	91
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398145
Seq. ID	LIB3431-011-P1-K1-C6
Method	BLASTX
NCBI GI	g132105
BLAST score	418
E value	1.0e-58
Match length	131
% identity	82
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	398146
Seq. ID	LIB3431-011-P1-K1-C7
Method	BLASTX
NCBI GI	g133999
BLAST score	493
E value	7.0e-50
Match length	100
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_70904_pir__R3RZ7 ribosomal protein S7 - rice chloroplast >gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_226657_prf__1603356CH ribosomal protein S7 [Oryza sativa]
Seq. No.	398147
Seq. ID	LIB3431-011-P1-K1-C8
Method	BLASTX
NCBI GI	g2625084
BLAST score	550
E value	1.0e-56
Match length	129
% identity	85
NCBI Description	(AF030382) ADP-glucose pyrophosphorylase small subunit [Cucumis melo var. markuwa Markino]
Seq. No.	398148
Seq. ID	LIB3431-011-P1-K1-C9
Method	BLASTN
NCBI GI	g4574134
BLAST score	123
E value	6.0e-63
Match length	146
% identity	97
NCBI Description	Oryza sativa cysteine synthase (rcs1) mRNA, complete cds
Seq. No.	398149
Seq. ID	LIB3431-011-P1-K1-D1
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	49
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	398150
Seq. ID	LIB3431-011-P1-K1-D11
Method	BLASTX

NCBI GI	g2570505
BLAST score	242
E value	4.0e-27
Match length	87
% identity	83
NCBI Description	(AF022735) proteasome component [Oryza sativa]

Seq. No.	398151
Seq. ID	LIB3431-011-P1-K1-D3
Method	BLASTN
NCBI GI	g3885891
BLAST score	110
E value	5.0e-55
Match length	181
% identity	97
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	398152
Seq. ID	LIB3431-011-P1-K1-D5
Method	BLASTX
NCBI GI	g5902394
BLAST score	440
E value	1.0e-43
Match length	114
% identity	76
NCBI Description	(AC008148) Putative phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	398153
Seq. ID	LIB3431-011-P1-K1-D7
Method	BLASTN
NCBI GI	g3810868
BLAST score	35
E value	8.0e-11
Match length	35
% identity	100
NCBI Description	Homo sapiens ST15 mRNA, complete cds

Seq. No.	398154
Seq. ID	LIB3431-011-P1-K1-D9
Method	BLASTX
NCBI GI	g2407281
BLAST score	543
E value	8.0e-56
Match length	105
% identity	95
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398155
Seq. ID	LIB3431-011-P1-K1-E1
Method	BLASTX
NCBI GI	g4929595
BLAST score	239
E value	4.0e-20
Match length	102

% identity	46
NCBI Description	(AF151821) CGI-63 protein [Homo sapiens]

Seq. No.	398156
Seq. ID	LIB3431-011-P1-K1-E10
Method	BLASTX
NCBI GI	g2072555
BLAST score	181
E value	1.0e-13
Match length	38
% identity	92
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398157
Seq. ID	LIB3431-011-P1-K1-E11
Method	BLASTX
NCBI GI	g4056427
BLAST score	289
E value	6.0e-26
Match length	105
% identity	53
NCBI Description	(AC005322) Contains similarity to gb_AJ006354 zinc finger protein (ZAC) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	398158
Seq. ID	LIB3431-011-P1-K1-E12
Method	BLASTX
NCBI GI	g115802
BLAST score	149
E value	2.0e-11
Match length	38
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No.	398159
Seq. ID	LIB3431-011-P1-K1-E2
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	1.0e-10
Match length	35
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	398160
Seq. ID	LIB3431-011-P1-K1-E3
Method	BLASTN
NCBI GI	g20262
BLAST score	233
E value	1.0e-128
Match length	273

% identity	96
NCBI Description	O.sativa light-induced mRNA

Seq. No.	398161
Seq. ID	LIB3431-011-P1-K1-E4
Method	BLASTX
NCBI GI	g3047109
BLAST score	206
E value	3.0e-16
Match length	90
% identity	49
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	398162
Seq. ID	LIB3431-011-P1-K1-E6
Method	BLASTX
NCBI GI	g3941480
BLAST score	288
E value	1.0e-25
Match length	129
% identity	49
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	398163
Seq. ID	LIB3431-011-P1-K1-E8
Method	BLASTX
NCBI GI	g5679336
BLAST score	253
E value	9.0e-22
Match length	94
% identity	49
NCBI Description	(AF171223) putative zinc finger protein [Oryza sativa]

Seq. No.	398164
Seq. ID	LIB3431-011-P1-K1-F10
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	4.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398165
Seq. ID	LIB3431-011-P1-K1-F4
Method	BLASTN
NCBI GI	g3377792
BLAST score	67
E value	7.0e-30
Match length	83
% identity	95
NCBI Description	Oryza sativa ribulose-1,5-bisphosphate carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No.	398166
Seq. ID	LIB3431-011-P1-K1-F5
Method	BLASTX
NCBI GI	g115796
BLAST score	517
E value	1.0e-52
Match length	119
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398167
Seq. ID	LIB3431-011-P1-K1-F8
Method	BLASTN
NCBI GI	g218171
BLAST score	43
E value	2.0e-15
Match length	43
% identity	100
NCBI Description	Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No.	398168
Seq. ID	LIB3431-011-P1-K1-F9
Method	BLASTX
NCBI GI	g70642
BLAST score	662
E value	1.0e-69
Match length	136
% identity	22
NCBI Description	ubiquitin precursor - Arabidopsis thaliana >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A poly-ubiquitin [Arabidopsis thaliana]

Seq. No.	398169
Seq. ID	LIB3431-011-P1-K1-G11
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398170
Seq. ID	LIB3431-011-P1-K1-G12
Method	BLASTX
NCBI GI	g3789952
BLAST score	516
E value	1.0e-52
Match length	103
% identity	98

NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	398171
Seq. ID	LIB3431-011-P1-K1-G2
Method	BLASTN
NCBI GI	g167086
BLAST score	43
E value	3.0e-15
Match length	74
% identity	90
NCBI Description	Hordeum vulgare photosystem I protein (PSI-L) mRNA, complete cds

Seq. No.	398172
Seq. ID	LIB3431-011-P1-K1-G4
Method	BLASTX
NCBI GI	g548605
BLAST score	570
E value	8.0e-59
Match length	124
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398173
Seq. ID	LIB3431-011-P1-K1-G5
Method	BLASTX
NCBI GI	g2499497
BLAST score	334
E value	5.0e-33
Match length	84
% identity	95
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_1161600_emb_CAA88841_ (Z48977) phosphoglycerate kinase [Nicotiana tabacum]

Seq. No.	398174
Seq. ID	LIB3431-011-P1-K1-G7
Method	BLASTX
NCBI GI	g2407281
BLAST score	513
E value	3.0e-52
Match length	109
% identity	90
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398175
Seq. ID	LIB3431-011-P1-K1-G9
Method	BLASTX
NCBI GI	g544437
BLAST score	323
E value	6.0e-30

Match length	70
% identity	87
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN) >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]

Seq. No.	398176
Seq. ID	LIB3431-011-P1-K1-H1
Method	BLASTX
NCBI GI	g3386621
BLAST score	412
E value	2.0e-40
Match length	97
% identity	84
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	398177
Seq. ID	LIB3431-011-P1-K1-H10
Method	BLASTX
NCBI GI	g2754849
BLAST score	578
E value	9.0e-60
Match length	139
% identity	77
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	398178
Seq. ID	LIB3431-011-P1-K1-H11
Method	BLASTX
NCBI GI	g3478700
BLAST score	461
E value	5.0e-46
Match length	144
% identity	61
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	398179
Seq. ID	LIB3431-011-P1-K1-H12
Method	BLASTN
NCBI GI	g3273244
BLAST score	58
E value	5.0e-24
Match length	74
% identity	95
NCBI Description	Oryza sativa DNA for NLS receptor, complete cds

Seq. No.	398180
Seq. ID	LIB3431-011-P1-K1-H2
Method	BLASTX
NCBI GI	g4079798
BLAST score	224
E value	1.0e-18
Match length	83
% identity	58
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	398181
Seq. ID	LIB3431-011-P1-K1-H4
Method	BLASTX
NCBI GI	g4886307
BLAST score	704
E value	1.0e-74
Match length	135
% identity	97
NCBI Description	(AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]

Seq. No.	398182
Seq. ID	LIB3431-011-P1-K1-H5
Method	BLASTX
NCBI GI	g3345477
BLAST score	314
E value	6.0e-29
Match length	111
% identity	58
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	398183
Seq. ID	LIB3431-011-P1-K1-H7
Method	BLASTX
NCBI GI	g733458
BLAST score	484
E value	9.0e-49
Match length	109
% identity	84
NCBI Description	(U23190) chlorophyll a/b-binding apoprotein CP24 precursor [Zea mays]

Seq. No.	398184
Seq. ID	LIB3431-011-P1-K1-H9
Method	BLASTX
NCBI GI	g320618
BLAST score	386
E value	1.0e-40
Match length	116
% identity	78
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398185
Seq. ID	LIB3431-011-P1-N1-A1
Method	BLASTX
NCBI GI	g542157
BLAST score	528
E value	5.0e-54
Match length	124
% identity	85
NCBI Description	ribosomal 5S RNA-binding protein - Rice

Seq. No.	398186

Seq. ID	LIB3431-011-P1-N1-A2
Method	BLASTX
NCBI GI	g21839
BLAST score	209
E value	2.0e-16
Match length	47
% identity	89
NCBI Description	(X57952) phosphoribulokinase [Triticum aestivum]

Seq. No.	398187
Seq. ID	LIB3431-011-P1-N1-A3
Method	BLASTX
NCBI GI	g129233
BLAST score	268
E value	2.0e-23
Match length	47
% identity	98
NCBI Description	ORYZAIN GAMMA CHAIN PRECURSOR >gi_67646_pir__KHRZOG oryzain (EC 3.4.22.-) gamma precursor - rice >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor [Oryza sativa]

Seq. No.	398188
Seq. ID	LIB3431-011-P1-N1-A8
Method	BLASTX
NCBI GI	g2384669
BLAST score	163
E value	3.0e-11
Match length	58
% identity	53
NCBI Description	(AF012656) putative potassium transporter AtKT1p [Arabidopsis thaliana]

Seq. No.	398189
Seq. ID	LIB3431-011-P1-N1-B10
Method	BLASTX
NCBI GI	g3873807
BLAST score	183
E value	2.0e-13
Match length	137
% identity	35
NCBI Description	(Z49907) B0491.1 [Caenorhabditis elegans]

Seq. No.	398190
Seq. ID	LIB3431-011-P1-N1-B12
Method	BLASTX
NCBI GI	g131225
BLAST score	178
E value	7.0e-15
Match length	58
% identity	63
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 398191

Seq. ID	LIB3431-011-P1-N1-B2
Method	BLASTX
NCBI GI	g3377848
BLAST score	198
E value	3.0e-15
Match length	95
% identity	38
NCBI Description	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]

Seq. No.	398192
Seq. ID	LIB3431-011-P1-N1-B3
Method	BLASTX
NCBI GI	g6093830
BLAST score	211
E value	1.0e-16
Match length	94
% identity	34
NCBI Description	PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

Seq. No.	398193
Seq. ID	LIB3431-011-P1-N1-B4
Method	BLASTN
NCBI GI	g11957
BLAST score	341
E value	0.0e+00
Match length	362
% identity	98
NCBI Description	Rice complete chloroplast genome

Seq. No.	398194
Seq. ID	LIB3431-011-P1-N1-B5
Method	BLASTX
NCBI GI	g3924605
BLAST score	251
E value	2.0e-21
Match length	59
% identity	71
NCBI Description	(AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]

Seq. No.	398195
Seq. ID	LIB3431-011-P1-N1-B6
Method	BLASTN
NCBI GI	g218207
BLAST score	298
E value	1.0e-167
Match length	298
% identity	100
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398196

Seq. ID	LIB3431-011-P1-N1-B9
Method	BLASTX
NCBI GI	g421855
BLAST score	151
E value	1.0e-09
Match length	79
% identity	44
NCBI Description	alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana (fragment)

Seq. No.	398197
Seq. ID	LIB3431-011-P1-N1-C10
Method	BLASTX
NCBI GI	g3929924
BLAST score	163
E value	3.0e-11
Match length	36
% identity	89
NCBI Description	(AB020502) catalase [Oryza sativa]

Seq. No.	398198
Seq. ID	LIB3431-011-P1-N1-C3
Method	BLASTX
NCBI GI	g1504052
BLAST score	270
E value	1.0e-23
Match length	52
% identity	100
NCBI Description	(D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No.	398199
Seq. ID	LIB3431-011-P1-N1-C5
Method	BLASTX
NCBI GI	g289920
BLAST score	217
E value	1.0e-17
Match length	42
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	398200
Seq. ID	LIB3431-011-P1-N1-C6
Method	BLASTX
NCBI GI	g132105
BLAST score	289
E value	8.0e-26
Match length	73
% identity	78
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No.	398201
Seq. ID	LIB3431-011-P1-N1-C8
Method	BLASTX
NCBI GI	g633678
BLAST score	145
E value	5.0e-09
Match length	32
% identity	91
NCBI Description	(X83500) ADP-glucose pyrophosphorylase [Spinacia oleracea]

Seq. No.	398202
Seq. ID	LIB3431-011-P1-N1-C9
Method	BLASTN
NCBI GI	g4574134
BLAST score	147
E value	3.0e-77
Match length	147
% identity	100
NCBI Description	Oryza sativa cysteine synthase (rcs1) mRNA, complete cds

Seq. No.	398203
Seq. ID	LIB3431-011-P1-N1-D11
Method	BLASTX
NCBI GI	g2570505
BLAST score	221
E value	3.0e-35
Match length	81
% identity	95
NCBI Description	(AF022735) proteasome component [Oryza sativa]

Seq. No.	398204
Seq. ID	LIB3431-011-P1-N1-D3
Method	BLASTX
NCBI GI	g3885892
BLAST score	426
E value	6.0e-42
Match length	83
% identity	98
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	398205
Seq. ID	LIB3431-011-P1-N1-D7
Method	BLASTX
NCBI GI	g6016427
BLAST score	292
E value	3.0e-26
Match length	58
% identity	84
NCBI Description	CASEIN KINASE II BETA-3 CHAIN (CK II) >gi_3493611 (AF068318) regulatory subunit of protein kinase CK2; CK2 beta-subunit [Arabidopsis thaliana]

Seq. No.	398206
Seq. ID	LIB3431-011-P1-N1-D9
Method	BLASTN

NCBI GI	g218209
BLAST score	149
E value	4.0e-78
Match length	299
% identity	97
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	398207
Seq. ID	LIB3431-011-P1-N1-E12
Method	BLASTX
NCBI GI	g115802
BLAST score	217
E value	1.0e-17
Match length	40
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No.	398208
Seq. ID	LIB3431-011-P1-N1-E3
Method	BLASTX
NCBI GI	g417260
BLAST score	326
E value	3.0e-30
Match length	81
% identity	77
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	398209
Seq. ID	LIB3431-011-P1-N1-E5
Method	BLASTX
NCBI GI	g517500
BLAST score	234
E value	1.0e-19
Match length	79
% identity	62
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	398210
Seq. ID	LIB3431-011-P1-N1-E9
Method	BLASTX
NCBI GI	g3212877
BLAST score	180
E value	3.0e-13
Match length	40
% identity	85
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	398211
Seq. ID	LIB3431-011-P1-N1-F11
Method	BLASTX
NCBI GI	g4115931
BLAST score	225
E value	2.0e-18
Match length	57
% identity	75
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	398212
Seq. ID	LIB3431-011-P1-N1-F12
Method	BLASTX
NCBI GI	g2072555
BLAST score	205
E value	5.0e-16
Match length	44
% identity	91
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398213
Seq. ID	LIB3431-011-P1-N1-F3
Method	BLASTX
NCBI GI	g131192
BLAST score	205
E value	3.0e-16
Match length	45
% identity	84
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937 photosystem I chain V precursor - barley >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide PSI-G precursor [Hordeum vulgare]

Seq. No.	398214
Seq. ID	LIB3431-011-P1-N1-F4
Method	BLASTX
NCBI GI	g132166
BLAST score	160
E value	6.0e-11
Match length	31
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	398215
Seq. ID	LIB3431-011-P1-N1-F5
Method	BLASTX
NCBI GI	g115802
BLAST score	143

E value	3.0e-09
Match length	30
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No.	398216
Seq. ID	LIB3431-011-P1-N1-F8
Method	BLASTX
NCBI GI	g3036949
BLAST score	264
E value	4.0e-23
Match length	50
% identity	100
NCBI Description	(AB012638) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	398217
Seq. ID	LIB3431-011-P1-N1-F9
Method	BLASTX
NCBI GI	g1076678
BLAST score	243
E value	1.0e-20
Match length	48
% identity	100
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	398218
Seq. ID	LIB3431-011-P1-N1-G1
Method	BLASTX
NCBI GI	g131176
BLAST score	304
E value	1.0e-27
Match length	59
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No.	398219
Seq. ID	LIB3431-011-P1-N1-G12
Method	BLASTN
NCBI GI	g3789951
BLAST score	191
E value	1.0e-103
Match length	414
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398220
Seq. ID	LIB3431-011-P1-N1-G2
Method	BLASTX
NCBI GI	g6006283
BLAST score	151
E value	8.0e-10
Match length	41
% identity	73
NCBI Description	(AB015861) photosystem I subunit PSI-L [Arabidopsis thaliana]

Seq. No.	398221
Seq. ID	LIB3431-011-P1-N1-G4
Method	BLASTX
NCBI GI	g548605
BLAST score	402
E value	9.0e-40
Match length	105
% identity	87
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398222
Seq. ID	LIB3431-011-P1-N1-G5
Method	BLASTX
NCBI GI	g3738261
BLAST score	416
E value	9.0e-41
Match length	91
% identity	92
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	398223
Seq. ID	LIB3431-011-P1-N1-G9
Method	BLASTX
NCBI GI	g485512
BLAST score	326
E value	3.0e-30
Match length	70
% identity	87
NCBI Description	salt-associated protein csaA - sweet orange

Seq. No.	398224
Seq. ID	LIB3431-011-P1-N1-H10
Method	BLASTX
NCBI GI	g2754849
BLAST score	186
E value	7.0e-14
Match length	43
% identity	84
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	398225
Seq. ID	LIB3431-011-P1-N1-H11
Method	BLASTN
NCBI GI	g531030
BLAST score	60
E value	5.0e-25
Match length	116
% identity	88
NCBI Description	Pennisetum ciliare apomixis-associated mRNA >gi_531483_emb_Z36546_PCAPOSPA3 P.ciliare (Higgins) apospory associated mRNA, 876bp >gi_549985_gb_U13149_PCU13149 Pennisetum ciliare possible apospory-associated mRNA clone pSUB 3-1a, partial cds

Seq. No.	398226
Seq. ID	LIB3431-011-P1-N1-H12
Method	BLASTN
NCBI GI	g3273244
BLAST score	59
E value	1.0e-24
Match length	95
% identity	91
NCBI Description	Oryza sativa DNA for NLS receptor, complete cds

Seq. No.	398227
Seq. ID	LIB3431-011-P1-N1-H2
Method	BLASTX
NCBI GI	g4079798
BLAST score	277
E value	1.0e-24
Match length	52
% identity	100
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	398228
Seq. ID	LIB3431-011-P1-N1-H4
Method	BLASTX
NCBI GI	g4886307
BLAST score	294
E value	2.0e-26
Match length	67
% identity	84
NCBI Description	(AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]

Seq. No.	398229
Seq. ID	LIB3431-011-P1-N1-H7
Method	BLASTX
NCBI GI	g543939
BLAST score	208
E value	2.0e-16
Match length	43
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 PRECURSOR >gi_541819_pir__S40210 chlorophyll a/b-binding protein CP24

precursor - spinach >gi_437991_emb_CAA81105.1_ (Z25886) 20 kDa protein of CP24 precursor protein [Spinacia oleracea]

Seq. No.	398230
Seq. ID	LIB3431-011-P1-N1-H9
Method	BLASTX
NCBI GI	g115787
BLAST score	449
E value	1.0e-44
Match length	96
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398231
Seq. ID	LIB3431-012-P1-K1-A10
Method	BLASTX
NCBI GI	g4732091
BLAST score	407
E value	1.0e-39
Match length	99
% identity	73
NCBI Description	(AF126742) bundle sheath defective protein 2 [Zea mays]

Seq. No.	398232
Seq. ID	LIB3431-012-P1-K1-A11
Method	BLASTX
NCBI GI	g3126854
BLAST score	477
E value	3.0e-48
Match length	90
% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398233
Seq. ID	LIB3431-012-P1-K1-A4
Method	BLASTX
NCBI GI	g4512684
BLAST score	397
E value	2.0e-38
Match length	96
% identity	80
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	398234
Seq. ID	LIB3431-012-P1-K1-B1
Method	BLASTX
NCBI GI	g3126854
BLAST score	510
E value	6.0e-52
Match length	102
% identity	94

NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	398235
Seq. ID	LIB3431-012-P1-K1-B10
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	2.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	398236
Seq. ID	LIB3431-012-P1-K1-B11
Method	BLASTN
NCBI GI	g6015437
BLAST score	43
E value	4.0e-15
Match length	43
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	398237
Seq. ID	LIB3431-012-P1-K1-B12
Method	BLASTX
NCBI GI	g2072555
BLAST score	221
E value	6.0e-18
Match length	44
% identity	93
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	398238
Seq. ID	LIB3431-012-P1-K1-B3
Method	BLASTX
NCBI GI	g4836934
BLAST score	187
E value	7.0e-14
Match length	86
% identity	43
NCBI Description	(AC006085) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	398239
Seq. ID	LIB3431-012-P1-K1-B4
Method	BLASTN
NCBI GI	g218207
BLAST score	253
E value	1.0e-140
Match length	257
% identity	100
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139
Seq. No.	398240

Seq. ID	LIB3431-012-P1-K1-B5
Method	BLASTN
NCBI GI	g3789951
BLAST score	62
E value	3.0e-26
Match length	121
% identity	88
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398241
Seq. ID	LIB3431-012-P1-K1-B6
Method	BLASTX
NCBI GI	g3075488
BLAST score	211
E value	3.0e-17
Match length	59
% identity	69
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398242
Seq. ID	LIB3431-012-P1-K1-B8
Method	BLASTX
NCBI GI	g548603
BLAST score	380
E value	1.0e-36
Match length	120
% identity	68
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	398243
Seq. ID	LIB3431-012-P1-K1-B9
Method	BLASTX
NCBI GI	g131225
BLAST score	378
E value	1.0e-36
Match length	85
% identity	88
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	398244
Seq. ID	LIB3431-012-P1-K1-C1
Method	BLASTX
NCBI GI	g1707018
BLAST score	460
E value	7.0e-46
Match length	104
% identity	86
NCBI Description	(U78721) CutA isolog [Arabidopsis thaliana]

Seq. No.	398245
Seq. ID	LIB3431-012-P1-K1-C11
Method	BLASTX
NCBI GI	g2244867
BLAST score	298
E value	6.0e-27
Match length	137
% identity	44
NCBI Description	(Z97337) hydroxynitrile lyase like protein [Arabidopsis thaliana]

Seq. No.	398246
Seq. ID	LIB3431-012-P1-K1-C2
Method	BLASTX
NCBI GI	g2072555
BLAST score	208
E value	3.0e-16
Match length	62
% identity	63
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398247
Seq. ID	LIB3431-012-P1-K1-C3
Method	BLASTX
NCBI GI	g4079798
BLAST score	223
E value	2.0e-18
Match length	46
% identity	96
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	398248
Seq. ID	LIB3431-012-P1-K1-C4
Method	BLASTX
NCBI GI	g2407281
BLAST score	304
E value	1.0e-27
Match length	87
% identity	68
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398249
Seq. ID	LIB3431-012-P1-K1-C5
Method	BLASTX
NCBI GI	g1353352
BLAST score	423
E value	2.0e-41
Match length	116
% identity	72
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	398250

Seq. ID	LIB3431-012-P1-K1-C7
Method	BLASTN
NCBI GI	g1944204
BLAST score	451
E value	0.0e+00
Match length	466
% identity	99
NCBI Description	Oryza sativa mRNA for RicMT, complete cds

Seq. No.	398251
Seq. ID	LIB3431-012-P1-K1-C8
Method	BLASTX
NCBI GI	g4585142
BLAST score	388
E value	2.0e-37
Match length	101
% identity	71
NCBI Description	(AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon esculentum]

Seq. No.	398252
Seq. ID	LIB3431-012-P1-K1-C9
Method	BLASTX
NCBI GI	g170131
BLAST score	176
E value	1.0e-12
Match length	48
% identity	62
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	398253
Seq. ID	LIB3431-012-P1-K1-D1
Method	BLASTX
NCBI GI	g5091623
BLAST score	521
E value	5.0e-53
Match length	125
% identity	82
NCBI Description	(AC007454) Similar to gb_U93048 somatic embryogenesis receptor-like kinase from Daucus carota, contains 4 PF_00560 Leucine Rich Repeat domains and a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No.	398254
Seq. ID	LIB3431-012-P1-K1-D10
Method	BLASTX
NCBI GI	g4510363
BLAST score	511
E value	6.0e-52
Match length	123
% identity	80
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	398255
Seq. ID	LIB3431-012-P1-K1-D12
Method	BLASTX

NCBI GI	g6056373
BLAST score	218
E value	1.0e-19
Match length	102
% identity	59
NCBI Description	(AC009894) elongation factor EF-2 [Arabidopsis thaliana]

Seq. No.	398256
Seq. ID	LIB3431-012-P1-K1-D2
Method	BLASTX
NCBI GI	g733454
BLAST score	575
E value	2.0e-59
Match length	133
% identity	82
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	398257
Seq. ID	LIB3431-012-P1-K1-D4
Method	BLASTN
NCBI GI	g20239
BLAST score	119
E value	4.0e-60
Match length	135
% identity	97
NCBI Description	O.sativa (rice) shoot-specific GOS5 gene for a putative chloroplast transit peptide

Seq. No.	398258
Seq. ID	LIB3431-012-P1-K1-D6
Method	BLASTX
NCBI GI	g1055130
BLAST score	220
E value	8.0e-18
Match length	131
% identity	44
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No.	398259
Seq. ID	LIB3431-012-P1-K1-D8
Method	BLASTX
NCBI GI	g3522929
BLAST score	589
E value	5.0e-61
Match length	126
% identity	87
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	398260
Seq. ID	LIB3431-012-P1-K1-D9

Method	BLASTX
NCBI GI	g115787
BLAST score	365
E value	4.0e-35
Match length	94
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398261
Seq. ID	LIB3431-012-P1-K1-E10
Method	BLASTX
NCBI GI	g115794
BLAST score	787
E value	3.0e-84
Match length	156
% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No.	398262
Seq. ID	LIB3431-012-P1-K1-E11
Method	BLASTX
NCBI GI	g4239891
BLAST score	617
E value	3.0e-67
Match length	151
% identity	87
NCBI Description	(AB016804) NADP-malic enzyme [Aloe arborescens]

Seq. No.	398263
Seq. ID	LIB3431-012-P1-K1-E12
Method	BLASTX
NCBI GI	g115787
BLAST score	352
E value	2.0e-33
Match length	90
% identity	80
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398264
Seq. ID	LIB3431-012-P1-K1-E4
Method	BLASTX
NCBI GI	g4531444
BLAST score	472
E value	3.0e-47
Match length	148

% identity	61
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	398265
Seq. ID	LIB3431-012-P1-K1-E6
Method	BLASTX
NCBI GI	g3075488
BLAST score	634
E value	3.0e-66
Match length	138
% identity	87
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398266
Seq. ID	LIB3431-012-P1-K1-E8
Method	BLASTX
NCBI GI	g1172874
BLAST score	251
E value	2.0e-21
Match length	129
% identity	42
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]

Seq. No.	398267
Seq. ID	LIB3431-012-P1-K1-E9
Method	BLASTX
NCBI GI	g100903
BLAST score	216
E value	2.0e-17
Match length	94
% identity	51
NCBI Description	nucleic acid-binding protein - maize >gi_168526 (M74566) nucleic acid-binding protein [Zea mays]

Seq. No.	398268
Seq. ID	LIB3431-012-P1-K1-F1
Method	BLASTX
NCBI GI	g3914557
BLAST score	671
E value	1.0e-70
Match length	134
% identity	94
NCBI Description	RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED PROTEIN) >gi_1155265 (U40219) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	398269
Seq. ID	LIB3431-012-P1-K1-F11
Method	BLASTX
NCBI GI	g733456
BLAST score	672
E value	9.0e-71
Match length	151

% identity	83
NCBI Description	(U23189) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	398270
Seq. ID	LIB3431-012-P1-K1-F12
Method	BLASTX
NCBI GI	g1835731
BLAST score	455
E value	2.0e-45
Match length	93
% identity	95
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	398271
Seq. ID	LIB3431-012-P1-K1-F9
Method	BLASTN
NCBI GI	g3885891
BLAST score	144
E value	3.0e-75
Match length	197
% identity	98
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	398272
Seq. ID	LIB3431-012-P1-K1-G1
Method	BLASTN
NCBI GI	g3885891
BLAST score	105
E value	3.0e-52
Match length	125
% identity	96
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	398273
Seq. ID	LIB3431-012-P1-K1-G10
Method	BLASTX
NCBI GI	g2754849
BLAST score	278
E value	4.0e-25
Match length	64
% identity	84
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	398274
Seq. ID	LIB3431-012-P1-K1-G12
Method	BLASTX
NCBI GI	g1632822
BLAST score	461
E value	3.0e-46
Match length	92
% identity	97
NCBI Description	(Y08962) transmembrane protein [Oryza sativa] >gi_1667594 (U77297) transmembrane protein [Oryza sativa]

Seq. No.	398275
Seq. ID	LIB3431-012-P1-K1-G2
Method	BLASTX
NCBI GI	g115525
BLAST score	162
E value	8.0e-19
Match length	78
% identity	67
NCBI Description	CALMODULIN >gi_71685_pir__MCSP calmodulin - spinach

Seq. No.	398276
Seq. ID	LIB3431-012-P1-K1-G3
Method	BLASTX
NCBI GI	g1709846
BLAST score	226
E value	2.0e-18
Match length	133
% identity	38
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) 22 kDa component of photosystem II [Lycopersicon esculentum]

Seq. No.	398277
Seq. ID	LIB3431-012-P1-K1-G5
Method	BLASTX
NCBI GI	g2407281
BLAST score	626
E value	2.0e-65
Match length	128
% identity	91
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398278
Seq. ID	LIB3431-012-P1-K1-G6
Method	BLASTX
NCBI GI	g1353352
BLAST score	342
E value	5.0e-32
Match length	104
% identity	63
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	398279
Seq. ID	LIB3431-012-P1-K1-G7
Method	BLASTX
NCBI GI	g122106
BLAST score	389
E value	1.0e-37
Match length	79
% identity	99
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum

aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	398280
Seq. ID	LIB3431-012-P1-K1-G9
Method	BLASTX
NCBI GI	g3075382
BLAST score	212
E value	7.0e-17
Match length	110
% identity	50
NCBI Description	(AC002505) putative peroxisome assembly protein PER8 [Arabidopsis thaliana] >gi_3075384 (AC004484) putative peroxisome assembly protein PER8 [Arabidopsis thaliana]

Seq. No.	398281
Seq. ID	LIB3431-012-P1-K1-H1
Method	BLASTX
NCBI GI	g3355477
BLAST score	441
E value	1.0e-43
Match length	105
% identity	44
NCBI Description	(AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No.	398282
Seq. ID	LIB3431-012-P1-K1-H10
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-11
Match length	36
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398283
Seq. ID	LIB3431-012-P1-K1-H2
Method	BLASTX
NCBI GI	g4102703
BLAST score	468
E value	1.0e-52
Match length	140
% identity	79
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	398284
Seq. ID	LIB3431-012-P1-K1-H3
Method	BLASTX
NCBI GI	g2653558
BLAST score	776
E value	6.0e-83
Match length	159
% identity	91
NCBI Description	(D50679) ferredoxin-sulfite reductase precursor [Zea mays]

Seq. No.	398285
Seq. ID	LIB3431-012-P1-K1-H5
Method	BLASTX
NCBI GI	g2982453
BLAST score	295
E value	4.0e-27
Match length	63
% identity	94
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	398286
Seq. ID	LIB3431-012-P1-K1-H7
Method	BLASTX
NCBI GI	g115787
BLAST score	280
E value	3.0e-25
Match length	77
% identity	77
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398287
Seq. ID	LIB3431-012-P1-K1-H8
Method	BLASTX
NCBI GI	g3345477
BLAST score	429
E value	3.0e-42
Match length	128
% identity	68
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	398288
Seq. ID	LIB3431-012-P1-K1-H9
Method	BLASTN
NCBI GI	g4887617
BLAST score	131
E value	2.0e-67
Match length	142
% identity	98
NCBI Description	Oryza sativa HOS59 mRNA, partial cds

Seq. No.	398289
Seq. ID	LIB3431-013-P1-K1-A10

Method	BLASTX
NCBI GI	g2673914
BLAST score	325
E value	8.0e-42
Match length	139
% identity	62
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	398290
Seq. ID	LIB3431-013-P1-K1-A12
Method	BLASTX
NCBI GI	g2660669
BLAST score	311
E value	2.0e-28
Match length	131
% identity	47
NCBI Description	(AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]

Seq. No.	398291
Seq. ID	LIB3431-013-P1-K1-A4
Method	BLASTX
NCBI GI	g132105
BLAST score	417
E value	5.0e-43
Match length	130
% identity	76
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398292
Seq. ID	LIB3431-013-P1-K1-A5
Method	BLASTX
NCBI GI	g4206195
BLAST score	213
E value	5.0e-17
Match length	54
% identity	67
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein [Arabidopsis thaliana]

Seq. No.	398293
Seq. ID	LIB3431-013-P1-K1-A6
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100

NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	398294
Seq. ID	LIB3431-013-P1-K1-A8
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.	398295
Seq. ID	LIB3431-013-P1-K1-A9
Method	BLASTX
NCBI GI	g2894534
BLAST score	537
E value	5.0e-55
Match length	116
% identity	91
NCBI Description	(AJ224327) aquaporin [Oryza sativa]
Seq. No.	398296
Seq. ID	LIB3431-013-P1-K1-B1
Method	BLASTX
NCBI GI	g1835731
BLAST score	348
E value	4.0e-33
Match length	69
% identity	99
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.	398297
Seq. ID	LIB3431-013-P1-K1-B10
Method	BLASTX
NCBI GI	g479406
BLAST score	649
E value	4.0e-68
Match length	126
% identity	94
NCBI Description	chlorophyll a/b-binding protein - garden pea >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding protein [Pisum sativum]
Seq. No.	398298
Seq. ID	LIB3431-013-P1-K1-B11
Method	BLASTX
NCBI GI	g320618
BLAST score	407
E value	9.0e-40
Match length	89
% identity	93
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398299
Seq. ID	LIB3431-013-P1-K1-B12
Method	BLASTX
NCBI GI	g1169798
BLAST score	336
E value	2.0e-31
Match length	85
% identity	79
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B) (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218) phosphoglucose isomerase (Pgi-b) [Oryza sativa]

Seq. No.	398300
Seq. ID	LIB3431-013-P1-K1-B2
Method	BLASTX
NCBI GI	g132105
BLAST score	501
E value	1.0e-52
Match length	134
% identity	81
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398301
Seq. ID	LIB3431-013-P1-K1-B3
Method	BLASTN
NCBI GI	g6002093
BLAST score	52
E value	9.0e-21
Match length	63
% identity	97
NCBI Description	Zizania latifolia cloroplast rps4 gene for ribosomal protein S4

Seq. No.	398302
Seq. ID	LIB3431-013-P1-K1-B4
Method	BLASTX
NCBI GI	g488573
BLAST score	600
E value	2.0e-62
Match length	122
% identity	98
NCBI Description	(U09463) histone H3.2 [Medicago sativa]

Seq. No.	398303
Seq. ID	LIB3431-013-P1-K1-B7
Method	BLASTX
NCBI GI	g3757521

BLAST score	331
E value	8.0e-31
Match length	129
% identity	49
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	398304
Seq. ID	LIB3431-013-P1-K1-B9
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	398305
Seq. ID	LIB3431-013-P1-K1-C1
Method	BLASTX
NCBI GI	g2632254
BLAST score	198
E value	1.0e-15
Match length	78
% identity	51
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	398306
Seq. ID	LIB3431-013-P1-K1-C10
Method	BLASTX
NCBI GI	g170131
BLAST score	375
E value	6.0e-36
Match length	150
% identity	53
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	398307
Seq. ID	LIB3431-013-P1-K1-C11
Method	BLASTN
NCBI GI	g596079
BLAST score	42
E value	3.0e-14
Match length	42
% identity	100
NCBI Description	Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA, complete cds

Seq. No.	398308
Seq. ID	LIB3431-013-P1-K1-C4
Method	BLASTX
NCBI GI	g3789952
BLAST score	645
E value	1.0e-67
Match length	127
% identity	98
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	398309
Seq. ID	LIB3431-013-P1-K1-C5
Method	BLASTX
NCBI GI	g131225
BLAST score	511
E value	6.0e-52
Match length	111
% identity	88
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	398310
Seq. ID	LIB3431-013-P1-K1-C6
Method	BLASTX
NCBI GI	g461899
BLAST score	184
E value	1.0e-13
Match length	116
% identity	40
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No.	398311
Seq. ID	LIB3431-013-P1-K1-C7
Method	BLASTX
NCBI GI	g3914466
BLAST score	199
E value	2.0e-15
Match length	36
% identity	97
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN subunit precursor [Zea mays]

Seq. No.	398312
Seq. ID	LIB3431-013-P1-K1-C9
Method	BLASTX
NCBI GI	g4512653
BLAST score	225
E value	2.0e-18
Match length	51
% identity	82
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	398313
Seq. ID	LIB3431-013-P1-K1-D10
Method	BLASTX
NCBI GI	g121343
BLAST score	729
E value	2.0e-77

Match length	138
% identity	99
NCBI Description	GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31) >gi_68598_pir__AJRZQD glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - rice >gi_20370_emb_CAA32462_ (X14246) precursor chloroplastic glutamine synthetase (AA -46 to 382) [Oryza sativa]

Seq. No.	398314
Seq. ID	LIB3431-013-P1-K1-D11
Method	BLASTX
NCBI GI	g3789952
BLAST score	566
E value	1.0e-58
Match length	127
% identity	94
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	398315
Seq. ID	LIB3431-013-P1-K1-D12
Method	BLASTX
NCBI GI	g3913240
BLAST score	401
E value	5.0e-39
Match length	94
% identity	90
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D) >gi_2239151_emb_CAA71128_ (Y10022) CHLD magnesium chelatase subunit [Nicotiana tabacum]

Seq. No.	398316
Seq. ID	LIB3431-013-P1-K1-D2
Method	BLASTX
NCBI GI	g132105
BLAST score	178
E value	2.0e-13
Match length	55
% identity	67
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398317
Seq. ID	LIB3431-013-P1-K1-D3
Method	BLASTX
NCBI GI	g82080
BLAST score	383
E value	6.0e-37

Match length	107
% identity	67
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	398318
Seq. ID	LIB3431-013-P1-K1-D5
Method	BLASTX
NCBI GI	g417260
BLAST score	421
E value	2.0e-41
Match length	128
% identity	66
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	398319
Seq. ID	LIB3431-013-P1-K1-D9
Method	BLASTX
NCBI GI	g100615
BLAST score	732
E value	8.0e-78
Match length	143
% identity	96
NCBI Description	ribulose-bisphosphate carboxylase activase A short form precursor - barley >gi_167091 (M55447) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	398320
Seq. ID	LIB3431-013-P1-K1-E1
Method	BLASTX
NCBI GI	g671740
BLAST score	558
E value	2.0e-57
Match length	107
% identity	96
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	398321
Seq. ID	LIB3431-013-P1-K1-E10
Method	BLASTX
NCBI GI	g3126854
BLAST score	705
E value	1.0e-74
Match length	133
% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398322
Seq. ID	LIB3431-013-P1-K1-E11
Method	BLASTX
NCBI GI	g115787
BLAST score	699
E value	6.0e-74

Match length	134
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398323
Seq. ID	LIB3431-013-P1-K1-E12
Method	BLASTX
NCBI GI	g3345477
BLAST score	362
E value	2.0e-34
Match length	115
% identity	63
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	398324
Seq. ID	LIB3431-013-P1-K1-E2
Method	BLASTN
NCBI GI	g409579
BLAST score	55
E value	4.0e-22
Match length	144
% identity	90
NCBI Description	Rice cbp1 gene for serine carboxypeptidase I, complete cds

Seq. No.	398325
Seq. ID	LIB3431-013-P1-K1-E3
Method	BLASTX
NCBI GI	g283038
BLAST score	357
E value	3.0e-34
Match length	75
% identity	91
NCBI Description	chlorophyll a/b-binding protein (cab-m7) precursor - maize >gi_22230_emb_CAA37474_ (X53398) light harvesting chlorophyll a /b binding protein [Zea mays]

Seq. No.	398326
Seq. ID	LIB3431-013-P1-K1-E4
Method	BLASTX
NCBI GI	g3582333
BLAST score	539
E value	7.0e-62
Match length	142
% identity	84
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	398327
Seq. ID	LIB3431-013-P1-K1-E5
Method	BLASTX
NCBI GI	g132105
BLAST score	614
E value	6.0e-64
Match length	132

% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398328
Seq. ID	LIB3431-013-P1-K1-E7
Method	BLASTX
NCBI GI	g1777312
BLAST score	259
E value	2.0e-22
Match length	75
% identity	65
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	398329
Seq. ID	LIB3431-013-P1-K1-E9
Method	BLASTN
NCBI GI	g4680189
BLAST score	169
E value	5.0e-90
Match length	185
% identity	98
NCBI Description	Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds

Seq. No.	398330
Seq. ID	LIB3431-013-P1-K1-F10
Method	BLASTN
NCBI GI	g2306980
BLAST score	103
E value	6.0e-51
Match length	163
% identity	91
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	398331
Seq. ID	LIB3431-013-P1-K1-F11
Method	BLASTX
NCBI GI	g3914603
BLAST score	684
E value	3.0e-72
Match length	134
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase [Oryza sativa]

Seq. No.	398332
Seq. ID	LIB3431-013-P1-K1-F2
Method	BLASTX
NCBI GI	g2290681
BLAST score	178
E value	7.0e-25
Match length	145
% identity	46
NCBI Description	(AF000135) acidic cellulase [Citrus sinensis]

Seq. No.	398333
Seq. ID	LIB3431-013-P1-K1-F3
Method	BLASTX
NCBI GI	g1777312
BLAST score	382
E value	8.0e-37
Match length	108
% identity	66
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	398334
Seq. ID	LIB3431-013-P1-K1-F7
Method	BLASTX
NCBI GI	g1729971
BLAST score	327
E value	2.0e-30
Match length	99
% identity	69
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa]

Seq. No.	398335
Seq. ID	LIB3431-013-P1-K1-F8
Method	BLASTX
NCBI GI	g4079798
BLAST score	293
E value	2.0e-26
Match length	104
% identity	59
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	398336
Seq. ID	LIB3431-013-P1-K1-G1
Method	BLASTX
NCBI GI	g2072555
BLAST score	228
E value	1.0e-18
Match length	44
% identity	98
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No.	398337
Seq. ID	LIB3431-013-P1-K1-G3
Method	BLASTX
NCBI GI	g347451
BLAST score	536
E value	7.0e-55
Match length	117
% identity	86
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	398338
Seq. ID	LIB3431-013-P1-K1-G4
Method	BLASTX
NCBI GI	g132105
BLAST score	665
E value	6.0e-70
Match length	144
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398339
Seq. ID	LIB3431-013-P1-K1-G6
Method	BLASTN
NCBI GI	g20262
BLAST score	157
E value	4.0e-83
Match length	187
% identity	96
NCBI Description	O.sativa light-induced mRNA

Seq. No.	398340
Seq. ID	LIB3431-013-P1-K1-G8
Method	BLASTX
NCBI GI	g729668
BLAST score	245
E value	6.0e-21
Match length	83
% identity	55
NCBI Description	HISTONE H1 >gi_2147479_pir__S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No.	398341
Seq. ID	LIB3431-013-P1-K1-G9
Method	BLASTX
NCBI GI	g4469021

BLAST score	245
E value	1.0e-20
Match length	72
% identity	69
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	398342
Seq. ID	LIB3431-013-P1-K1-H1
Method	BLASTN
NCBI GI	g3041776
BLAST score	60
E value	2.0e-25
Match length	88
% identity	92
NCBI Description	Oryza sativa mRNA for fructose-1,6-bisphosphatase (plastidic isoform), complete cds

Seq. No.	398343
Seq. ID	LIB3431-013-P1-K1-H11
Method	BLASTX
NCBI GI	g3789954
BLAST score	368
E value	4.0e-35
Match length	110
% identity	68
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	398344
Seq. ID	LIB3431-013-P1-K1-H12
Method	BLASTX
NCBI GI	g4079798
BLAST score	376
E value	5.0e-36
Match length	125
% identity	62
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	398345
Seq. ID	LIB3431-013-P1-K1-H3
Method	BLASTN
NCBI GI	g2072554
BLAST score	102
E value	2.0e-50
Match length	118
% identity	97
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398346
Seq. ID	LIB3431-013-P1-K1-H5
Method	BLASTX
NCBI GI	g2586083
BLAST score	206
E value	2.0e-17
Match length	117

% identity	43
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	398347
Seq. ID	LIB3431-013-P1-K1-H9
Method	BLASTX
NCBI GI	g2407281
BLAST score	709
E value	4.0e-75
Match length	133
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398348
Seq. ID	LIB3431-014-P1-K1-A10
Method	BLASTX
NCBI GI	g120657
BLAST score	540
E value	2.0e-55
Match length	135
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_66024_pir__DEZMG3 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No.	398349
Seq. ID	LIB3431-014-P1-K1-A4
Method	BLASTX
NCBI GI	g131225
BLAST score	220
E value	4.0e-18
Match length	68
% identity	69
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	398350
Seq. ID	LIB3431-014-P1-K1-A5
Method	BLASTX
NCBI GI	g2072555
BLAST score	214
E value	3.0e-17
Match length	44
% identity	91
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398351

Seq. ID	LIB3431-014-P1-K1-A6
Method	BLASTX
NCBI GI	g3913018
BLAST score	321
E value	7.0e-30
Match length	80
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	398352
Seq. ID	LIB3431-014-P1-K1-A7
Method	BLASTX
NCBI GI	g3551958
BLAST score	267
E value	1.0e-25
Match length	87
% identity	71
NCBI Description	(AF082032) senescence-associated protein 12 [Hemerocallis hybrid cultivar]

Seq. No.	398353
Seq. ID	LIB3431-014-P1-K1-A8
Method	BLASTX
NCBI GI	g3158476
BLAST score	348
E value	6.0e-33
Match length	93
% identity	69
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	398354
Seq. ID	LIB3431-014-P1-K1-B10
Method	BLASTX
NCBI GI	g132105
BLAST score	505
E value	3.0e-51
Match length	110
% identity	85
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398355
Seq. ID	LIB3431-014-P1-K1-B11
Method	BLASTX
NCBI GI	g4559339
BLAST score	610
E value	1.0e-63
Match length	138

% identity	86
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	398356
Seq. ID	LIB3431-014-P1-K1-B12
Method	BLASTX
NCBI GI	g1001794
BLAST score	161
E value	4.0e-11
Match length	41
% identity	71
NCBI Description	(D64005) hypothetical protein [Synechocystis sp.]

Seq. No.	398357
Seq. ID	LIB3431-014-P1-K1-B2
Method	BLASTN
NCBI GI	g5478796
BLAST score	57
E value	1.0e-23
Match length	73
% identity	96
NCBI Description	Oryza sativa CAO mRNA for chlorophyll b synthase, partial cds

Seq. No.	398358
Seq. ID	LIB3431-014-P1-K1-B3
Method	BLASTN
NCBI GI	g19094
BLAST score	46
E value	6.0e-17
Match length	54
% identity	96
NCBI Description	H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No.	398359
Seq. ID	LIB3431-014-P1-K1-B6
Method	BLASTX
NCBI GI	g4741205
BLAST score	395
E value	2.0e-38
Match length	107
% identity	64
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	398360
Seq. ID	LIB3431-014-P1-K1-B8
Method	BLASTX
NCBI GI	g1262849
BLAST score	266
E value	1.0e-25
Match length	64
% identity	95
NCBI Description	(U51633) type 1 light-harvesting chlorophyll a/b-binding polypeptide [Pinus palustris]

Seq. No.	398361

Seq. ID	LIB3431-014-P1-K1-C1
Method	BLASTN
NCBI GI	g3063523
BLAST score	45
E value	6.0e-17
Match length	49
% identity	98
NCBI Description	Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	398362
Seq. ID	LIB3431-014-P1-K1-C10
Method	BLASTN
NCBI GI	g3885891
BLAST score	41
E value	5.0e-14
Match length	85
% identity	87
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	398363
Seq. ID	LIB3431-014-P1-K1-C11
Method	BLASTX
NCBI GI	g3122914
BLAST score	213
E value	6.0e-17
Match length	147
% identity	31
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_1890130_gb_AAB49704.1_ (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	398364
Seq. ID	LIB3431-014-P1-K1-C2
Method	BLASTX
NCBI GI	g3126854
BLAST score	609
E value	2.0e-63
Match length	119
% identity	96
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398365
Seq. ID	LIB3431-014-P1-K1-C7
Method	BLASTN
NCBI GI	g3126853
BLAST score	172
E value	7.0e-92
Match length	210
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398366
Seq. ID	LIB3431-014-P1-K1-C8

Method	BLASTX
NCBI GI	g3126854
BLAST score	707
E value	8.0e-75
Match length	137
% identity	97
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398367
Seq. ID	LIB3431-014-P1-K1-D1
Method	BLASTX
NCBI GI	g1931640
BLAST score	445
E value	4.0e-44
Match length	125
% identity	61
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	398368
Seq. ID	LIB3431-014-P1-K1-D10
Method	BLASTN
NCBI GI	g1835730
BLAST score	288
E value	1.0e-161
Match length	308
% identity	99
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No.	398369
Seq. ID	LIB3431-014-P1-K1-D11
Method	BLASTX
NCBI GI	g19184
BLAST score	498
E value	4.0e-51
Match length	125
% identity	82
NCBI Description	(X61287) Type I (26 kD) CP29 polypeptide [Lycopersicon esculentum]

Seq. No.	398370
Seq. ID	LIB3431-014-P1-K1-D12
Method	BLASTX
NCBI GI	g2280518
BLAST score	157
E value	2.0e-10
Match length	116
% identity	31
NCBI Description	(AB005878) BYJ15 [Nicotiana tabacum]

Seq. No.	398371
Seq. ID	LIB3431-014-P1-K1-D2
Method	BLASTX
NCBI GI	g854731
BLAST score	662
E value	1.0e-69

Match length	140
% identity	94
NCBI Description	(U19183) acetyl-coenzyme A carboxylase [Zea mays]

Seq. No.	398372
Seq. ID	LIB3431-014-P1-K1-D3
Method	BLASTX
NCBI GI	g2306981
BLAST score	480
E value	4.0e-48
Match length	101
% identity	83
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No.	398373
Seq. ID	LIB3431-014-P1-K1-D4
Method	BLASTN
NCBI GI	g1835730
BLAST score	73
E value	8.0e-33
Match length	89
% identity	96
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No.	398374
Seq. ID	LIB3431-014-P1-K1-D5
Method	BLASTX
NCBI GI	g2160322
BLAST score	281
E value	5.0e-25
Match length	66
% identity	85
NCBI Description	(D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]

Seq. No.	398375
Seq. ID	LIB3431-014-P1-K1-D9
Method	BLASTX
NCBI GI	g132105
BLAST score	304
E value	1.0e-27
Match length	78
% identity	79
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398376
Seq. ID	LIB3431-014-P1-K1-E1
Method	BLASTX

NCBI GI	g3914603
BLAST score	664
E value	6.0e-70
Match length	130
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	398377
Seq. ID	LIB3431-014-P1-K1-E10
Method	BLASTX
NCBI GI	g3025189
BLAST score	455
E value	3.0e-45
Match length	141
% identity	61
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]

Seq. No.	398378
Seq. ID	LIB3431-014-P1-K1-E11
Method	BLASTX
NCBI GI	g2894534
BLAST score	746
E value	2.0e-79
Match length	146
% identity	99
NCBI Description	(AJ224327) aquaporin [Oryza sativa]

Seq. No.	398379
Seq. ID	LIB3431-014-P1-K1-E12
Method	BLASTX
NCBI GI	g3345477
BLAST score	534
E value	1.0e-54
Match length	149
% identity	70
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	398380
Seq. ID	LIB3431-014-P1-K1-E2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398381
Seq. ID	LIB3431-014-P1-K1-E4
Method	BLASTX

NCBI GI	g115787
BLAST score	236
E value	5.0e-20
Match length	67
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398382
Seq. ID	LIB3431-014-P1-K1-E5
Method	BLASTX
NCBI GI	g3808101
BLAST score	306
E value	7.0e-28
Match length	75
% identity	85
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	398383
Seq. ID	LIB3431-014-P1-K1-E6
Method	BLASTX
NCBI GI	g82080
BLAST score	501
E value	1.0e-50
Match length	137
% identity	69
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	398384
Seq. ID	LIB3431-014-P1-K1-E8
Method	BLASTX
NCBI GI	g2407279
BLAST score	575
E value	2.0e-59
Match length	117
% identity	93
NCBI Description	(AF017362) aldolase [Oryza sativa]

Seq. No.	398385
Seq. ID	LIB3431-014-P1-K1-E9
Method	BLASTX
NCBI GI	g2982362
BLAST score	479
E value	4.0e-48
Match length	103
% identity	85
NCBI Description	(AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No.	398386
Seq. ID	LIB3431-014-P1-K1-F1
Method	BLASTX
NCBI GI	g548605

BLAST score 608
E value 3.0e-63
Match length 133
% identity 91
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 398387
Seq. ID LIB3431-014-P1-K1-F10
Method BLASTX
NCBI GI g3548815
BLAST score 254
E value 1.0e-21
Match length 109
% identity 50
NCBI Description (AC005313) similar to axoneme-associated protein mst101 [Arabidopsis thaliana]

Seq. No. 398388
Seq. ID LIB3431-014-P1-K1-F11
Method BLASTX
NCBI GI g1903364
BLAST score 296
E value 1.0e-26
Match length 145
% identity 43
NCBI Description (AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No. 398389
Seq. ID LIB3431-014-P1-K1-F2
Method BLASTX
NCBI GI g3738285
BLAST score 320
E value 2.0e-29
Match length 101
% identity 61
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 398390
Seq. ID LIB3431-014-P1-K1-F4
Method BLASTX
NCBI GI g3548815
BLAST score 255
E value 6.0e-22
Match length 105
% identity 48
NCBI Description (AC005313) similar to axoneme-associated protein mst101 [Arabidopsis thaliana]

Seq. No. 398391
Seq. ID LIB3431-014-P1-K1-F6
Method BLASTX
NCBI GI g1346771

BLAST score	778
E value	4.0e-83
Match length	158
% identity	91
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP] >gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase (PCK1) - Urochloa panicoides >gi_607752 (U09241) phosphoenolpyruvate carboxykinase [Urochloa panicoides]

Seq. No.	398392
Seq. ID	LIB3431-014-P1-K1-F9
Method	BLASTX
NCBI GI	g3789954
BLAST score	328
E value	7.0e-31
Match length	66
% identity	94
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	398393
Seq. ID	LIB3431-014-P1-K1-G1
Method	BLASTX
NCBI GI	g2501189
BLAST score	464
E value	1.0e-46
Match length	101
% identity	88
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	398394
Seq. ID	LIB3431-014-P1-K1-G10
Method	BLASTX
NCBI GI	g2626753
BLAST score	376
E value	4.0e-36
Match length	109
% identity	67
NCBI Description	(AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No.	398395
Seq. ID	LIB3431-014-P1-K1-G12
Method	BLASTX
NCBI GI	g1769887
BLAST score	456
E value	1.0e-45
Match length	110
% identity	76
NCBI Description	(X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.	398396
Seq. ID	LIB3431-014-P1-K1-G2
Method	BLASTX
NCBI GI	g3913018

BLAST score 809
E value 8.0e-87
Match length 154
% identity 99
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 398397
Seq. ID LIB3431-014-P1-K1-G4
Method BLASTN
NCBI GI g20262
BLAST score 205
E value 1.0e-111
Match length 273
% identity 94
NCBI Description O.sativa light-induced mRNA

Seq. No. 398398
Seq. ID LIB3431-014-P1-K1-G5
Method BLASTX
NCBI GI g3288821
BLAST score 655
E value 1.0e-68
Match length 143
% identity 86
NCBI Description (AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 398399
Seq. ID LIB3431-014-P1-K1-G6
Method BLASTX
NCBI GI g462195
BLAST score 516
E value 2.0e-52
Match length 115
% identity 88
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 398400
Seq. ID LIB3431-014-P1-K1-G7
Method BLASTX
NCBI GI g283039
BLAST score 175
E value 1.0e-17
Match length 63
% identity 76
NCBI Description gene iojap protein - maize >gi_22349_emb_CAA78772_ (Z15063) putative iojap protein [Zea mays]

Seq. No. 398401

Seq. ID	LIB3431-014-P1-K1-H1
Method	BLASTX
NCBI GI	g729477
BLAST score	331
E value	9.0e-31
Match length	133
% identity	50
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_320548_pir__A44974 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - common ice plant >gi_167256 (M25528) ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1) [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A ferredoxin NADP reductase [Mesembryanthemum crystallinum]

Seq. No.	398402
Seq. ID	LIB3431-014-P1-K1-H11
Method	BLASTX
NCBI GI	g266893
BLAST score	768
E value	5.0e-82
Match length	151
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	398403
Seq. ID	LIB3431-014-P1-K1-H3
Method	BLASTN
NCBI GI	g3075487
BLAST score	281
E value	1.0e-157
Match length	285
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	398404
Seq. ID	LIB3431-014-P1-K1-H4
Method	BLASTX
NCBI GI	g4056507
BLAST score	267
E value	3.0e-23
Match length	85
% identity	62
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	398405
Seq. ID	LIB3431-014-P1-K1-H5
Method	BLASTX
NCBI GI	g320618
BLAST score	635
E value	2.0e-66
Match length	138

% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	398406
Seq. ID	LIB3431-014-P1-K1-H6
Method	BLASTX
NCBI GI	g606817
BLAST score	649
E value	3.0e-71
Match length	147
% identity	95
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]
Seq. No.	398407
Seq. ID	LIB3431-014-P1-K1-H8
Method	BLASTX
NCBI GI	g4666287
BLAST score	581
E value	3.0e-60
Match length	121
% identity	97
NCBI Description	(D85764) cytosolic monodehydroascorbate reductase [Oryza sativa]
Seq. No.	398408
Seq. ID	LIB3431-014-P1-K1-H9
Method	BLASTX
NCBI GI	g3075488
BLAST score	694
E value	5.0e-76
Match length	147
% identity	97
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.	398409
Seq. ID	LIB3431-014-P1-N1-A3
Method	BLASTN
NCBI GI	g3789951
BLAST score	88
E value	7.0e-42
Match length	213
% identity	85
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	398410
Seq. ID	LIB3431-014-P1-N1-A6
Method	BLASTN
NCBI GI	g218154
BLAST score	65

E value	5.0e-28
Match length	80
% identity	98
NCBI Description	Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No.	398411
Seq. ID	LIB3431-014-P1-N1-B10
Method	BLASTX
NCBI GI	g347451
BLAST score	207
E value	2.0e-16
Match length	39
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	398412
Seq. ID	LIB3431-014-P1-N1-B12
Method	BLASTX
NCBI GI	g1001794
BLAST score	168
E value	6.0e-12
Match length	41
% identity	73
NCBI Description	(D64005) hypothetical protein [Synechocystis sp.]

Seq. No.	398413
Seq. ID	LIB3431-014-P1-N1-B3
Method	BLASTX
NCBI GI	g3914466
BLAST score	302
E value	2.0e-27
Match length	71
% identity	79
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN subunit precursor [Zea mays]

Seq. No.	398414
Seq. ID	LIB3431-014-P1-N1-B8
Method	BLASTN
NCBI GI	g20181
BLAST score	138
E value	1.0e-71
Match length	145
% identity	99
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398415
Seq. ID	LIB3431-014-P1-N1-C1
Method	BLASTN
NCBI GI	g218207
BLAST score	94
E value	1.0e-45
Match length	138

% identity	92
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398416
Seq. ID	LIB3431-014-P1-N1-C10
Method	BLASTX
NCBI GI	g3885892
BLAST score	342
E value	4.0e-32
Match length	66
% identity	100
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	398417
Seq. ID	LIB3431-014-P1-N1-C2
Method	BLASTX
NCBI GI	g3126854
BLAST score	272
E value	6.0e-24
Match length	57
% identity	93
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398418
Seq. ID	LIB3431-014-P1-N1-C7
Method	BLASTN
NCBI GI	g3126853
BLAST score	145
E value	8.0e-76
Match length	207
% identity	97
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398419
Seq. ID	LIB3431-014-P1-N1-C8
Method	BLASTX
NCBI GI	g3126854
BLAST score	456
E value	9.0e-46
Match length	103
% identity	94
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398420
Seq. ID	LIB3431-014-P1-N1-D10
Method	BLASTX
NCBI GI	g1835731
BLAST score	236
E value	6.0e-20
Match length	56
% identity	82
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	398421
Seq. ID	LIB3431-014-P1-N1-D11
Method	BLASTX
NCBI GI	g733454
BLAST score	210
E value	1.0e-16
Match length	48
% identity	85
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	398422
Seq. ID	LIB3431-014-P1-N1-D3
Method	BLASTX
NCBI GI	g99486
BLAST score	275
E value	4.0e-24
Match length	67
% identity	79
NCBI Description	chlorophyll a/b-binding protein (clone pINEab 31) - Scotch pine >gi_20792_emb_CAA41406_ (X58516) Type II chlorophyll a /b-binding protein [Pinus sylvestris]

Seq. No.	398423
Seq. ID	LIB3431-014-P1-N1-D6
Method	BLASTN
NCBI GI	g168525
BLAST score	37
E value	3.0e-11
Match length	53
% identity	92
NCBI Description	Zea mays nucleic acid-binding protein (NBP)

Seq. No.	398424
Seq. ID	LIB3431-014-P1-N1-D8
Method	BLASTX
NCBI GI	g80783
BLAST score	190
E value	3.0e-14
Match length	120
% identity	36
NCBI Description	hypothetical 31.7K protein (aphE region) - Streptomyces griseus >gi_153164 (M37378) streptomycin-3'-phosphotransferase [Streptomyces griseus]

Seq. No.	398425
Seq. ID	LIB3431-014-P1-N1-D9
Method	BLASTX
NCBI GI	g671740
BLAST score	225
E value	2.0e-18
Match length	44
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	398426

Seq. ID	LIB3431-014-P1-N1-E1
Method	BLASTX
NCBI GI	g132166
BLAST score	149
E value	1.0e-09
Match length	31
% identity	81
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	398427
Seq. ID	LIB3431-014-P1-N1-E11
Method	BLASTX
NCBI GI	g2696804
BLAST score	308
E value	4.0e-28
Match length	56
% identity	100
NCBI Description	(AB009665) water channel protein [Oryza sativa]

Seq. No.	398428
Seq. ID	LIB3431-014-P1-N1-E12
Method	BLASTN
NCBI GI	g606816
BLAST score	350
E value	0.0e+00
Match length	364
% identity	99
NCBI Description	Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds

Seq. No.	398429
Seq. ID	LIB3431-014-P1-N1-E2
Method	BLASTN
NCBI GI	g2072554
BLAST score	343
E value	0.0e+00
Match length	377
% identity	98
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398430
Seq. ID	LIB3431-014-P1-N1-E4
Method	BLASTX
NCBI GI	g3036951
BLAST score	233
E value	2.0e-19
Match length	57
% identity	93
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	398431
Seq. ID	LIB3431-014-P1-N1-E5
Method	BLASTX
NCBI GI	g3808101
BLAST score	181
E value	2.0e-13
Match length	43
% identity	84
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	398432
Seq. ID	LIB3431-014-P1-N1-E8
Method	BLASTX
NCBI GI	g2407279
BLAST score	200
E value	8.0e-25
Match length	67
% identity	93
NCBI Description	(AF017362) aldolase [Oryza sativa]

Seq. No.	398433
Seq. ID	LIB3431-014-P1-N1-E9
Method	BLASTX
NCBI GI	g2982362
BLAST score	494
E value	6.0e-50
Match length	100
% identity	89
NCBI Description	(AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No.	398434
Seq. ID	LIB3431-014-P1-N1-F1
Method	BLASTX
NCBI GI	g548605
BLAST score	232
E value	1.0e-20
Match length	64
% identity	88
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398435
Seq. ID	LIB3431-014-P1-N1-F5
Method	BLASTN
NCBI GI	g11957
BLAST score	63
E value	7.0e-27
Match length	143
% identity	43
NCBI Description	Rice complete chloroplast genome

Seq. No.	398436
Seq. ID	LIB3431-014-P1-N1-F6
Method	BLASTX

NCBI GI	g1346771
BLAST score	189
E value	2.0e-17
Match length	67
% identity	78
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP] >gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase (PCK1) - Urochloa panicoides >gi_607752 (U09241) phosphoenolpyruvate carboxykinase [Urochloa panicoides]

Seq. No.	398437
Seq. ID	LIB3431-014-P1-N1-F9
Method	BLASTX
NCBI GI	g3789954
BLAST score	277
E value	2.0e-24
Match length	54
% identity	94
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	398438
Seq. ID	LIB3431-014-P1-N1-G2
Method	BLASTX
NCBI GI	g2407279
BLAST score	149
E value	2.0e-11
Match length	45
% identity	81
NCBI Description	(AF017362) aldolase [Oryza sativa]

Seq. No.	398439
Seq. ID	LIB3431-014-P1-N1-G4
Method	BLASTN
NCBI GI	g20262
BLAST score	300
E value	1.0e-168
Match length	345
% identity	97
NCBI Description	O.sativa light-induced mRNA

Seq. No.	398440
Seq. ID	LIB3431-014-P1-N1-G6
Method	BLASTN
NCBI GI	g3789949
BLAST score	142
E value	2.0e-74
Match length	146
% identity	99
NCBI Description	Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No.	398441
Seq. ID	LIB3431-014-P1-N1-G7
Method	BLASTX
NCBI GI	g283039
BLAST score	157

E value	2.0e-10
Match length	39
% identity	79
NCBI Description	gene iojap protein - maize >gi_22349_emb_CAA78772_ (Z15063) putative iojap protein [Zea mays]

Seq. No.	398442
Seq. ID	LIB3431-014-P1-N1-H1
Method	BLASTX
NCBI GI	g729478
BLAST score	247
E value	1.0e-23
Match length	60
% identity	83
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	398443
Seq. ID	LIB3431-014-P1-N1-H3
Method	BLASTN
NCBI GI	g3075487
BLAST score	80
E value	5.0e-37
Match length	205
% identity	90
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	398444
Seq. ID	LIB3431-014-P1-N1-H8
Method	BLASTX
NCBI GI	g4666287
BLAST score	336
E value	1.0e-31
Match length	65
% identity	100
NCBI Description	(D85764) cytosolic monodehydroascorbate reductase [Oryza sativa]

Seq. No.	398445
Seq. ID	LIB3431-014-P1-N1-H9
Method	BLASTN
NCBI GI	g3075487
BLAST score	241
E value	1.0e-133
Match length	253
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	398446
Seq. ID	LIB3431-015-P1-K1-A10
Method	BLASTX

NCBI GI	g2072727
BLAST score	700
E value	4.0e-74
Match length	140
% identity	97
NCBI Description	(Y12595) Fd-GOGAT protein [Oryza sativa]

Seq. No.	398447
Seq. ID	LIB3431-015-P1-K1-A11
Method	BLASTN
NCBI GI	g1398998
BLAST score	86
E value	8.0e-41
Match length	173
% identity	99
NCBI Description	Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II, complete cds

Seq. No.	398448
Seq. ID	LIB3431-015-P1-K1-A12
Method	BLASTX
NCBI GI	g4138179
BLAST score	338
E value	4.0e-32
Match length	69
% identity	93
NCBI Description	(AJ223969) elongation factor 1 alpha subunit [Malus domestica]

Seq. No.	398449
Seq. ID	LIB3431-015-P1-K1-A4
Method	BLASTX
NCBI GI	g488571
BLAST score	515
E value	2.0e-52
Match length	103
% identity	99
NCBI Description	(U09462) histone H3.2 [Medicago sativa]

Seq. No.	398450
Seq. ID	LIB3431-015-P1-K1-A5
Method	BLASTX
NCBI GI	g4138290
BLAST score	576
E value	1.0e-59
Match length	124
% identity	86
NCBI Description	(AJ005841) thioredoxin M [Oryza sativa]

Seq. No.	398451
Seq. ID	LIB3431-015-P1-K1-A6
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100

NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	398452
Seq. ID	LIB3431-015-P1-K1-A7
Method	BLASTX
NCBI GI	g2293480
BLAST score	246
E value	3.0e-21
Match length	48
% identity	98
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]
Seq. No.	398453
Seq. ID	LIB3431-015-P1-K1-A8
Method	BLASTX
NCBI GI	g3142698
BLAST score	534
E value	1.0e-54
Match length	129
% identity	71
NCBI Description	(AF064542) protein farnesyltransferase subunit A [Arabidopsis thaliana]
Seq. No.	398454
Seq. ID	LIB3431-015-P1-K1-B1
Method	BLASTX
NCBI GI	g2407281
BLAST score	570
E value	6.0e-59
Match length	109
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]
Seq. No.	398455
Seq. ID	LIB3431-015-P1-K1-B10
Method	BLASTX
NCBI GI	g115787
BLAST score	438
E value	1.0e-43
Match length	97
% identity	86
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]
Seq. No.	398456
Seq. ID	LIB3431-015-P1-K1-B11
Method	BLASTX
NCBI GI	g2501647
BLAST score	292
E value	3.0e-26
Match length	80
% identity	69
NCBI Description	UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)

>gi_1362120_pir__S55732 uroporphyrinogen decarboxylase - common tobacco >gi_1009429_emb_CAA58040_ (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]

Seq. No.	398457
Seq. ID	LIB3431-015-P1-K1-B12
Method	BLASTN
NCBI GI	g218171
BLAST score	236
E value	1.0e-130
Match length	236
% identity	100
NCBI Description	Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No.	398458
Seq. ID	LIB3431-015-P1-K1-B3
Method	BLASTX
NCBI GI	g3122724
BLAST score	313
E value	9.0e-29
Match length	69
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal protein L38 isolog [Arabidopsis thaliana]

Seq. No.	398459
Seq. ID	LIB3431-015-P1-K1-B4
Method	BLASTX
NCBI GI	g347451
BLAST score	173
E value	1.0e-12
Match length	75
% identity	51
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	398460
Seq. ID	LIB3431-015-P1-K1-B9
Method	BLASTX
NCBI GI	g3193290
BLAST score	213
E value	3.0e-17
Match length	73
% identity	59
NCBI Description	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido

Seq. No.	398461
Seq. ID	LIB3431-015-P1-K1-C10
Method	BLASTX
NCBI GI	g5007084
BLAST score	706

E value	8.0e-75
Match length	137
% identity	98
NCBI Description	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]

Seq. No.	398462
Seq. ID	LIB3431-015-P1-K1-C11
Method	BLASTX
NCBI GI	g3885513
BLAST score	237
E value	7.0e-20
Match length	59
% identity	66
NCBI Description	(AF084201) similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]

Seq. No.	398463
Seq. ID	LIB3431-015-P1-K1-C2
Method	BLASTX
NCBI GI	g2072555
BLAST score	348
E value	7.0e-33
Match length	62
% identity	98
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398464
Seq. ID	LIB3431-015-P1-K1-C4
Method	BLASTN
NCBI GI	g4519195
BLAST score	40
E value	5.0e-13
Match length	68
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	398465
Seq. ID	LIB3431-015-P1-K1-C7
Method	BLASTX
NCBI GI	g1532135
BLAST score	339
E value	6.0e-32
Match length	112
% identity	60
NCBI Description	(U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea]

Seq. No.	398466
Seq. ID	LIB3431-015-P1-K1-C8
Method	BLASTX
NCBI GI	g2623298
BLAST score	532
E value	2.0e-54

Match length	116
% identity	84
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No.	398467
Seq. ID	LIB3431-015-P1-K1-C9
Method	BLASTX
NCBI GI	g3868756
BLAST score	494
E value	3.0e-50
Match length	99
% identity	91
NCBI Description	(D86611) catalase [Oryza sativa]

Seq. No.	398468
Seq. ID	LIB3431-015-P1-K1-D1
Method	BLASTX
NCBI GI	g1055130
BLAST score	275
E value	3.0e-24
Match length	126
% identity	44
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No.	398469
Seq. ID	LIB3431-015-P1-K1-D11
Method	BLASTX
NCBI GI	g3126854
BLAST score	437
E value	4.0e-58
Match length	114
% identity	92
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398470
Seq. ID	LIB3431-015-P1-K1-D2
Method	BLASTN
NCBI GI	g20262
BLAST score	175
E value	1.0e-93
Match length	175
% identity	100
NCBI Description	O.sativa light-induced mRNA

Seq. No.	398471
Seq. ID	LIB3431-015-P1-K1-D3
Method	BLASTX
NCBI GI	g347451
BLAST score	165
E value	1.0e-24
Match length	92
% identity	59

09560760.960704

NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	398472
Seq. ID	LIB3431-015-P1-K1-D5
Method	BLASTX
NCBI GI	g2196672
BLAST score	444
E value	4.0e-44
Match length	93
% identity	89
NCBI Description	(Y08807) HMGd1 [Zea mays]

Seq. No.	398473
Seq. ID	LIB3431-015-P1-K1-D7
Method	BLASTX
NCBI GI	g4455180
BLAST score	184
E value	1.0e-13
Match length	44
% identity	82
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	398474
Seq. ID	LIB3431-015-P1-K1-D9
Method	BLASTX
NCBI GI	g3885888
BLAST score	282
E value	3.0e-25
Match length	63
% identity	90
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	398475
Seq. ID	LIB3431-015-P1-K1-E1
Method	BLASTN
NCBI GI	g295500
BLAST score	50
E value	4.0e-19
Match length	102
% identity	87
NCBI Description	Triticum aestivum heat shock protein 16.9C (hsp16.9C) mRNA, 3' end

Seq. No.	398476
Seq. ID	LIB3431-015-P1-K1-E11
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	3.0e-11
Match length	48
% identity	66
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398477
Seq. ID	LIB3431-015-P1-K1-E12
Method	BLASTN

NCBI GI	g5410347
BLAST score	40
E value	3.0e-13
Match length	56
% identity	93
NCBI Description	Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No.	398478
Seq. ID	LIB3431-015-P1-K1-E2
Method	BLASTN
NCBI GI	g168608
BLAST score	43
E value	7.0e-15
Match length	67
% identity	91
NCBI Description	Maize 17S ribosomal RNA gene and flanks

Seq. No.	398479
Seq. ID	LIB3431-015-P1-K1-E3
Method	BLASTX
NCBI GI	g3292814
BLAST score	169
E value	7.0e-12
Match length	47
% identity	74
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	398480
Seq. ID	LIB3431-015-P1-K1-E6
Method	BLASTN
NCBI GI	g304219
BLAST score	33
E value	3.0e-09
Match length	65
% identity	88
NCBI Description	Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No.	398481
Seq. ID	LIB3431-015-P1-K1-E7
Method	BLASTN
NCBI GI	g5410347
BLAST score	41
E value	1.0e-13
Match length	57
% identity	93
NCBI Description	Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No.	398482
Seq. ID	LIB3431-015-P1-K1-E9
Method	BLASTX
NCBI GI	g4539333
BLAST score	425
E value	8.0e-42
Match length	129
% identity	64
NCBI Description	(AL035539) putative amino acid transport protein

[Arabidopsis thaliana]

Seq. No.	398483
Seq. ID	LIB3431-015-P1-K1-F10
Method	BLASTX
NCBI GI	g399213
BLAST score	501
E value	6.0e-51
Match length	119
% identity	82
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato >gi_170435 (M32604) ATP-dependent protease (CD4B) [Lycopersicon esculentum]

Seq. No.	398484
Seq. ID	LIB3431-015-P1-K1-F11
Method	BLASTX
NCBI GI	g3128228
BLAST score	520
E value	1.0e-54
Match length	124
% identity	88
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	398485
Seq. ID	LIB3431-015-P1-K1-F2
Method	BLASTX
NCBI GI	g2497903
BLAST score	220
E value	6.0e-18
Match length	59
% identity	68
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like protein [Oryza sativa] >gi_1815628 (U43530) metallothionein-like type 2 [Oryza sativa]

Seq. No.	398486
Seq. ID	LIB3431-015-P1-K1-F3
Method	BLASTX
NCBI GI	g115787
BLAST score	578
E value	6.0e-60
Match length	112
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398487
Seq. ID	LIB3431-015-P1-K1-F4
Method	BLASTX

NCBI GI	g82080
BLAST score	422
E value	2.0e-41
Match length	120
% identity	68
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	398488
Seq. ID	LIB3431-015-P1-K1-F8
Method	BLASTX
NCBI GI	g3885888
BLAST score	230
E value	4.0e-19
Match length	93
% identity	57
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	398489
Seq. ID	LIB3431-015-P1-K1-G1
Method	BLASTX
NCBI GI	g100102
BLAST score	156
E value	3.0e-10
Match length	86
% identity	38
NCBI Description	seed protein precursor - tick bean >gi_22043_emb_CAA39696_ (X56240) unknown seed protein [Vicia faba]

Seq. No.	398490
Seq. ID	LIB3431-015-P1-K1-G10
Method	BLASTX
NCBI GI	g2281089
BLAST score	376
E value	4.0e-36
Match length	79
% identity	90
NCBI Description	(AC002333) Sm protein F isolog [Arabidopsis thaliana]

Seq. No.	398491
Seq. ID	LIB3431-015-P1-K1-G11
Method	BLASTX
NCBI GI	g2306981
BLAST score	175
E value	8.0e-13
Match length	32
% identity	91
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No.	398492
Seq. ID	LIB3431-015-P1-K1-G12
Method	BLASTX
NCBI GI	g82080
BLAST score	322
E value	7.0e-30
Match length	86

% identity	71
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	398493
Seq. ID	LIB3431-015-P1-K1-G2
Method	BLASTX
NCBI GI	g82080
BLAST score	432
E value	1.0e-42
Match length	122
% identity	68
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	398494
Seq. ID	LIB3431-015-P1-K1-G3
Method	BLASTX
NCBI GI	g548605
BLAST score	519
E value	6.0e-53
Match length	113
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398495
Seq. ID	LIB3431-015-P1-K1-G4
Method	BLASTX
NCBI GI	g5295988
BLAST score	177
E value	9.0e-13
Match length	51
% identity	75
NCBI Description	(AB003327) MADS box-like protein [Oryza sativa]

Seq. No.	398496
Seq. ID	LIB3431-015-P1-K1-G5
Method	BLASTX
NCBI GI	g5734720
BLAST score	212
E value	6.0e-17
Match length	100
% identity	48
NCBI Description	(AC008075) Contains PF_01426 BAH (bromo-adjacent homology) domain. ESTs gb_N96349, gb_T42710, gb_H77084, gb_AA395147 and gb_AA605500 come from this gene. [Arabidopsis thaliana]

Seq. No.	398497
Seq. ID	LIB3431-015-P1-K1-G6
Method	BLASTN
NCBI GI	g1002914

BLAST score	40
E value	4.0e-13
Match length	56
% identity	93
NCBI Description	Oryza sativa cap-binding protein p26 mRNA, complete cds

Seq. No.	398498
Seq. ID	LIB3431-015-P1-K1-G7
Method	BLASTX
NCBI GI	g1495768
BLAST score	266
E value	3.0e-23
Match length	108
% identity	51
NCBI Description	(Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]

Seq. No.	398499
Seq. ID	LIB3431-015-P1-K1-G8
Method	BLASTX
NCBI GI	g166410
BLAST score	408
E value	7.0e-40
Match length	111
% identity	69
NCBI Description	(L07291) Alfin-1 [Medicago sativa]

Seq. No.	398500
Seq. ID	LIB3431-015-P1-K1-G9
Method	BLASTX
NCBI GI	g3126854
BLAST score	616
E value	3.0e-64
Match length	115
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398501
Seq. ID	LIB3431-015-P1-K1-H11
Method	BLASTN
NCBI GI	g6103440
BLAST score	51
E value	2.0e-20
Match length	55
% identity	98
NCBI Description	Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds

Seq. No.	398502
Seq. ID	LIB3431-015-P1-K1-H12
Method	BLASTN
NCBI GI	g3135542
BLAST score	39
E value	1.0e-12
Match length	67
% identity	90
NCBI Description	Oryza sativa aquaporin (PIP2a) mRNA, complete cds

Seq. No.	398503
Seq. ID	LIB3431-015-P1-K1-H2
Method	BLASTX
NCBI GI	g4455180
BLAST score	396
E value	1.0e-38
Match length	108
% identity	71
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	398504
Seq. ID	LIB3431-015-P1-K1-H3
Method	BLASTX
NCBI GI	g3913811
BLAST score	704
E value	1.0e-74
Match length	141
% identity	99
NCBI Description	GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR) >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA reductase [Oryza sativa]

Seq. No.	398505
Seq. ID	LIB3431-015-P1-K1-H6
Method	BLASTN
NCBI GI	g2072554
BLAST score	212
E value	1.0e-116
Match length	260
% identity	96
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398506
Seq. ID	LIB3431-015-P1-K1-H7
Method	BLASTX
NCBI GI	g3075488
BLAST score	211
E value	6.0e-17
Match length	57
% identity	72
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398507
Seq. ID	LIB3431-015-P1-K1-H8
Method	BLASTX
NCBI GI	g3915309
BLAST score	159
E value	9.0e-11
Match length	93
% identity	32
NCBI Description	D-XYLOSE-PROTON SYMPORT (D-XYLOSE TRANSPORTER) >gi_2895856 (AF045552) D-xylose proton-symporter [Lactobacillus brevis]

Seq. No.	398508
Seq. ID	LIB3431-015-P1-K1-H9

Method	BLASTX
NCBI GI	g4803952
BLAST score	446
E value	2.0e-44
Match length	113
% identity	76
NCBI Description	(AC006202) hypothetical protein [Arabidopsis thaliana]

Seq. No.	398509
Seq. ID	LIB3431-016-P1-K1-A11
Method	BLASTX
NCBI GI	g6093830
BLAST score	155
E value	3.0e-10
Match length	37
% identity	81
NCBI Description	PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

Seq. No.	398510
Seq. ID	LIB3431-016-P1-K1-A12
Method	BLASTX
NCBI GI	g895845
BLAST score	165
E value	2.0e-11
Match length	103
% identity	38
NCBI Description	(X87689) putative start codon [Homo sapiens]

Seq. No.	398511
Seq. ID	LIB3431-016-P1-K1-A2
Method	BLASTX
NCBI GI	g5912299
BLAST score	672
E value	7.0e-71
Match length	133
% identity	100
NCBI Description	(AJ133787) gigantea homologue [Oryza sativa]

Seq. No.	398512
Seq. ID	LIB3431-016-P1-K1-A3
Method	BLASTX
NCBI GI	g4680685
BLAST score	214
E value	4.0e-17
Match length	100
% identity	42
NCBI Description	(AF132957) CGI-23 protein [Homo sapiens]

Seq. No.	398513
Seq. ID	LIB3431-016-P1-K1-A5
Method	BLASTX
NCBI GI	g3126854
BLAST score	620
E value	9.0e-65

Match length	116
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398514
Seq. ID	LIB3431-016-P1-K1-A6
Method	BLASTX
NCBI GI	g320618
BLAST score	481
E value	2.0e-48
Match length	107
% identity	85
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398515
Seq. ID	LIB3431-016-P1-K1-A7
Method	BLASTN
NCBI GI	g6015437
BLAST score	34
E value	6.0e-10
Match length	38
% identity	97
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398516
Seq. ID	LIB3431-016-P1-K1-A8
Method	BLASTX
NCBI GI	g4079798
BLAST score	342
E value	4.0e-32
Match length	98
% identity	71
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	398517
Seq. ID	LIB3431-016-P1-K1-A9
Method	BLASTX
NCBI GI	g121343
BLAST score	198
E value	4.0e-24
Match length	107
% identity	63
NCBI Description	GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31) >gi_68598_pir__AJRZQD glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - rice >gi_20370_emb_CAA32462_ (X14246) precursor chloroplastic glutamine synthetase (AA -46 to 382) [Oryza sativa]

Seq. No.	398518
Seq. ID	LIB3431-016-P1-K1-B1
Method	BLASTX

NCBI GI	g3789954
BLAST score	684
E value	3.0e-72
Match length	128
% identity	98
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	398519
Seq. ID	LIB3431-016-P1-K1-B10
Method	BLASTX
NCBI GI	g3461820
BLAST score	212
E value	6.0e-17
Match length	112
% identity	44
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	398520
Seq. ID	LIB3431-016-P1-K1-B11
Method	BLASTN
NCBI GI	g2570514
BLAST score	178
E value	2.0e-95
Match length	186
% identity	99
NCBI Description	Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	398521
Seq. ID	LIB3431-016-P1-K1-B12
Method	BLASTX
NCBI GI	g871931
BLAST score	260
E value	2.0e-22
Match length	80
% identity	66
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	398522
Seq. ID	LIB3431-016-P1-K1-B2
Method	BLASTX
NCBI GI	g6093869
BLAST score	599
E value	3.0e-62
Match length	128
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi_2982259 (AF051212) probable 60s ribosomal protein L13a [Picea mariana]

Seq. No.	398523
Seq. ID	LIB3431-016-P1-K1-B4
Method	BLASTX
NCBI GI	g5006853
BLAST score	372
E value	7.0e-36
Match length	96
% identity	80

NCBI Description	(AF145728) homeodomain leucine zipper protein [Oryza sativa]

Seq. No.	398524
Seq. ID	LIB3431-016-P1-K1-B5
Method	BLASTX
NCBI GI	g5702015
BLAST score	338
E value	1.0e-31
Match length	105
% identity	65
NCBI Description	(AJ012215) GAL83 protein [Solanum tuberosum]

Seq. No.	398525
Seq. ID	LIB3431-016-P1-K1-B6
Method	BLASTX
NCBI GI	g2407281
BLAST score	541
E value	2.0e-55
Match length	109
% identity	94
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398526
Seq. ID	LIB3431-016-P1-K1-B7
Method	BLASTX
NCBI GI	g1346698
BLAST score	610
E value	1.0e-63
Match length	131
% identity	93
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_21272_emb_CAA48479_ (X68430) phosphoglycerate kinase [Spinacia oleracea]

Seq. No.	398527
Seq. ID	LIB3431-016-P1-K1-B8
Method	BLASTX
NCBI GI	g4666287
BLAST score	523
E value	2.0e-53
Match length	102
% identity	100
NCBI Description	(D85764) cytosolic monodehydroascorbate reductase [Oryza sativa]

Seq. No.	398528
Seq. ID	LIB3431-016-P1-K1-C1
Method	BLASTX
NCBI GI	g3345477
BLAST score	504
E value	4.0e-51
Match length	96
% identity	100
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	398529
Seq. ID	LIB3431-016-P1-K1-C10
Method	BLASTX
NCBI GI	g3913641
BLAST score	314
E value	5.0e-29
Match length	61
% identity	100
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041777_dbj_BAA25423_ (AB007194) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	398530
Seq. ID	LIB3431-016-P1-K1-C11
Method	BLASTX
NCBI GI	g3868756
BLAST score	289
E value	1.0e-41
Match length	120
% identity	72
NCBI Description	(D86611) catalase [Oryza sativa]

Seq. No.	398531
Seq. ID	LIB3431-016-P1-K1-C12
Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	1.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	398532
Seq. ID	LIB3431-016-P1-K1-C2
Method	BLASTX
NCBI GI	g1706260
BLAST score	648
E value	5.0e-68
Match length	132
% identity	90
NCBI Description	CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597 cysteine proteinase 1 precursor - maize >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No.	398533
Seq. ID	LIB3431-016-P1-K1-C5
Method	BLASTX
NCBI GI	g3075488
BLAST score	660
E value	2.0e-69
Match length	126
% identity	100
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398534

Seq. ID	LIB3431-016-P1-K1-C6
Method	BLASTN
NCBI GI	g2072554
BLAST score	301
E value	1.0e-169
Match length	301
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398535
Seq. ID	LIB3431-016-P1-K1-C7
Method	BLASTX
NCBI GI	g3345477
BLAST score	371
E value	1.0e-35
Match length	117
% identity	63
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	398536
Seq. ID	LIB3431-016-P1-K1-C8
Method	BLASTN
NCBI GI	g11957
BLAST score	371
E value	0.0e+00
Match length	392
% identity	98
NCBI Description	Rice complete chloroplast genome

Seq. No.	398537
Seq. ID	LIB3431-016-P1-K1-C9
Method	BLASTX
NCBI GI	g2330739
BLAST score	295
E value	1.0e-26
Match length	90
% identity	58
NCBI Description	(Z98598) putative transcriptional regulator [Schizosaccharomyces pombe]

Seq. No.	398538
Seq. ID	LIB3431-016-P1-K1-D1
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398539
Seq. ID	LIB3431-016-P1-K1-D10
Method	BLASTN
NCBI GI	g20177
BLAST score	43
E value	8.0e-16

Match length	43
% identity	100
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398540
Seq. ID	LIB3431-016-P1-K1-D11
Method	BLASTX
NCBI GI	g4914457
BLAST score	303
E value	1.0e-27
Match length	105
% identity	52
NCBI Description	(AL050400) putative protein [Arabidopsis thaliana]

Seq. No.	398541
Seq. ID	LIB3431-016-P1-K1-D12
Method	BLASTX
NCBI GI	g927025
BLAST score	196
E value	5.0e-15
Match length	116
% identity	38
NCBI Description	(L44134) SPF1-like DNA-binding protein [Cucumis sativus]

Seq. No.	398542
Seq. ID	LIB3431-016-P1-K1-D2
Method	BLASTX
NCBI GI	g2129950
BLAST score	646
E value	8.0e-68
Match length	132
% identity	98
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP9) - common tobacco

Seq. No.	398543
Seq. ID	LIB3431-016-P1-K1-D4
Method	BLASTX
NCBI GI	g115813
BLAST score	423
E value	1.0e-41
Match length	117
% identity	73
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398544
Seq. ID	LIB3431-016-P1-K1-D6
Method	BLASTX
NCBI GI	g3789954
BLAST score	743
E value	4.0e-79
Match length	134
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No.	398545
Seq. ID	LIB3431-016-P1-K1-D7
Method	BLASTX
NCBI GI	g3618310
BLAST score	331
E value	7.0e-31
Match length	97
% identity	67
NCBI Description	(AB001883) zinc finger protein [Oryza sativa]

Seq. No.	398546
Seq. ID	LIB3431-016-P1-K1-D9
Method	BLASTX
NCBI GI	g2245136
BLAST score	289
E value	6.0e-26
Match length	92
% identity	62
NCBI Description	(Z97344) trehalose-6-phosphate synthase like protein [Arabidopsis thaliana]

Seq. No.	398547
Seq. ID	LIB3431-016-P1-K1-E10
Method	BLASTX
NCBI GI	g3126854
BLAST score	698
E value	6.0e-74
Match length	129
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398548
Seq. ID	LIB3431-016-P1-K1-E11
Method	BLASTX
NCBI GI	g132105
BLAST score	715
E value	7.0e-76
Match length	132
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398549
Seq. ID	LIB3431-016-P1-K1-E12
Method	BLASTX
NCBI GI	g115787
BLAST score	518
E value	9.0e-53

Match length	119
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398550
Seq. ID	LIB3431-016-P1-K1-E2
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398551
Seq. ID	LIB3431-016-P1-K1-E5
Method	BLASTX
NCBI GI	g2245120
BLAST score	319
E value	3.0e-30
Match length	128
% identity	57
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	398552
Seq. ID	LIB3431-016-P1-K1-E6
Method	BLASTX
NCBI GI	g320618
BLAST score	690
E value	6.0e-73
Match length	129
% identity	99
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398553
Seq. ID	LIB3431-016-P1-K1-E7
Method	BLASTX
NCBI GI	g1617206
BLAST score	190
E value	2.0e-14
Match length	54
% identity	69
NCBI Description	(Z72489) CP12 [Pisum sativum]

Seq. No.	398554
Seq. ID	LIB3431-016-P1-K1-E8
Method	BLASTN
NCBI GI	g5410347
BLAST score	37

E value	3.0e-11
Match length	57
% identity	91
NCBI Description	Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No.	398555
Seq. ID	LIB3431-016-P1-K1-F10
Method	BLASTX
NCBI GI	g730456
BLAST score	569
E value	9.0e-59
Match length	108
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	398556
Seq. ID	LIB3431-016-P1-K1-F2
Method	BLASTX
NCBI GI	g2493318
BLAST score	171
E value	4.0e-12
Match length	72
% identity	46
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	398557
Seq. ID	LIB3431-016-P1-K1-F5
Method	BLASTX
NCBI GI	g2072555
BLAST score	232
E value	7.0e-20
Match length	44
% identity	98
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398558
Seq. ID	LIB3431-016-P1-K1-F7
Method	BLASTX
NCBI GI	g1707998
BLAST score	262
E value	2.0e-23
Match length	52
% identity	98
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir__S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No.	398559
Seq. ID	LIB3431-016-P1-K1-F8
Method	BLASTX

NCBI GI	g4220481
BLAST score	205
E value	4.0e-16
Match length	107
% identity	43
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	398560
Seq. ID	LIB3431-016-P1-K1-G1
Method	BLASTX
NCBI GI	g115787
BLAST score	695
E value	2.0e-73
Match length	134
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398561
Seq. ID	LIB3431-016-P1-K1-G10
Method	BLASTX
NCBI GI	g4455323
BLAST score	397
E value	1.0e-38
Match length	136
% identity	59
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	398562
Seq. ID	LIB3431-016-P1-K1-G11
Method	BLASTX
NCBI GI	g462195
BLAST score	423
E value	1.0e-41
Match length	88
% identity	91
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	398563
Seq. ID	LIB3431-016-P1-K1-G12
Method	BLASTX
NCBI GI	g2501189
BLAST score	402
E value	3.0e-39
Match length	111
% identity	72
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

Seq. No.	398564
Seq. ID	LIB3431-016-P1-K1-G3
Method	BLASTX
NCBI GI	g115787
BLAST score	554
E value	6.0e-57
Match length	125
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398565
Seq. ID	LIB3431-016-P1-K1-G4
Method	BLASTX
NCBI GI	g710308
BLAST score	268
E value	1.0e-23
Match length	49
% identity	96
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	398566
Seq. ID	LIB3431-016-P1-K1-G5
Method	BLASTX
NCBI GI	g2570511
BLAST score	590
E value	3.0e-61
Match length	111
% identity	99
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	398567
Seq. ID	LIB3431-016-P1-K1-G6
Method	BLASTX
NCBI GI	g3789954
BLAST score	515
E value	2.0e-52
Match length	96
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	398568
Seq. ID	LIB3431-016-P1-K1-G7
Method	BLASTX
NCBI GI	g1899188
BLAST score	359
E value	4.0e-34
Match length	132
% identity	55
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	398569
Seq. ID	LIB3431-016-P1-K1-G8
Method	BLASTX
NCBI GI	g556409
BLAST score	366
E value	6.0e-35
Match length	112
% identity	72
NCBI Description	(L34551) transcriptional activator protein [Oryza sativa]

Seq. No.	398570
Seq. ID	LIB3431-016-P1-K1-G9
Method	BLASTX
NCBI GI	g4886307
BLAST score	662
E value	1.0e-69
Match length	133
% identity	92
NCBI Description	(AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]

Seq. No.	398571
Seq. ID	LIB3431-016-P1-K1-H1
Method	BLASTX
NCBI GI	g1778149
BLAST score	563
E value	4.0e-58
Match length	119
% identity	93
NCBI Description	(U66404) phosphate/phosphoenolpyruvate translocator precursor [Zea mays]

Seq. No.	398572
Seq. ID	LIB3431-016-P1-K1-H12
Method	BLASTX
NCBI GI	g3868758
BLAST score	370
E value	2.0e-35
Match length	92
% identity	77
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	398573
Seq. ID	LIB3431-016-P1-K1-H2
Method	BLASTX
NCBI GI	g5306269
BLAST score	256
E value	5.0e-22
Match length	128
% identity	25
NCBI Description	(AC006233) unknown protein [Arabidopsis thaliana]

Seq. No.	398574
Seq. ID	LIB3431-016-P1-K1-H3
Method	BLASTX
NCBI GI	g451193
BLAST score	442

E value	7.0e-44
Match length	100
% identity	87
NCBI Description	(L28008) wali7 [Triticum aestivum] >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]

Seq. No.	398575
Seq. ID	LIB3431-016-P1-K1-H6
Method	BLASTX
NCBI GI	g3913018
BLAST score	447
E value	2.0e-44
Match length	90
% identity	100
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	398576
Seq. ID	LIB3431-016-P1-K1-H7
Method	BLASTX
NCBI GI	g131225
BLAST score	525
E value	1.0e-53
Match length	125
% identity	82
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	398577
Seq. ID	LIB3431-016-P1-K1-H8
Method	BLASTN
NCBI GI	g3126853
BLAST score	178
E value	2.0e-95
Match length	216
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398578
Seq. ID	LIB3431-016-P1-K1-H9
Method	BLASTX
NCBI GI	g5824411
BLAST score	360
E value	3.0e-34
Match length	121
% identity	55
NCBI Description	(Z68882) Similarity to Bovine inorganic pyrophosphatase (SW:IPYR_BOVIN); cDNA EST EMBL:D66533 comes from this gene; cDNA EST EMBL:D70345 comes from this gene; cDNA EST yk338a8.3 comes from this gene; cDNA EST yk338a8.5 comes

Seq. No.	398579

Seq. ID	LIB3431-017-P1-K1-A1
Method	BLASTX
NCBI GI	g2498465
BLAST score	150
E value	1.0e-09
Match length	115
% identity	43
NCBI Description	28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF ASSOCIATED PROTEIN) >gi_2143777_pir__S62782 heat and acid-stable phosphoprotein, 28K - rat >gi_847785 (U26541) HASPP28 [Rattus norvegicus] >gi_1588241_prf__2208261A casein kinase II substrate [Rattus norvegicus]

Seq. No.	398580
Seq. ID	LIB3431-017-P1-K1-A10
Method	BLASTN
NCBI GI	g2072554
BLAST score	36
E value	1.0e-10
Match length	88
% identity	85
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398581
Seq. ID	LIB3431-017-P1-K1-A12
Method	BLASTX
NCBI GI	g82080
BLAST score	372
E value	1.0e-35
Match length	105
% identity	70
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	398582
Seq. ID	LIB3431-017-P1-K1-A3
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	7.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398583
Seq. ID	LIB3431-017-P1-K1-A4
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398584
Seq. ID	LIB3431-017-P1-K1-A5
Method	BLASTX
NCBI GI	g132105
BLAST score	548
E value	3.0e-56
Match length	122
% identity	84
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398585
Seq. ID	LIB3431-017-P1-K1-A6
Method	BLASTX
NCBI GI	g510907
BLAST score	659
E value	3.0e-69
Match length	141
% identity	80
NCBI Description	(Z35108) calnexin [Helianthus tuberosus]

Seq. No.	398586
Seq. ID	LIB3431-017-P1-K1-A7
Method	BLASTX
NCBI GI	g132096
BLAST score	228
E value	2.0e-19
Match length	55
% identity	82
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_ (D00644) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa]

Seq. No.	398587
Seq. ID	LIB3431-017-P1-K1-A8
Method	BLASTX
NCBI GI	g2497746
BLAST score	287
E value	1.0e-25
Match length	88
% identity	65
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2) >gi_951334 (U31766) lipid transfer protein precursor [Oryza sativa]

Seq. No.	398588
Seq. ID	LIB3431-017-P1-K1-A9
Method	BLASTX
NCBI GI	g4337192
BLAST score	292
E value	3.0e-26
Match length	90
% identity	66
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	398589
Seq. ID	LIB3431-017-P1-K1-B1
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398590
Seq. ID	LIB3431-017-P1-K1-B10
Method	BLASTX
NCBI GI	g733454
BLAST score	589
E value	4.0e-61
Match length	124
% identity	87
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	398591
Seq. ID	LIB3431-017-P1-K1-B11
Method	BLASTX
NCBI GI	g542200
BLAST score	263
E value	7.0e-23
Match length	98
% identity	56
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	398592
Seq. ID	LIB3431-017-P1-K1-B2
Method	BLASTN
NCBI GI	g21843
BLAST score	96
E value	2.0e-46
Match length	312
% identity	87
NCBI Description	Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II

Seq. No.	398593
Seq. ID	LIB3431-017-P1-K1-B3
Method	BLASTX
NCBI GI	g2618704
BLAST score	619
E value	1.0e-64
Match length	136
% identity	85
NCBI Description	(AC002510) putative thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	398594
Seq. ID	LIB3431-017-P1-K1-B4
Method	BLASTX
NCBI GI	g129233
BLAST score	491
E value	1.0e-49
Match length	120
% identity	82
NCBI Description	ORYZAIN GAMMA CHAIN PRECURSOR >gi_67646_pir__KHRZOG oryzain (EC 3.4.22.-) gamma precursor - rice >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor [Oryza sativa]

Seq. No.	398595
Seq. ID	LIB3431-017-P1-K1-B5
Method	BLASTX
NCBI GI	g5541681
BLAST score	363
E value	1.0e-34
Match length	133
% identity	59
NCBI Description	(AL096859) putative protein [Arabidopsis thaliana]

Seq. No.	398596
Seq. ID	LIB3431-017-P1-K1-B7
Method	BLASTX
NCBI GI	g120661
BLAST score	228
E value	8.0e-19
Match length	45
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	398597
Seq. ID	LIB3431-017-P1-K1-C1
Method	BLASTX
NCBI GI	g3184098
BLAST score	355
E value	1.0e-33
Match length	118
% identity	56
NCBI Description	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]

Seq. No.	398598
Seq. ID	LIB3431-017-P1-K1-C10
Method	BLASTX
NCBI GI	g2072727
BLAST score	699
E value	5.0e-74
Match length	140
% identity	97
NCBI Description	(Y12595) Fd-GOGAT protein [Oryza sativa]

Seq. No.	398599
Seq. ID	LIB3431-017-P1-K1-C11
Method	BLASTX
NCBI GI	g131225
BLAST score	589
E value	4.0e-61
Match length	122
% identity	93
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	398600
Seq. ID	LIB3431-017-P1-K1-C12
Method	BLASTN
NCBI GI	g3885891
BLAST score	41
E value	1.0e-13
Match length	60
% identity	93
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	398601
Seq. ID	LIB3431-017-P1-K1-C2
Method	BLASTX
NCBI GI	g282833
BLAST score	686
E value	2.0e-72
Match length	143
% identity	97
NCBI Description	phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)

Seq. No.	398602
Seq. ID	LIB3431-017-P1-K1-C3
Method	BLASTX
NCBI GI	g585421
BLAST score	429
E value	3.0e-42
Match length	147
% identity	53
NCBI Description	LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir__JQ2391 lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana >gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No.	398603

Seq. ID	LIB3431-017-P1-K1-C6
Method	BLASTX
NCBI GI	g2407281
BLAST score	754
E value	2.0e-80
Match length	142
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398604
Seq. ID	LIB3431-017-P1-K1-C7
Method	BLASTX
NCBI GI	g482311
BLAST score	634
E value	2.0e-66
Match length	123
% identity	98
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	398605
Seq. ID	LIB3431-017-P1-K1-D10
Method	BLASTX
NCBI GI	g462195
BLAST score	405
E value	2.0e-39
Match length	96
% identity	82
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	398606
Seq. ID	LIB3431-017-P1-K1-D12
Method	BLASTX
NCBI GI	g132105
BLAST score	694
E value	2.0e-73
Match length	130
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398607
Seq. ID	LIB3431-017-P1-K1-D2
Method	BLASTX

NCBI GI	g4581207
BLAST score	504
E value	4.0e-51
Match length	144
% identity	73
NCBI Description	(Y17914) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	398608
Seq. ID	LIB3431-017-P1-K1-D3
Method	BLASTX
NCBI GI	g3075488
BLAST score	533
E value	2.0e-54
Match length	120
% identity	85
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398609
Seq. ID	LIB3431-017-P1-K1-D5
Method	BLASTX
NCBI GI	g3927827
BLAST score	190
E value	3.0e-14
Match length	104
% identity	43
NCBI Description	(AC005727) osmotin-like protein precursor [Arabidopsis thaliana]

Seq. No.	398610
Seq. ID	LIB3431-017-P1-K1-D6
Method	BLASTN
NCBI GI	g11957
BLAST score	292
E value	1.0e-163
Match length	308
% identity	99
NCBI Description	Rice complete chloroplast genome

Seq. No.	398611
Seq. ID	LIB3431-017-P1-K1-D7
Method	BLASTX
NCBI GI	g5902390
BLAST score	386
E value	3.0e-37
Match length	126
% identity	60
NCBI Description	(AC008148) Unknown protein [Arabidopsis thaliana]

Seq. No.	398612
Seq. ID	LIB3431-017-P1-K1-D8
Method	BLASTX
NCBI GI	g400879
BLAST score	211
E value	6.0e-17
Match length	103
% identity	50

NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_479690_pir__S35159 photosystem I chain psaN - barley >gi_19095_emb_CAA47056_ (X66428) photosystem I subunit N [Hordeum vulgare]
Seq. No.	398613
Seq. ID	LIB3431-017-P1-K1-D9
Method	BLASTX
NCBI GI	g3341648
BLAST score	566
E value	2.0e-58
Match length	115
% identity	90
NCBI Description	(AJ005343) DNA directed RNA polymerase [Zea mays]
Seq. No.	398614
Seq. ID	LIB3431-017-P1-K1-E1
Method	BLASTX
NCBI GI	g129233
BLAST score	739
E value	1.0e-78
Match length	145
% identity	98
NCBI Description	ORYZAIN GAMMA CHAIN PRECURSOR >gi_67646_pir__KHRZOG oryzain (EC 3.4.22.-) gamma precursor - rice >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor [Oryza sativa]
Seq. No.	398615
Seq. ID	LIB3431-017-P1-K1-E10
Method	BLASTX
NCBI GI	g517500
BLAST score	535
E value	8.0e-55
Match length	132
% identity	77
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]
Seq. No.	398616
Seq. ID	LIB3431-017-P1-K1-E11
Method	BLASTX
NCBI GI	g517500
BLAST score	250
E value	2.0e-21
Match length	113
% identity	48
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]
Seq. No.	398617
Seq. ID	LIB3431-017-P1-K1-E12
Method	BLASTX
NCBI GI	g5903092
BLAST score	354

E value	1.0e-33
Match length	110
% identity	70
NCBI Description	(AC008017) Highly similar to developmental protein DG1118 [Arabidopsis thaliana]

Seq. No.	398618
Seq. ID	LIB3431-017-P1-K1-E3
Method	BLASTX
NCBI GI	g1703200
BLAST score	377
E value	3.0e-36
Match length	119
% identity	62
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	398619
Seq. ID	LIB3431-017-P1-K1-E6
Method	BLASTN
NCBI GI	g20270
BLAST score	147
E value	8.0e-77
Match length	162
% identity	99
NCBI Description	Rice nia1 gene for nitrate reductase apoenzyme (exon 1-2)

Seq. No.	398620
Seq. ID	LIB3431-017-P1-K1-E7
Method	BLASTX
NCBI GI	g115772
BLAST score	535
E value	6.0e-55
Match length	101
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_ (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No.	398621
Seq. ID	LIB3431-017-P1-K1-E8
Method	BLASTX
NCBI GI	g3885888
BLAST score	165
E value	2.0e-11
Match length	78
% identity	51
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	398622
Seq. ID	LIB3431-017-P1-K1-F1
Method	BLASTX

NCBI GI	g1617197
BLAST score	245
E value	1.0e-20
Match length	66
% identity	73
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	398623
Seq. ID	LIB3431-017-P1-K1-F10
Method	BLASTX
NCBI GI	g1706260
BLAST score	561
E value	9.0e-58
Match length	121
% identity	85
NCBI Description	CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597 cysteine proteinase 1 precursor - maize >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No.	398624
Seq. ID	LIB3431-017-P1-K1-F4
Method	BLASTN
NCBI GI	g2773153
BLAST score	418
E value	0.0e+00
Match length	450
% identity	98
NCBI Description	Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds

Seq. No.	398625
Seq. ID	LIB3431-017-P1-K1-F5
Method	BLASTN
NCBI GI	g2072554
BLAST score	161
E value	3.0e-85
Match length	161
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398626
Seq. ID	LIB3431-017-P1-K1-F6
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398627
Seq. ID	LIB3431-017-P1-K1-F8
Method	BLASTX

NCBI GI	g4585882
BLAST score	611
E value	1.0e-63
Match length	135
% identity	79
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	398628
Seq. ID	LIB3431-017-P1-K1-G10
Method	BLASTX
NCBI GI	g68843
BLAST score	342
E value	4.0e-32
Match length	86
% identity	80
NCBI Description	phospholipid transfer protein homolog - rice >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer Protein >gi_5107522_pdb_1BV2_ Lipid Transfer Protein From Rice Seeds, Nmr, 14 Structures

Seq. No.	398629
Seq. ID	LIB3431-017-P1-K1-G12
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	6.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398630
Seq. ID	LIB3431-017-P1-K1-G2
Method	BLASTX
NCBI GI	g132105
BLAST score	595
E value	9.0e-62
Match length	128
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398631
Seq. ID	LIB3431-017-P1-K1-G3
Method	BLASTX
NCBI GI	g2570511
BLAST score	660
E value	2.0e-69

Match length	126
% identity	98
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	398632
Seq. ID	LIB3431-017-P1-K1-G4
Method	BLASTX
NCBI GI	g2293480
BLAST score	337
E value	9.0e-32
Match length	71
% identity	92
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	398633
Seq. ID	LIB3431-017-P1-K1-G5
Method	BLASTX
NCBI GI	g3135543
BLAST score	553
E value	8.0e-57
Match length	136
% identity	82
NCBI Description	(AF062393) aquaporin [Oryza sativa]

Seq. No.	398634
Seq. ID	LIB3431-017-P1-K1-G6
Method	BLASTX
NCBI GI	g2570511
BLAST score	607
E value	3.0e-63
Match length	115
% identity	99
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	398635
Seq. ID	LIB3431-017-P1-K1-G8
Method	BLASTX
NCBI GI	g3063524
BLAST score	168
E value	8.0e-12
Match length	107
% identity	47
NCBI Description	(AF052305) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398636
Seq. ID	LIB3431-017-P1-K1-G9
Method	BLASTX
NCBI GI	g1236961
BLAST score	280
E value	7.0e-25
Match length	97
% identity	52
NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No.	398637
Seq. ID	LIB3431-017-P1-K1-H10

Method	BLASTX
NCBI GI	g3789952
BLAST score	383
E value	3.0e-37
Match length	85
% identity	98
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	398638
Seq. ID	LIB3431-017-P1-K1-H11
Method	BLASTX
NCBI GI	g5919219
BLAST score	202
E value	1.0e-15
Match length	133
% identity	13
NCBI Description	(AF186273) leucine-rich repeats containing F-box protein FBL3 [Homo sapiens]

Seq. No.	398639
Seq. ID	LIB3431-017-P1-K1-H12
Method	BLASTN
NCBI GI	g6015437
BLAST score	33
E value	4.0e-09
Match length	33
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398640
Seq. ID	LIB3431-017-P1-K1-H2
Method	BLASTX
NCBI GI	g3885892
BLAST score	442
E value	8.0e-44
Match length	85
% identity	98
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	398641
Seq. ID	LIB3431-017-P1-K1-H3
Method	BLASTX
NCBI GI	g3075488
BLAST score	426
E value	6.0e-42
Match length	82
% identity	99
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398642
Seq. ID	LIB3431-017-P1-K1-H4
Method	BLASTX
NCBI GI	g1173189
BLAST score	220
E value	8.0e-18
Match length	42

% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_2119091_pir__S58629 ribosomal protein S12 - maize chloroplast >gi_342619 (M17841) ribosomal protein S12 [Zea mays] >gi_1216141_emb_CAA60309_ (X86563) ribosomal protein S12 [Zea mays]

Seq. No.	398643
Seq. ID	LIB3431-017-P1-K1-H5
Method	BLASTN
NCBI GI	g4105560
BLAST score	37
E value	5.0e-12
Match length	37
% identity	100
NCBI Description	Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA, complete cds

Seq. No.	398644
Seq. ID	LIB3431-017-P1-K1-H6
Method	BLASTX
NCBI GI	g1617197
BLAST score	305
E value	1.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	398645
Seq. ID	LIB3431-017-P1-K1-H7
Method	BLASTX
NCBI GI	g4126473
BLAST score	252
E value	1.0e-21
Match length	140
% identity	45
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No.	398646
Seq. ID	LIB3431-017-P1-K1-H8
Method	BLASTN
NCBI GI	g487317
BLAST score	97
E value	5.0e-47
Match length	101
% identity	99
NCBI Description	Rice mRNA EN56, partial sequence

Seq. No.	398647
Seq. ID	LIB3431-017-P1-N1-A12
Method	BLASTX
NCBI GI	g115813
BLAST score	171
E value	4.0e-12
Match length	40
% identity	80

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398648
Seq. ID	LIB3431-017-P1-N1-A4
Method	BLASTN
NCBI GI	g2072554
BLAST score	361
E value	0.0e+00
Match length	369
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398649
Seq. ID	LIB3431-017-P1-N1-A5
Method	BLASTX
NCBI GI	g347451
BLAST score	365
E value	6.0e-35
Match length	69
% identity	99
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	398650
Seq. ID	LIB3431-017-P1-N1-A7
Method	BLASTN
NCBI GI	g218209
BLAST score	187
E value	1.0e-101
Match length	235
% identity	95
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	398651
Seq. ID	LIB3431-017-P1-N1-A8
Method	BLASTN
NCBI GI	g886692
BLAST score	377
E value	0.0e+00
Match length	385
% identity	99
NCBI Description	O.sativa mRNA for lipid transfer protein, b1

Seq. No.	398652
Seq. ID	LIB3431-017-P1-N1-B1
Method	BLASTN
NCBI GI	g2072554
BLAST score	160
E value	8.0e-85
Match length	244
% identity	91
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No.	398653
Seq. ID	LIB3431-017-P1-N1-B10
Method	BLASTX
NCBI GI	g733454
BLAST score	317
E value	3.0e-29
Match length	67
% identity	93
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	398654
Seq. ID	LIB3431-017-P1-N1-B2
Method	BLASTX
NCBI GI	g482311
BLAST score	260
E value	1.0e-22
Match length	51
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	398655
Seq. ID	LIB3431-017-P1-N1-B4
Method	BLASTX
NCBI GI	g1841466
BLAST score	205
E value	4.0e-16
Match length	37
% identity	95
NCBI Description	(Y11003) putative pre-pro-cysteine proteinase [Nicotiana tabacum]

Seq. No.	398656
Seq. ID	LIB3431-017-P1-N1-B5
Method	BLASTX
NCBI GI	g5541681
BLAST score	182
E value	2.0e-13
Match length	79
% identity	58
NCBI Description	(AL096859) putative protein [Arabidopsis thaliana]

Seq. No.	398657
Seq. ID	LIB3431-017-P1-N1-C1
Method	BLASTX
NCBI GI	g586339
BLAST score	182
E value	2.0e-13
Match length	67
% identity	46
NCBI Description	PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir__S46098 probable AMP-binding protein - yeast (Saccharomyces cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c

[Saccharomyces cerevisiae]

Seq. No.	398658
Seq. ID	LIB3431-017-P1-N1-C10
Method	BLASTN
NCBI GI	g2072726
BLAST score	350
E value	0.0e+00
Match length	369
% identity	99
NCBI Description	O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No.	398659
Seq. ID	LIB3431-017-P1-N1-C11
Method	BLASTX
NCBI GI	g131225
BLAST score	284
E value	2.0e-25
Match length	70
% identity	77
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	398660
Seq. ID	LIB3431-017-P1-N1-C12
Method	BLASTX
NCBI GI	g3885892
BLAST score	272
E value	5.0e-24
Match length	55
% identity	98
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	398661
Seq. ID	LIB3431-017-P1-N1-C2
Method	BLASTX
NCBI GI	g2499497
BLAST score	236
E value	8.0e-20
Match length	70
% identity	76
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_1161600_emb_CAA88841_ (Z48977) phosphoglycerate kinase [Nicotiana tabacum]

Seq. No.	398662
Seq. ID	LIB3431-017-P1-N1-C3
Method	BLASTX
NCBI GI	g450231
BLAST score	186
E value	8.0e-14
Match length	56
% identity	59
NCBI Description	(U05041) lipoxygenase [Cuscuta reflexa]

Seq. No.	398663
Seq. ID	LIB3431-017-P1-N1-C6
Method	BLASTX
NCBI GI	g132105
BLAST score	174
E value	1.0e-20
Match length	57
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398664
Seq. ID	LIB3431-017-P1-N1-C7
Method	BLASTX
NCBI GI	g482311
BLAST score	175
E value	1.0e-12
Match length	34
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	398665
Seq. ID	LIB3431-017-P1-N1-C8
Method	BLASTX
NCBI GI	g4678346
BLAST score	187
E value	5.0e-14
Match length	44
% identity	77
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	398666
Seq. ID	LIB3431-017-P1-N1-C9
Method	BLASTX
NCBI GI	g3341699
BLAST score	238
E value	7.0e-20
Match length	153
% identity	37
NCBI Description	(AC003672) putative giberellin beta-hydroxylase [Arabidopsis thaliana]

Seq. No.	398667
Seq. ID	LIB3431-017-P1-N1-D10
Method	BLASTX
NCBI GI	g462195
BLAST score	234
E value	1.0e-19

Match length	45
% identity	100
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	398668
Seq. ID	LIB3431-017-P1-N1-D12
Method	BLASTX
NCBI GI	g671740
BLAST score	179
E value	4.0e-13
Match length	34
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	398669
Seq. ID	LIB3431-017-P1-N1-D3
Method	BLASTN
NCBI GI	g3075487
BLAST score	309
E value	1.0e-173
Match length	325
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	398670
Seq. ID	LIB3431-017-P1-N1-D6
Method	BLASTN
NCBI GI	g11957
BLAST score	94
E value	2.0e-45
Match length	209
% identity	86
NCBI Description	Rice complete chloroplast genome

Seq. No.	398671
Seq. ID	LIB3431-017-P1-N1-D8
Method	BLASTX
NCBI GI	g3914466
BLAST score	369
E value	2.0e-35
Match length	67
% identity	99
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN subunit precursor [Zea mays]

Seq. No.	398672
Seq. ID	LIB3431-017-P1-N1-D9
Method	BLASTN
NCBI GI	g2239152
BLAST score	348

E value	0.0e+00
Match length	380
% identity	98
NCBI Description	O.sativa mRNA for putative T3/T7-like RNA polymerase, partial

Seq. No.	398673
Seq. ID	LIB3431-017-P1-N1-E1
Method	BLASTX
NCBI GI	g129233
BLAST score	240
E value	3.0e-26
Match length	60
% identity	98
NCBI Description	ORYZAIN GAMMA CHAIN PRECURSOR >gi_67646_pir__KHRZOG oryzain (EC 3.4.22.-) gamma precursor - rice >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor [Oryza sativa]

Seq. No.	398674
Seq. ID	LIB3431-017-P1-N1-E10
Method	BLASTN
NCBI GI	g169133
BLAST score	56
E value	1.0e-22
Match length	168
% identity	83
NCBI Description	Zea mays precursor of the oxygen evolving complex 17 kDa protein mRNA, complete cds

Seq. No.	398675
Seq. ID	LIB3431-017-P1-N1-E11
Method	BLASTX
NCBI GI	g347451
BLAST score	173
E value	2.0e-12
Match length	33
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	398676
Seq. ID	LIB3431-017-P1-N1-E3
Method	BLASTX
NCBI GI	g1703199
BLAST score	150
E value	9.0e-10
Match length	45
% identity	62
NCBI Description	PROTEIN KINASE AFC1 >gi_601787 (U16176) protein kinase [Arabidopsis thaliana]

Seq. No.	398677
Seq. ID	LIB3431-017-P1-N1-E4
Method	BLASTN
NCBI GI	g3789953
BLAST score	56

E value	9.0e-23
Match length	248
% identity	82
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398678
Seq. ID	LIB3431-017-P1-N1-E6
Method	BLASTX
NCBI GI	g128186
BLAST score	251
E value	1.0e-21
Match length	50
% identity	90
NCBI Description	NITRATE REDUCTASE 1 (NR1) >gi_82490_pir__S07554 nitrate reductase (NADH) (EC 1.6.6.1) - rice

Seq. No.	398679
Seq. ID	LIB3431-017-P1-N1-E7
Method	BLASTX
NCBI GI	g421916
BLAST score	195
E value	6.0e-15
Match length	36
% identity	100
NCBI Description	chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No.	398680
Seq. ID	LIB3431-017-P1-N1-E8
Method	BLASTN
NCBI GI	g3885887
BLAST score	405
E value	0.0e+00
Match length	456
% identity	97
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	398681
Seq. ID	LIB3431-017-P1-N1-F12
Method	BLASTX
NCBI GI	g482311
BLAST score	307
E value	4.0e-28
Match length	61
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	398682
Seq. ID	LIB3431-017-P1-N1-F8
Method	BLASTX
NCBI GI	g115813

BLAST score	152
E value	6.0e-10
Match length	33
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398683
Seq. ID	LIB3431-017-P1-N1-G10
Method	BLASTN
NCBI GI	g1619603
BLAST score	306
E value	1.0e-172
Match length	322
% identity	99
NCBI Description	O.sativa mRNA for lipid transfer protein >gi_1667589_gb_U77295_OSU77295 Oryza sativa lipid transfer protein (LTP) mRNA, complete cds

Seq. No.	398684
Seq. ID	LIB3431-017-P1-N1-G12
Method	BLASTN
NCBI GI	g2072554
BLAST score	290
E value	1.0e-162
Match length	290
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398685
Seq. ID	LIB3431-017-P1-N1-G2
Method	BLASTX
NCBI GI	g132105
BLAST score	251
E value	4.0e-32
Match length	71
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398686
Seq. ID	LIB3431-017-P1-N1-G3
Method	BLASTX
NCBI GI	g2570511
BLAST score	163
E value	8.0e-22
Match length	63
% identity	81

NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	398687
Seq. ID	LIB3431-017-P1-N1-G4
Method	BLASTX
NCBI GI	g482311
BLAST score	193
E value	1.0e-14
Match length	48
% identity	81
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	398688
Seq. ID	LIB3431-017-P1-N1-G5
Method	BLASTN
NCBI GI	g5381215
BLAST score	116
E value	8.0e-59
Match length	152
% identity	95
NCBI Description	Oryza sativa rwc-2 mRNA for water channel protein, partial cds

Seq. No.	398689
Seq. ID	LIB3431-017-P1-N1-G6
Method	BLASTX
NCBI GI	g479406
BLAST score	307
E value	3.0e-28
Match length	66
% identity	89
NCBI Description	chlorophyll a/b-binding protein - garden pea >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No.	398690
Seq. ID	LIB3431-017-P1-N1-G8
Method	BLASTX
NCBI GI	g4741942
BLAST score	221
E value	5.0e-18
Match length	60
% identity	72
NCBI Description	(AF134121) Lhca5 protein [Arabidopsis thaliana]

Seq. No.	398691
Seq. ID	LIB3431-017-P1-N1-G9
Method	BLASTX
NCBI GI	g1236961
BLAST score	231
E value	3.0e-19
Match length	64
% identity	64
NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No.	398692
Seq. ID	LIB3431-017-P1-N1-H2
Method	BLASTN
NCBI GI	g3885891
BLAST score	207
E value	1.0e-113
Match length	247
% identity	96
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	398693
Seq. ID	LIB3431-017-P1-N1-H3
Method	BLASTX
NCBI GI	g3075488
BLAST score	176
E value	9.0e-13
Match length	33
% identity	100
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398694
Seq. ID	LIB3431-017-P1-N1-H4
Method	BLASTN
NCBI GI	g2072554
BLAST score	140
E value	7.0e-73
Match length	248
% identity	88
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398695
Seq. ID	LIB3431-017-P1-N1-H5
Method	BLASTN
NCBI GI	g4105560
BLAST score	141
E value	2.0e-73
Match length	190
% identity	94
NCBI Description	Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA, complete cds

Seq. No.	398696
Seq. ID	LIB3431-017-P1-N1-H7
Method	BLASTX
NCBI GI	g4126473
BLAST score	195
E value	5.0e-15
Match length	47
% identity	81
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No.	398697
Seq. ID	LIB3431-017-P1-N1-H9
Method	BLASTN

NCBI GI	g2267594
BLAST score	101
E value	1.0e-49
Match length	196
% identity	99
NCBI Description	Oryza sativa plastocyanin precursor, mRNA, complete cds

Seq. No.	398698
Seq. ID	LIB3431-018-P1-K1-A10
Method	BLASTN
NCBI GI	g2072554
BLAST score	56
E value	6.0e-23
Match length	111
% identity	89
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398699
Seq. ID	LIB3431-018-P1-K1-A12
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	398700
Seq. ID	LIB3431-018-P1-K1-A4
Method	BLASTX
NCBI GI	g4038034
BLAST score	273
E value	6.0e-24
Match length	76
% identity	68
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	398701
Seq. ID	LIB3431-018-P1-K1-A6
Method	BLASTX
NCBI GI	g3914603
BLAST score	1128
E value	1.0e-124
Match length	220
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	398702
Seq. ID	LIB3431-018-P1-K1-B10
Method	BLASTX
NCBI GI	g2088647
BLAST score	388
E value	3.0e-37

Match length	127
% identity	58
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No.	398703
Seq. ID	LIB3431-018-P1-K1-B4
Method	BLASTN
NCBI GI	g473980
BLAST score	56
E value	2.0e-22
Match length	83
% identity	90
NCBI Description	Rice mRNA, partial homologous to glycine-rich protein gene

Seq. No.	398704
Seq. ID	LIB3431-018-P1-K1-B5
Method	BLASTX
NCBI GI	g1839022
BLAST score	269
E value	1.0e-23
Match length	65
% identity	71
NCBI Description	(Y11121) amino acid carrier [Ricinus communis]

Seq. No.	398705
Seq. ID	LIB3431-018-P1-K1-B7
Method	BLASTX
NCBI GI	g417154
BLAST score	910
E value	2.0e-98
Match length	201
% identity	90
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	398706
Seq. ID	LIB3431-018-P1-K1-B9
Method	BLASTN
NCBI GI	g11957
BLAST score	487
E value	0.0e+00
Match length	543
% identity	97
NCBI Description	Rice complete chloroplast genome

Seq. No.	398707
Seq. ID	LIB3431-018-P1-K1-C10
Method	BLASTX
NCBI GI	g115793
BLAST score	688
E value	1.0e-72
Match length	154
% identity	84

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]
Seq. No.	398708
Seq. ID	LIB3431-018-P1-K1-C12
Method	BLASTX
NCBI GI	g2501578
BLAST score	515
E value	3.0e-52
Match length	125
% identity	82
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]
Seq. No.	398709
Seq. ID	LIB3431-018-P1-K1-C4
Method	BLASTX
NCBI GI	g132105
BLAST score	739
E value	2.0e-78
Match length	137
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	398710
Seq. ID	LIB3431-018-P1-K1-C6
Method	BLASTX
NCBI GI	g2497746
BLAST score	380
E value	2.0e-36
Match length	99
% identity	76
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2) >gi_951334 (U31766) lipid transfer protein precursor [Oryza sativa]
Seq. No.	398711
Seq. ID	LIB3431-018-P1-K1-C7
Method	BLASTX
NCBI GI	g3789952
BLAST score	252
E value	2.0e-21
Match length	151
% identity	49

NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	398712
Seq. ID	LIB3431-018-P1-K1-C8
Method	BLASTX
NCBI GI	g3980400
BLAST score	489
E value	3.0e-49
Match length	142
% identity	66
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	398713
Seq. ID	LIB3431-018-P1-K1-D10
Method	BLASTN
NCBI GI	g4959460
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	398714
Seq. ID	LIB3431-018-P1-K1-D11
Method	BLASTX
NCBI GI	g170131
BLAST score	276
E value	3.0e-24
Match length	75
% identity	65
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	398715
Seq. ID	LIB3431-018-P1-K1-D12
Method	BLASTX
NCBI GI	g115813
BLAST score	424
E value	1.0e-41
Match length	118
% identity	73
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398716
Seq. ID	LIB3431-018-P1-K1-D2
Method	BLASTX
NCBI GI	g115787
BLAST score	782
E value	2.0e-83
Match length	170
% identity	91
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398717
Seq. ID	LIB3431-018-P1-K1-D3
Method	BLASTX
NCBI GI	g548603
BLAST score	690
E value	1.0e-72
Match length	136
% identity	96
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	398718
Seq. ID	LIB3431-018-P1-K1-D4
Method	BLASTX
NCBI GI	g115787
BLAST score	767
E value	9.0e-82
Match length	169
% identity	91
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398719
Seq. ID	LIB3431-018-P1-K1-D5
Method	BLASTX
NCBI GI	g121343
BLAST score	871
E value	5.0e-94
Match length	177
% identity	93
NCBI Description	GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31) >gi_68598_pir__AJRZQD glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - rice >gi_20370_emb_CAA32462_ (X14246) precursor chloroplastic glutamine synthetase (AA -46 to 382) [Oryza sativa]

Seq. No.	398720
Seq. ID	LIB3431-018-P1-K1-D6
Method	BLASTX
NCBI GI	g2130069
BLAST score	1038
E value	1.0e-113
Match length	199
% identity	96
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No. 398721

Seq. ID	LIB3431-018-P1-K1-D7
Method	BLASTX
NCBI GI	g4803952
BLAST score	461
E value	8.0e-46
Match length	115
% identity	77
NCBI Description	(AC006202) hypothetical protein [Arabidopsis thaliana]

Seq. No.	398722
Seq. ID	LIB3431-018-P1-K1-E10
Method	BLASTX
NCBI GI	g125580
BLAST score	791
E value	2.0e-84
Match length	181
% identity	85
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608) phosphoribulokinase [Triticum aestivum]

Seq. No.	398723
Seq. ID	LIB3431-018-P1-K1-E12
Method	BLASTX
NCBI GI	g671740
BLAST score	342
E value	4.0e-32
Match length	63
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	398724
Seq. ID	LIB3431-018-P1-K1-E3
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	1.0e-19
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398725
Seq. ID	LIB3431-018-P1-K1-E7
Method	BLASTN
NCBI GI	g2331140
BLAST score	279
E value	1.0e-155
Match length	420
% identity	97
NCBI Description	Oryza sativa water-stress inducible protein (WSI) mRNA, complete cds

Seq. No.	398726

Seq. ID	LIB3431-018-P1-K1-E9
Method	BLASTX
NCBI GI	g320618
BLAST score	746
E value	2.0e-79
Match length	159
% identity	90
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398727
Seq. ID	LIB3431-018-P1-K1-F10
Method	BLASTX
NCBI GI	g548605
BLAST score	595
E value	1.0e-61
Match length	130
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398728
Seq. ID	LIB3431-018-P1-K1-F11
Method	BLASTX
NCBI GI	g131388
BLAST score	658
E value	6.0e-69
Match length	189
% identity	72
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No.	398729
Seq. ID	LIB3431-018-P1-K1-F12
Method	BLASTX
NCBI GI	g548605
BLAST score	377
E value	3.0e-36
Match length	78
% identity	95
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398730
Seq. ID	LIB3431-018-P1-K1-F8
Method	BLASTX
NCBI GI	g2570499
BLAST score	191
E value	1.0e-14
Match length	38
% identity	100
NCBI Description	(AF022732) 23kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	398731
Seq. ID	LIB3431-018-P1-K1-G10
Method	BLASTX
NCBI GI	g5305740
BLAST score	759
E value	8.0e-81
Match length	186
% identity	84
NCBI Description	(AF135862) precursor monofunctional aspartokinase [Glycine max]

Seq. No.	398732
Seq. ID	LIB3431-018-P1-K1-G11
Method	BLASTX
NCBI GI	g115787
BLAST score	691
E value	7.0e-73
Match length	133
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398733
Seq. ID	LIB3431-018-P1-K1-G12
Method	BLASTX
NCBI GI	g5921185
BLAST score	395
E value	6.0e-47
Match length	213
% identity	50
NCBI Description	CYTOCHROME P450 76C1 >gi_2979548 (AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	398734
Seq. ID	LIB3431-018-P1-K1-G2
Method	BLASTX
NCBI GI	g1173347
BLAST score	932
E value	1.0e-101
Match length	185
% identity	95
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)

>gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	398735
Seq. ID	LIB3431-018-P1-K1-G4
Method	BLASTX
NCBI GI	g132096
BLAST score	803
E value	6.0e-86
Match length	150
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_ (D00644) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa]

Seq. No.	398736
Seq. ID	LIB3431-018-P1-K1-G5
Method	BLASTX
NCBI GI	g6014904
BLAST score	296
E value	1.0e-26
Match length	74
% identity	77
NCBI Description	DAG PROTEIN, CHLOROPLAST PRECURSOR >gi_1200205_emb_CAA65064_ (X95753) DAG [Antirrhinum majus]

Seq. No.	398737
Seq. ID	LIB3431-018-P1-K1-G6
Method	BLASTX
NCBI GI	g2501189
BLAST score	643
E value	3.0e-67
Match length	164
% identity	79
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	398738
Seq. ID	LIB3431-018-P1-K1-G7
Method	BLASTX
NCBI GI	g320618
BLAST score	728
E value	3.0e-77
Match length	156
% identity	89
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398739
Seq. ID	LIB3431-018-P1-K1-G9
Method	BLASTX
NCBI GI	g3885888
BLAST score	326
E value	4.0e-30
Match length	89
% identity	76
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	398740
Seq. ID	LIB3431-018-P1-K1-H10
Method	BLASTX
NCBI GI	g115793
BLAST score	869
E value	1.0e-93
Match length	192
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]

Seq. No.	398741
Seq. ID	LIB3431-018-P1-K1-H12
Method	BLASTX
NCBI GI	g710308
BLAST score	987
E value	1.0e-107
Match length	224
% identity	85
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	398742
Seq. ID	LIB3431-018-P1-K1-H3
Method	BLASTX
NCBI GI	g113466
BLAST score	282
E value	8.0e-25
Match length	82
% identity	65
NCBI Description	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_72020_pir__XWNC ADP,ATP carrier protein - Neurospora crassa >gi_2977_emb_CAA25104_ (X00363) ADP/ATP carrier protein [Neurospora crassa]

Seq. No.	398743
Seq. ID	LIB3431-018-P1-K1-H4
Method	BLASTX
NCBI GI	g3126854
BLAST score	731
E value	2.0e-77
Match length	186
% identity	80
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398744
Seq. ID	LIB3431-018-P1-K1-H5
Method	BLASTX
NCBI GI	g121530
BLAST score	866
E value	3.0e-93
Match length	194
% identity	86
NCBI Description	(S)-2-HYDROXY-ACID OXIDASE, PEROXISOMAL (GLYCOLATE OXIDASE) (GOX) (SHORT CHAIN ALPHA-HYDROXY ACID OXIDASE) >gi_65974_pir__OXSPH (S)-2-hydroxy-acid oxidase (EC 1.1.3.15), peroxisomal - spinach >gi_229945_pdb_1GOX_ Glycolate Oxidase (E.C.1.1.3.1) >gi_170113 (J03492) glycolate oxidase (EC 1.1.3.15) [Spinacia oleracea]

Seq. No.	398745
Seq. ID	LIB3431-018-P1-K1-H7
Method	BLASTX
NCBI GI	g3345477
BLAST score	813
E value	4.0e-87
Match length	201
% identity	79
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	398746
Seq. ID	LIB3431-018-P1-N1-A1
Method	BLASTX
NCBI GI	g70772
BLAST score	292
E value	2.0e-26
Match length	58
% identity	100
NCBI Description	histone H4 - wheat >gi_70773_pir__HSPM4 histone H4 - garden pea

Seq. No.	398747
Seq. ID	LIB3431-018-P1-N1-A2
Method	BLASTX
NCBI GI	g3789954
BLAST score	390
E value	1.0e-37
Match length	72
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	398748
Seq. ID	LIB3431-018-P1-N1-A4
Method	BLASTX
NCBI GI	g4038034
BLAST score	222
E value	4.0e-19
Match length	76
% identity	68
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	398749
Seq. ID	LIB3431-018-P1-N1-A6
Method	BLASTX
NCBI GI	g132166
BLAST score	158
E value	1.0e-10
Match length	31
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	398750
Seq. ID	LIB3431-018-P1-N1-A7
Method	BLASTX
NCBI GI	g4836912
BLAST score	238
E value	5.0e-20
Match length	73
% identity	66
NCBI Description	(AC007153) 60811 [Arabidopsis thaliana]

Seq. No.	398751
Seq. ID	LIB3431-018-P1-N1-A8
Method	BLASTX
NCBI GI	g2326947
BLAST score	158
E value	1.0e-10
Match length	29
% identity	100
NCBI Description	(Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays]

Seq. No.	398752
Seq. ID	LIB3431-018-P1-N1-A9
Method	BLASTN
NCBI GI	g2570514
BLAST score	259
E value	1.0e-143
Match length	332
% identity	97
NCBI Description	Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	398753
Seq. ID	LIB3431-018-P1-N1-B3
Method	BLASTX
NCBI GI	g1172818
BLAST score	179
E value	2.0e-25
Match length	67
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf__2111468A

ribosomal protein S16 [Oryza sativa]

Seq. No.	398754
Seq. ID	LIB3431-018-P1-N1-B4
Method	BLASTN
NCBI GI	g2331130
BLAST score	171
E value	2.0e-91
Match length	191
% identity	98
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No.	398755
Seq. ID	LIB3431-018-P1-N1-B6
Method	BLASTX
NCBI GI	g115813
BLAST score	224
E value	3.0e-18
Match length	78
% identity	69
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398756
Seq. ID	LIB3431-018-P1-N1-B7
Method	BLASTX
NCBI GI	g829283
BLAST score	200
E value	1.0e-15
Match length	51
% identity	80
NCBI Description	(Z15018) heat shock protein hsp82 [Oryza sativa]

Seq. No.	398757
Seq. ID	LIB3431-018-P1-N1-B9
Method	BLASTN
NCBI GI	g11957
BLAST score	68
E value	4.0e-30
Match length	156
% identity	87
NCBI Description	Rice complete chloroplast genome

Seq. No.	398758
Seq. ID	LIB3431-018-P1-N1-C3
Method	BLASTX
NCBI GI	g6063542
BLAST score	253
E value	2.0e-40
Match length	88
% identity	91
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No.	398759
Seq. ID	LIB3431-018-P1-N1-C4
Method	BLASTX
NCBI GI	g671740
BLAST score	244
E value	8.0e-21
Match length	58
% identity	79
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	398760
Seq. ID	LIB3431-018-P1-N1-C5
Method	BLASTX
NCBI GI	g548605
BLAST score	338
E value	9.0e-32
Match length	73
% identity	92
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398761
Seq. ID	LIB3431-018-P1-N1-C6
Method	BLASTX
NCBI GI	g2407273
BLAST score	268
E value	1.0e-23
Match length	53
% identity	96
NCBI Description	(AF017359) lipid transfer protein LPT II [Oryza sativa]

Seq. No.	398762
Seq. ID	LIB3431-018-P1-N1-C8
Method	BLASTX
NCBI GI	g3980406
BLAST score	313
E value	8.0e-29
Match length	93
% identity	61
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	398763
Seq. ID	LIB3431-018-P1-N1-D12
Method	BLASTX
NCBI GI	g115813
BLAST score	267
E value	3.0e-23
Match length	83
% identity	69
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398764
Seq. ID	LIB3431-018-P1-N1-D2
Method	BLASTX
NCBI GI	g3036951
BLAST score	243
E value	3.0e-27
Match length	65
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	398765
Seq. ID	LIB3431-018-P1-N1-D3
Method	BLASTX
NCBI GI	g548603
BLAST score	325
E value	3.0e-30
Match length	63
% identity	97
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	398766
Seq. ID	LIB3431-018-P1-N1-D4
Method	BLASTN
NCBI GI	g20181
BLAST score	183
E value	2.0e-98
Match length	190
% identity	99
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398767
Seq. ID	LIB3431-018-P1-N1-D5
Method	BLASTN
NCBI GI	g20369
BLAST score	252
E value	1.0e-139
Match length	263
% identity	99
NCBI Description	Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31) >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase

Seq. No.	398768
Seq. ID	LIB3431-018-P1-N1-D6
Method	BLASTN
NCBI GI	g20191
BLAST score	430
E value	0.0e+00
Match length	466
% identity	98

NCBI Description	O.sativa mRNA for catalase
Seq. No.	398769
Seq. ID	LIB3431-018-P1-N1-E1
Method	BLASTX
NCBI GI	g3913641
BLAST score	434
E value	1.0e-60
Match length	126
% identity	96
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041777_dbj_BAA25423_ (AB007194) fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.	398770
Seq. ID	LIB3431-018-P1-N1-E10
Method	BLASTN
NCBI GI	g21838
BLAST score	67
E value	3.0e-29
Match length	204
% identity	85
NCBI Description	T.aestivum PRK gene for ribulose-5-phosphate kinase
Seq. No.	398771
Seq. ID	LIB3431-018-P1-N1-E11
Method	BLASTX
NCBI GI	g2864617
BLAST score	200
E value	2.0e-15
Match length	85
% identity	53
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1_ (AJ245574) ATP synthase beta chain precursor (subunit II) [Arabidopsis thaliana]
Seq. No.	398772
Seq. ID	LIB3431-018-P1-N1-E12
Method	BLASTX
NCBI GI	g671740
BLAST score	284
E value	3.0e-25
Match length	63
% identity	84
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	398773
Seq. ID	LIB3431-018-P1-N1-E2
Method	BLASTX
NCBI GI	g2407279
BLAST score	279
E value	4.0e-42
Match length	94
% identity	93

NCBI Description	(AF017362) aldolase [Oryza sativa]
Seq. No.	398774
Seq. ID	LIB3431-018-P1-N1-E3
Method	BLASTN
NCBI GI	g2072554
BLAST score	455
E value	0.0e+00
Match length	483
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds
Seq. No.	398775
Seq. ID	LIB3431-018-P1-N1-E5
Method	BLASTX
NCBI GI	g2582822
BLAST score	285
E value	3.0e-34
Match length	90
% identity	82
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]
Seq. No.	398776
Seq. ID	LIB3431-018-P1-N1-E7
Method	BLASTN
NCBI GI	g2331130
BLAST score	162
E value	6.0e-86
Match length	254
% identity	91
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds
Seq. No.	398777
Seq. ID	LIB3431-018-P1-N1-E9
Method	BLASTX
NCBI GI	g3036951
BLAST score	291
E value	3.0e-26
Match length	56
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]
Seq. No.	398778
Seq. ID	LIB3431-018-P1-N1-F1
Method	BLASTN
NCBI GI	g2072554
BLAST score	140
E value	7.0e-73
Match length	272
% identity	88
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398779
Seq. ID	LIB3431-018-P1-N1-F10
Method	BLASTX
NCBI GI	g548605
BLAST score	368
E value	3.0e-35
Match length	76
% identity	95
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	398780
Seq. ID	LIB3431-018-P1-N1-F11
Method	BLASTX
NCBI GI	g482311
BLAST score	297
E value	3.0e-41
Match length	91
% identity	99
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	398781
Seq. ID	LIB3431-018-P1-N1-F5
Method	BLASTN
NCBI GI	g20369
BLAST score	382
E value	0.0e+00
Match length	382
% identity	100
NCBI Description	Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31) >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase

Seq. No.	398782
Seq. ID	LIB3431-018-P1-N1-F7
Method	BLASTX
NCBI GI	g1477428
BLAST score	294
E value	2.0e-26
Match length	59
% identity	97
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No.	398783
Seq. ID	LIB3431-018-P1-N1-F8
Method	BLASTX
NCBI GI	g4079798
BLAST score	298
E value	8.0e-43
Match length	93
% identity	88

NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	398784
Seq. ID	LIB3431-018-P1-N1-G10
Method	BLASTX
NCBI GI	g4376158
BLAST score	227
E value	2.0e-18
Match length	75
% identity	63
NCBI Description	(X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No.	398785
Seq. ID	LIB3431-018-P1-N1-G11
Method	BLASTX
NCBI GI	g421916
BLAST score	154
E value	3.0e-10
Match length	29
% identity	97
NCBI Description	chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No.	398786
Seq. ID	LIB3431-018-P1-N1-G4
Method	BLASTN
NCBI GI	g218209
BLAST score	57
E value	2.0e-23
Match length	153
% identity	85
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	398787
Seq. ID	LIB3431-018-P1-N1-G7
Method	BLASTX
NCBI GI	g3036951
BLAST score	282
E value	3.0e-25
Match length	54
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	398788
Seq. ID	LIB3431-018-P1-N1-G8
Method	BLASTX
NCBI GI	g5262756
BLAST score	221
E value	5.0e-27
Match length	80
% identity	75
NCBI Description	(AL080283) putative protein [Arabidopsis thaliana]

Seq. No.	398789
Seq. ID	LIB3431-018-P1-N1-G9
Method	BLASTN
NCBI GI	g3885887
BLAST score	365
E value	0.0e+00
Match length	365
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	398790
Seq. ID	LIB3431-018-P1-N1-H10
Method	BLASTX
NCBI GI	g115794
BLAST score	542
E value	2.0e-55
Match length	114
% identity	90
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No.	398791
Seq. ID	LIB3431-018-P1-N1-H12
Method	BLASTN
NCBI GI	g710307
BLAST score	36
E value	1.0e-10
Match length	52
% identity	92
NCBI Description	Avena sativa victorin binding protein mRNA, complete cds

Seq. No.	398792
Seq. ID	LIB3431-018-P1-N1-H2
Method	BLASTX
NCBI GI	g3881189
BLAST score	146
E value	2.0e-15
Match length	93
% identity	43
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y

Seq. No.	398793
Seq. ID	LIB3431-018-P1-N1-H4
Method	BLASTX
NCBI GI	g115802
BLAST score	195
E value	5.0e-15
Match length	40
% identity	90

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No.	398794
Seq. ID	LIB3431-018-P1-N1-H5
Method	BLASTN
NCBI GI	g2570514
BLAST score	266
E value	1.0e-148
Match length	325
% identity	98
NCBI Description	Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	398795
Seq. ID	LIB3431-018-P1-N1-H6
Method	BLASTX
NCBI GI	g5042409
BLAST score	148
E value	3.0e-09
Match length	39
% identity	72
NCBI Description	(AC006193) Putative membrane related protein [Arabidopsis thaliana]

Seq. No.	398796
Seq. ID	LIB3431-018-P1-N1-H7
Method	BLASTX
NCBI GI	g606817
BLAST score	188
E value	5.0e-25
Match length	61
% identity	78
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]

Seq. No.	398797
Seq. ID	LIB3431-018-P1-N1-H8
Method	BLASTN
NCBI GI	g4206059
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Homo sapiens map 20q13.3; 51cR from D20S173 repeat region, complete sequence

Seq. No.	398798
Seq. ID	LIB3431-019-P1-K1-A10
Method	BLASTN
NCBI GI	g2072554
BLAST score	239
E value	1.0e-132
Match length	239

% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398799
Seq. ID	LIB3431-019-P1-K1-A11
Method	BLASTX
NCBI GI	g1085987
BLAST score	231
E value	2.0e-19
Match length	45
% identity	98
NCBI Description	light harvesting chlorophyll a protein precursor - Norway spruce >gi_607148_emb_CAA57407_ (X81808) light harvesting chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]

Seq. No.	398800
Seq. ID	LIB3431-019-P1-K1-A12
Method	BLASTN
NCBI GI	g4761113
BLAST score	47
E value	3.0e-17
Match length	51
% identity	98
NCBI Description	Allium grayi 5S ribosomal RNA gene, complete sequence

Seq. No.	398801
Seq. ID	LIB3431-019-P1-K1-A4
Method	BLASTX
NCBI GI	g3789954
BLAST score	691
E value	4.0e-73
Match length	127
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	398802
Seq. ID	LIB3431-019-P1-K1-A5
Method	BLASTX
NCBI GI	g126894
BLAST score	535
E value	1.0e-54
Match length	137
% identity	78
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_319832_pir__DEPUGW malate dehydrogenase (EC 1.1.1.37) precursor, glyoxysomal - watermelon >gi_167284 (M33148) glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37) [Citrullus vulgaris]

Seq. No.	398803
Seq. ID	LIB3431-019-P1-K1-A6
Method	BLASTX
NCBI GI	g5442410
BLAST score	390
E value	1.0e-37

Match length	137
% identity	57
NCBI Description	(AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No.	398804
Seq. ID	LIB3431-019-P1-K1-A7
Method	BLASTX
NCBI GI	g320618
BLAST score	689
E value	9.0e-73
Match length	150
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398805
Seq. ID	LIB3431-019-P1-K1-A9
Method	BLASTX
NCBI GI	g2982453
BLAST score	149
E value	9.0e-15
Match length	77
% identity	58
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	398806
Seq. ID	LIB3431-019-P1-K1-B1
Method	BLASTX
NCBI GI	g2809245
BLAST score	298
E value	6.0e-27
Match length	78
% identity	72
NCBI Description	(AC002560) F21B7.14 [Arabidopsis thaliana]

Seq. No.	398807
Seq. ID	LIB3431-019-P1-K1-B11
Method	BLASTX
NCBI GI	g4038594
BLAST score	280
E value	8.0e-25
Match length	84
% identity	62
NCBI Description	(AJ222798) tDET1 protein [Lycopersicon esculentum] >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [Lycopersicon esculentum]

Seq. No.	398808
Seq. ID	LIB3431-019-P1-K1-B12
Method	BLASTX
NCBI GI	g3885882
BLAST score	390
E value	7.0e-38

Match length	74
% identity	100
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No.	398809
Seq. ID	LIB3431-019-P1-K1-B4
Method	BLASTX
NCBI GI	g4585882
BLAST score	590
E value	3.0e-61
Match length	134
% identity	78
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	398810
Seq. ID	LIB3431-019-P1-K1-B6
Method	BLASTX
NCBI GI	g2921158
BLAST score	554
E value	4.0e-57
Match length	122
% identity	89
NCBI Description	(AF022909) ClpC [Arabidopsis thaliana]

Seq. No.	398811
Seq. ID	LIB3431-019-P1-K1-B7
Method	BLASTX
NCBI GI	g320618
BLAST score	753
E value	3.0e-80
Match length	142
% identity	99
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398812
Seq. ID	LIB3431-019-P1-K1-B8
Method	BLASTX
NCBI GI	g132105
BLAST score	427
E value	3.0e-42
Match length	103
% identity	83
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398813
Seq. ID	LIB3431-019-P1-K1-B9
Method	BLASTX
NCBI GI	g2982453
BLAST score	568
E value	1.0e-58
Match length	129
% identity	86
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	398814
Seq. ID	LIB3431-019-P1-K1-C1
Method	BLASTX
NCBI GI	g126201
BLAST score	409
E value	6.0e-40
Match length	117
% identity	68
NCBI Description	3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_81676_pir__S20510 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor - rape >gi_17827_emb_CAA42596_ (X59970) 3-isopropylmalate dehydrogenase [Brassica napus]

Seq. No.	398815
Seq. ID	LIB3431-019-P1-K1-C11
Method	BLASTX
NCBI GI	g5031281
BLAST score	345
E value	2.0e-32
Match length	115
% identity	60
NCBI Description	(AF139499) unknown [Prunus armeniaca]

Seq. No.	398816
Seq. ID	LIB3431-019-P1-K1-C2
Method	BLASTX
NCBI GI	g3292814
BLAST score	248
E value	4.0e-21
Match length	117
% identity	44
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	398817
Seq. ID	LIB3431-019-P1-K1-C3
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398818
Seq. ID	LIB3431-019-P1-K1-C4
Method	BLASTX
NCBI GI	g3913018
BLAST score	712
E value	2.0e-75
Match length	136
% identity	99
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	398819
Seq. ID	LIB3431-019-P1-K1-C5
Method	BLASTX
NCBI GI	g3776005
BLAST score	372
E value	1.0e-35
Match length	76
% identity	95
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	398820
Seq. ID	LIB3431-019-P1-K1-C6
Method	BLASTX
NCBI GI	g3776005
BLAST score	287
E value	1.0e-25
Match length	76
% identity	78
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	398821
Seq. ID	LIB3431-019-P1-K1-C7
Method	BLASTX
NCBI GI	g1173347
BLAST score	473
E value	2.0e-47
Match length	107
% identity	89
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	398822
Seq. ID	LIB3431-019-P1-K1-C8
Method	BLASTX
NCBI GI	g132105
BLAST score	538
E value	4.0e-55
Match length	120
% identity	85
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398823
Seq. ID	LIB3431-019-P1-K1-[illegible]
Method	BLASTX
NCBI GI	g2239089
BLAST score	218
E value	1.0e-17
Match length	100
% identity	41
NCBI Description	(Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	398824
Seq. ID	LIB3431-019-P1-K1-D10
Method	BLASTX
NCBI GI	g1835731
BLAST score	512
E value	4.0e-52
Match length	97
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	398825
Seq. ID	LIB3431-019-P1-K1-D11
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	6.0e-11
Match length	47
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398826
Seq. ID	LIB3431-019-P1-K1-D12
Method	BLASTX
NCBI GI	g671740
BLAST score	588
E value	5.0e-61
Match length	108
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	398827
Seq. ID	LIB3431-019-P1-K1-D3
Method	BLASTX
NCBI GI	g2501646
BLAST score	631

E value	5.0e-66
Match length	139
% identity	91
NCBI Description	UROPORPHYRINOGEN DECARBOXYLASE (UPD) >gi_1362169_pir__S55733 uroporphyrinogen decarboxylase - barley >gi_1016347_emb_CAA58039_ (X82832) uroporphyrinogen decarboxylase [Hordeum vulgare]

Seq. No.	398828
Seq. ID	LIB3431-019-P1-K1-D4
Method	BLASTN
NCBI GI	g6015437
BLAST score	38
E value	7.0e-12
Match length	38
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398829
Seq. ID	LIB3431-019-P1-K1-D5
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	398830
Seq. ID	LIB3431-019-P1-K1-D7
Method	BLASTX
NCBI GI	g115787
BLAST score	508
E value	1.0e-51
Match length	117
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398831
Seq. ID	LIB3431-019-P1-K1-D8
Method	BLASTX
NCBI GI	g132105
BLAST score	609
E value	2.0e-63
Match length	131
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398832
Seq. ID	LIB3431-019-P1-K1-D9
Method	BLASTX
NCBI GI	g320618
BLAST score	380
E value	2.0e-36
Match length	96
% identity	83
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398833
Seq. ID	LIB3431-019-P1-K1-E1
Method	BLASTX
NCBI GI	g4874311
BLAST score	433
E value	8.0e-43
Match length	132
% identity	66
NCBI Description	(AC006053) unknown protein [Arabidopsis thaliana]

Seq. No.	398834
Seq. ID	LIB3431-019-P1-K1-E10
Method	BLASTX
NCBI GI	g5103831
BLAST score	221
E value	6.0e-18
Match length	66
% identity	64
NCBI Description	(AC007591) ESTs gb_H37032, gb_R6425, gb_Z34651, gb_N37268, gb_AA713172 and gb_Z34241 come from this gene. [Arabidopsis thaliana]

Seq. No.	398835
Seq. ID	LIB3431-019-P1-K1-E11
Method	BLASTX
NCBI GI	g1076724
BLAST score	601
E value	2.0e-62
Match length	127
% identity	84
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No.	398836
Seq. ID	LIB3431-019-P1-K1-E3
Method	BLASTX
NCBI GI	g1871192
BLAST score	288
E value	9.0e-26

Match length	137
% identity	45
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	398837
Seq. ID	LIB3431-019-P1-K1-E4
Method	BLASTX
NCBI GI	g4539332
BLAST score	296
E value	1.0e-26
Match length	90
% identity	68
NCBI Description	(AL035539) glycosyltransferase like protein (fragment) [Arabidopsis thaliana]

Seq. No.	398838
Seq. ID	LIB3431-019-P1-K1-E5
Method	BLASTN
NCBI GI	g6015437
BLAST score	39
E value	2.0e-12
Match length	39
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	398839
Seq. ID	LIB3431-019-P1-K1-E6
Method	BLASTX
NCBI GI	g2293480
BLAST score	416
E value	7.0e-41
Match length	85
% identity	94
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	398840
Seq. ID	LIB3431-019-P1-K1-E7
Method	BLASTX
NCBI GI	g2623298
BLAST score	512
E value	5.0e-52
Match length	143
% identity	64
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No.	398841
Seq. ID	LIB3431-019-P1-K1-E9
Method	BLASTX
NCBI GI	g1076746
BLAST score	163
E value	3.0e-11
Match length	30
% identity	97
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70

[Oryza sativa]

Seq. No.	398842
Seq. ID	LIB3431-019-P1-K1-F1
Method	BLASTX
NCBI GI	g134034
BLAST score	261
E value	1.0e-22
Match length	110
% identity	50
NCBI Description	30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5) (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1) >gi_279640_pir__R3SPS5 ribosomal protein CS-S22 precursor, chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270) chloroplast ribosomal protein S22 [Spinacia oleracea] >gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein [Spinacia oleracea]

Seq. No.	398843
Seq. ID	LIB3431-019-P1-K1-F10
Method	BLASTX
NCBI GI	g3075488
BLAST score	439
E value	2.0e-43
Match length	104
% identity	82
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	398844
Seq. ID	LIB3431-019-P1-K1-F11
Method	BLASTX
NCBI GI	g3914005
BLAST score	314
E value	8.0e-29
Match length	70
% identity	89
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays]

Seq. No.	398845
Seq. ID	LIB3431-019-P1-K1-F2
Method	BLASTX
NCBI GI	g1777961
BLAST score	482
E value	2.0e-48
Match length	152
% identity	62
NCBI Description	(U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No.	398846
Seq. ID	LIB3431-019-P1-K1-F4
Method	BLASTX
NCBI GI	g82080
BLAST score	336
E value	2.0e-31
Match length	95

% identity	69
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	398847
Seq. ID	LIB3431-019-P1-K1-F5
Method	BLASTX
NCBI GI	g2130082
BLAST score	260
E value	2.0e-22
Match length	128
% identity	41
NCBI Description	protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443 (U37133) receptor kinase-like protein [Oryza sativa] >gi_2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] >gi_1586408_prf__2203451A receptor kinase-like protein [Oryza sativa]

Seq. No.	398848
Seq. ID	LIB3431-019-P1-K1-F6
Method	BLASTX
NCBI GI	g710308
BLAST score	716
E value	7.0e-76
Match length	156
% identity	88
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	398849
Seq. ID	LIB3431-019-P1-K1-F7
Method	BLASTX
NCBI GI	g3126854
BLAST score	583
E value	2.0e-60
Match length	111
% identity	98
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398850
Seq. ID	LIB3431-019-P1-K1-F8
Method	BLASTX
NCBI GI	g1835731
BLAST score	531
E value	3.0e-54
Match length	101
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	398851
Seq. ID	LIB3431-019-P1-K1-F9
Method	BLASTX
NCBI GI	g3075488
BLAST score	500
E value	1.0e-50
Match length	117
% identity	83

NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.	398852
Seq. ID	LIB3431-019-P1-K1-G1
Method	BLASTX
NCBI GI	g4996602
BLAST score	316
E value	5.0e-29
Match length	142
% identity	50
NCBI Description	(AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana tabacum]
Seq. No.	398853
Seq. ID	LIB3431-019-P1-K1-G3
Method	BLASTX
NCBI GI	g5834807
BLAST score	161
E value	7.0e-11
Match length	50
% identity	64
NCBI Description	(AL117212) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	398854
Seq. ID	LIB3431-019-P1-K1-G5
Method	BLASTX
NCBI GI	g320618
BLAST score	380
E value	4.0e-44
Match length	108
% identity	86
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	398855
Seq. ID	LIB3431-019-P1-K1-G7
Method	BLASTX
NCBI GI	g132105
BLAST score	390
E value	3.0e-52
Match length	125
% identity	81
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	398856
Seq. ID	LIB3431-019-P1-K1-G8

Method	BLASTX
NCBI GI	g4506221
BLAST score	206
E value	3.0e-16
Match length	102
% identity	45
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 >gi_1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit p55 [Homo sapiens]

Seq. No.	398857
Seq. ID	LIB3431-019-P1-K1-H1
Method	BLASTX
NCBI GI	g4079800
BLAST score	502
E value	7.0e-51
Match length	101
% identity	96
NCBI Description	(AF052503) S-phase-specific ribosomal protein [Oryza sativa]

Seq. No.	398858
Seq. ID	LIB3431-019-P1-K1-H11
Method	BLASTX
NCBI GI	g3885882
BLAST score	317
E value	2.0e-29
Match length	83
% identity	75
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No.	398859
Seq. ID	LIB3431-019-P1-K1-H2
Method	BLASTX
NCBI GI	g5903092
BLAST score	382
E value	8.0e-37
Match length	114
% identity	72
NCBI Description	(AC008017) Highly similar to developmental protein DG1118 [Arabidopsis thaliana]

Seq. No.	398860
Seq. ID	LIB3431-019-P1-K1-H4
Method	BLASTX
NCBI GI	g3885888
BLAST score	316
E value	5.0e-29
Match length	142
% identity	52
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	398861
Seq. ID	LIB3431-019-P1-K1-H5
Method	BLASTX
NCBI GI	g3885882
BLAST score	409

E value	3.0e-42
Match length	95
% identity	95
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No.	398862
Seq. ID	LIB3431-019-P1-K1-H6
Method	BLASTX
NCBI GI	g2795806
BLAST score	498
E value	2.0e-50
Match length	141
% identity	70
NCBI Description	(AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	398863
Seq. ID	LIB3431-019-P1-K1-H7
Method	BLASTX
NCBI GI	g1164988
BLAST score	345
E value	2.0e-32
Match length	124
% identity	55
NCBI Description	(X94335) YOR3513c [Saccharomyces cerevisiae]

Seq. No.	398864
Seq. ID	LIB3431-019-P1-K1-H9
Method	BLASTX
NCBI GI	g266893
BLAST score	661
E value	1.0e-69
Match length	130
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	398865
Seq. ID	LIB3431-019-P1-N1-A10
Method	BLASTN
NCBI GI	g2072554
BLAST score	233
E value	1.0e-128
Match length	237
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398866
Seq. ID	LIB3431-019-P1-N1-A11
Method	BLASTX
NCBI GI	g1085987
BLAST score	231
E value	2.0e-19
Match length	45

% identity	98
NCBI Description	light harvesting chlorophyll a protein precursor - Norway spruce >gi_607148_emb_CAA57407_ (X81808) light harvesting chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]

Seq. No.	398867
Seq. ID	LIB3431-019-P1-N1-A2
Method	BLASTN
NCBI GI	g218207
BLAST score	161
E value	2.0e-85
Match length	245
% identity	91
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398868
Seq. ID	LIB3431-019-P1-N1-A4
Method	BLASTX
NCBI GI	g3789954
BLAST score	390
E value	1.0e-37
Match length	72
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	398869
Seq. ID	LIB3431-019-P1-N1-A6
Method	BLASTX
NCBI GI	g5442410
BLAST score	179
E value	5.0e-13
Match length	78
% identity	49
NCBI Description	(AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No.	398870
Seq. ID	LIB3431-019-P1-N1-A7
Method	BLASTX
NCBI GI	g115787
BLAST score	409
E value	6.0e-40
Match length	77
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398871
Seq. ID	LIB3431-019-P1-N1-A9
Method	BLASTX
NCBI GI	g2191138
BLAST score	287

E value	1.0e-25
Match length	64
% identity	83
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No.	398872
Seq. ID	LIB3431-019-P1-N1-B1
Method	BLASTX
NCBI GI	g2809245
BLAST score	283
E value	3.0e-25
Match length	64
% identity	83
NCBI Description	(AC002560) F21B7.14 [Arabidopsis thaliana]

Seq. No.	398873
Seq. ID	LIB3431-019-P1-N1-B11
Method	BLASTX
NCBI GI	g4038594
BLAST score	233
E value	2.0e-19
Match length	67
% identity	63
NCBI Description	(AJ222798) tDET1 protein [Lycopersicon esculentum] >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [Lycopersicon esculentum]

Seq. No.	398874
Seq. ID	LIB3431-019-P1-N1-B12
Method	BLASTN
NCBI GI	g3885881
BLAST score	345
E value	0.0e+00
Match length	373
% identity	98
NCBI Description	Oryza sativa inorganic pyrophosphatase (IPP) mRNA, complete cds

Seq. No.	398875
Seq. ID	LIB3431-019-P1-N1-B4
Method	BLASTX
NCBI GI	g115813
BLAST score	176
E value	1.0e-12
Match length	41
% identity	80
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398876
Seq. ID	LIB3431-019-P1-N1-B6
Method	BLASTX
NCBI GI	g461753
BLAST score	406
E value	1.0e-39

Match length	103
% identity	77
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi_169128 (L09547) nuclear encoded precursor to chloroplast protein [Pisum sativum]

Seq. No.	398877
Seq. ID	LIB3431-019-P1-N1-B7
Method	BLASTN
NCBI GI	g20181
BLAST score	139
E value	3.0e-72
Match length	150
% identity	98
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398878
Seq. ID	LIB3431-019-P1-N1-B8
Method	BLASTX
NCBI GI	g671740
BLAST score	363
E value	2.0e-34
Match length	72
% identity	94
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	398879
Seq. ID	LIB3431-019-P1-N1-C11
Method	BLASTX
NCBI GI	g5031281
BLAST score	237
E value	9.0e-20
Match length	51
% identity	80
NCBI Description	(AF139499) unknown [Prunus armeniaca]

Seq. No.	398880
Seq. ID	LIB3431-019-P1-N1-C3
Method	BLASTN
NCBI GI	g2072554
BLAST score	282
E value	1.0e-157
Match length	286
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398881
Seq. ID	LIB3431-019-P1-N1-C4
Method	BLASTN
NCBI GI	g218154
BLAST score	50
E value	4.0e-19

Match length	78
% identity	91
NCBI Description	Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No.	398882
Seq. ID	LIB3431-019-P1-N1-C5
Method	BLASTX
NCBI GI	g3776005
BLAST score	162
E value	6.0e-11
Match length	36
% identity	89
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	398883
Seq. ID	LIB3431-019-P1-N1-C7
Method	BLASTN
NCBI GI	g14264
BLAST score	51
E value	1.0e-19
Match length	87
% identity	90
NCBI Description	T.aestivum gene for sedoheptulose-1,7-bisphoshatase

Seq. No.	398884
Seq. ID	LIB3431-019-P1-N1-C8
Method	BLASTN
NCBI GI	g218207
BLAST score	163
E value	1.0e-86
Match length	279
% identity	90
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	398885
Seq. ID	LIB3431-019-P1-N1-D10
Method	BLASTX
NCBI GI	g1835731
BLAST score	280
E value	6.0e-25
Match length	64
% identity	84
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	398886
Seq. ID	LIB3431-019-P1-N1-D11
Method	BLASTX
NCBI GI	g517500
BLAST score	176
E value	8.0e-13
Match length	53
% identity	68
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II

OE17 protein [Pisum sativum]

Seq. No.	398887
Seq. ID	LIB3431-019-P1-N1-D3
Method	BLASTX
NCBI GI	g6014938
BLAST score	173
E value	2.0e-12
Match length	34
% identity	94
NCBI Description	UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi_3420233 (AF058763) uroporphyrinogen decarboxylase [Zea mays]

Seq. No.	398888
Seq. ID	LIB3431-019-P1-N1-D7
Method	BLASTX
NCBI GI	g421916
BLAST score	162
E value	4.0e-11
Match length	29
% identity	100
NCBI Description	chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No.	398889
Seq. ID	LIB3431-019-P1-N1-D8
Method	BLASTX
NCBI GI	g347451
BLAST score	387
E value	2.0e-37
Match length	72
% identity	97
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	398890
Seq. ID	LIB3431-019-P1-N1-D9
Method	BLASTX
NCBI GI	g3036951
BLAST score	310
E value	2.0e-28
Match length	61
% identity	98
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	398891
Seq. ID	LIB3431-019-P1-N1-E4
Method	BLASTX
NCBI GI	g5764049
BLAST score	252
E value	2.0e-21
Match length	67
% identity	70
NCBI Description	(Y16832) alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase [Nicotiana

tabacum]

Seq. No.	398892
Seq. ID	LIB3431-019-P1-N1-E6
Method	BLASTN
NCBI GI	g2331130
BLAST score	189
E value	1.0e-102
Match length	193
% identity	99
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No.	398893
Seq. ID	LIB3431-019-P1-N1-F10
Method	BLASTN
NCBI GI	g3075487
BLAST score	240
E value	1.0e-132
Match length	260
% identity	98
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	398894
Seq. ID	LIB3431-019-P1-N1-F2
Method	BLASTX
NCBI GI	g1777961
BLAST score	194
E value	1.0e-14
Match length	73
% identity	58
NCBI Description	(U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No.	398895
Seq. ID	LIB3431-019-P1-N1-F4
Method	BLASTX
NCBI GI	g115813
BLAST score	243
E value	1.0e-20
Match length	55
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	398896
Seq. ID	LIB3431-019-P1-N1-F6
Method	BLASTX
NCBI GI	g710308
BLAST score	147
E value	2.0e-09
Match length	27
% identity	96
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	398897
Seq. ID	LIB3431-019-P1-N1-F7
Method	BLASTX
NCBI GI	g3126854
BLAST score	345
E value	1.0e-32
Match length	65
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398898
Seq. ID	LIB3431-019-P1-N1-F8
Method	BLASTN
NCBI GI	g1835730
BLAST score	219
E value	1.0e-120
Match length	255
% identity	96
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No.	398899
Seq. ID	LIB3431-019-P1-N1-F9
Method	BLASTN
NCBI GI	g3075487
BLAST score	338
E value	0.0e+00
Match length	338
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	398900
Seq. ID	LIB3431-019-P1-N1-G1
Method	BLASTX
NCBI GI	g1321627
BLAST score	231
E value	3.0e-19
Match length	55
% identity	82
NCBI Description	(D83656) thylakoid-bound ascorbate peroxidase [Cucurbita sp.]

Seq. No.	398901
Seq. ID	LIB3431-019-P1-N1-G10
Method	BLASTX
NCBI GI	g289920
BLAST score	286
E value	1.0e-25
Match length	58
% identity	95
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	398902
Seq. ID	LIB3431-019-P1-N1-G2
Method	BLASTX

NCBI GI	g120661
BLAST score	251
E value	2.0e-21
Match length	50
% identity	92
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	398903
Seq. ID	LIB3431-019-P1-N1-G5
Method	BLASTN
NCBI GI	g218171
BLAST score	215
E value	1.0e-117
Match length	243
% identity	97
NCBI Description	Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No.	398904
Seq. ID	LIB3431-019-P1-N1-G6
Method	BLASTX
NCBI GI	g1652203
BLAST score	153
E value	5.0e-10
Match length	78
% identity	38
NCBI Description	(D90903) hypothetical protein [Synechocystis sp.]

Seq. No.	398905
Seq. ID	LIB3431-019-P1-N1-G7
Method	BLASTX
NCBI GI	g132105
BLAST score	310
E value	1.0e-30
Match length	68
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398906
Seq. ID	LIB3431-019-P1-N1-H11
Method	BLASTX
NCBI GI	g3789954
BLAST score	184
E value	9.0e-14
Match length	33
% identity	97

NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
Seq. No.	398907
Seq. ID	LIB3431-019-P1-N1-H4
Method	BLASTN
NCBI GI	g3885887
BLAST score	374
E value	0.0e+00
Match length	378
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds
Seq. No.	398908
Seq. ID	LIB3431-019-P1-N1-H5
Method	BLASTX
NCBI GI	g3885882
BLAST score	189
E value	3.0e-14
Match length	39
% identity	97
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]
Seq. No.	398909
Seq. ID	LIB3431-019-P1-N1-H7
Method	BLASTX
NCBI GI	g1164988
BLAST score	341
E value	6.0e-32
Match length	94
% identity	68
NCBI Description	(X94335) YOR3513c [Saccharomyces cerevisiae]
Seq. No.	398910
Seq. ID	LIB3431-019-P1-N1-H8
Method	BLASTN
NCBI GI	g12470
BLAST score	76
E value	5.0e-35
Match length	99
% identity	94
NCBI Description	Z.mays chloroplast rRNA-operon
Seq. No.	398911
Seq. ID	LIB3431-019-P1-N1-H9
Method	BLASTX
NCBI GI	g132166
BLAST score	160
E value	6.0e-11
Match length	31
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 -

473) [Arabidopsis thaliana]

Seq. No.	398912
Seq. ID	LIB3431-020-P1-K1-A1
Method	BLASTX
NCBI GI	g2494116
BLAST score	171
E value	8.0e-26
Match length	67
% identity	75
NCBI Description	(AC002376) Similar to Synechocystis hypothetical protein (gb_D90915). [Arabidopsis thaliana]

Seq. No.	398913
Seq. ID	LIB3431-020-P1-K1-A12
Method	BLASTX
NCBI GI	g115787
BLAST score	516
E value	2.0e-52
Match length	120
% identity	86
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398914
Seq. ID	LIB3431-020-P1-K1-A7
Method	BLASTX
NCBI GI	g5931655
BLAST score	199
E value	2.0e-15
Match length	100
% identity	41
NCBI Description	(AJ011629) squamosa promoter binding protein-like 1 [Arabidopsis thaliana]

Seq. No.	398915
Seq. ID	LIB3431-020-P1-K1-A8
Method	BLASTX
NCBI GI	g3550982
BLAST score	156
E value	2.0e-10
Match length	82
% identity	48
NCBI Description	(AB010690) mutM homologue-1 [Arabidopsis thaliana] >gi_5903053_gb_AAD55612.1_AC008016_22 (AC008016) Identical to gb_AB010690 mutM homologue-1 (formamidopyrimidine-DNA glycosylase 1) from Arabidopsis thaliana. EST gb_Z18192 comes from this gene

Seq. No.	398916
Seq. ID	LIB3431-020-P1-K1-B12
Method	BLASTX
NCBI GI	g121446
BLAST score	160

E value	2.0e-11
Match length	60
% identity	58
NCBI Description	FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR (FD-GOGAT) >gi_100877_pir__A38596 glutamate synthase (ferredoxin) (EC 1.4.7.1) - maize >gi_168477 (M59190) ferredoxin-dependent glutamate synthase [Zea mays]

Seq. No.	398917
Seq. ID	LIB3431-020-P1-K1-B4
Method	BLASTX
NCBI GI	g417260
BLAST score	421
E value	3.0e-41
Match length	128
% identity	66
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	398918
Seq. ID	LIB3431-020-P1-K1-B5
Method	BLASTX
NCBI GI	g4063821
BLAST score	756
E value	1.0e-80
Match length	144
% identity	99
NCBI Description	(AB015204) plastidic ATP sulfurylase [Oryza sativa]

Seq. No.	398919
Seq. ID	LIB3431-020-P1-K1-B6
Method	BLASTX
NCBI GI	g3789952
BLAST score	588
E value	7.0e-61
Match length	115
% identity	95
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	398920
Seq. ID	LIB3431-020-P1-K1-B7
Method	BLASTX
NCBI GI	g4138290
BLAST score	582
E value	2.0e-60
Match length	125
% identity	86
NCBI Description	(AJ005841) thioredoxin M [Oryza sativa]

Seq. No.	398921
Seq. ID	LIB3431-020-P1-K1-B8
Method	BLASTX
NCBI GI	g2673912
BLAST score	262
E value	1.0e-22

Match length	90
% identity	58
NCBI Description	(AC002561) unknown protein [Arabidopsis thaliana]

Seq. No.	398922
Seq. ID	LIB3431-020-P1-K1-B9
Method	BLASTX
NCBI GI	g132105
BLAST score	391
E value	7.0e-38
Match length	124
% identity	64
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398923
Seq. ID	LIB3431-020-P1-K1-C1
Method	BLASTX
NCBI GI	g170404
BLAST score	565
E value	3.0e-68
Match length	137
% identity	96
NCBI Description	(M14444) chlorophyll a/b-binding protein Cab-3C [Lycopersicon esculentum]

Seq. No.	398924
Seq. ID	LIB3431-020-P1-K1-C10
Method	BLASTX
NCBI GI	g1346874
BLAST score	152
E value	8.0e-10
Match length	49
% identity	61
NCBI Description	PHOTOSYSTEM II REACTION CENTER W PROTEIN >gi_1016177 (U30821) subunit of the water oxidation complex on the lumenal surface of the photosystem II reaction center complex [Cyanophora paradoxa]

Seq. No.	398925
Seq. ID	LIB3431-020-P1-K1-C11
Method	BLASTX
NCBI GI	g3126854
BLAST score	646
E value	1.0e-67
Match length	140
% identity	89
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398926

Seq. ID	LIB3431-020-P1-K1-C2
Method	BLASTX
NCBI GI	g473878
BLAST score	168
E value	3.0e-12
Match length	46
% identity	70
NCBI Description	(U08315) calnexin homolog [Arabidopsis thaliana]

Seq. No.	398927
Seq. ID	LIB3431-020-P1-K1-C3
Method	BLASTX
NCBI GI	g5729754
BLAST score	175
E value	1.0e-12
Match length	77
% identity	49
NCBI Description	transcription factor CA150 >gi_2460124 (AF017789) putative transcription factor CA150 [Homo sapiens]

Seq. No.	398928
Seq. ID	LIB3431-020-P1-K1-C5
Method	BLASTX
NCBI GI	g500734
BLAST score	374
E value	7.0e-36
Match length	131
% identity	54
NCBI Description	(U10414) Contains similarity to Pfam domain: PF00005 (ABC_tran), Score=245.2, E-value=3e-70, N=2 [Caenorhabditis elegans]

Seq. No.	398929
Seq. ID	LIB3431-020-P1-K1-C7
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398930
Seq. ID	LIB3431-020-P1-K1-C8
Method	BLASTX
NCBI GI	g1519251
BLAST score	537
E value	4.0e-55
Match length	108
% identity	100
NCBI Description	(U65957) GF14-c protein [Oryza sativa]

Seq. No.	398931
Seq. ID	LIB3431-020-P1-K1-D10
Method	BLASTX

NCBI GI	g3915131
BLAST score	582
E value	3.0e-60
Match length	112
% identity	100
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza sativa]

Seq. No.	398932
Seq. ID	LIB3431-020-P1-K1-D4
Method	BLASTX
NCBI GI	g2570511
BLAST score	662
E value	1.0e-69
Match length	127
% identity	98
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	398933
Seq. ID	LIB3431-020-P1-K1-D5
Method	BLASTX
NCBI GI	g3047117
BLAST score	740
E value	1.0e-78
Match length	144
% identity	97
NCBI Description	(AF058919) similar to ATP-dependent RNA helicases [Arabidopsis thaliana]

Seq. No.	398934
Seq. ID	LIB3431-020-P1-K1-D7
Method	BLASTX
NCBI GI	g1617206
BLAST score	180
E value	3.0e-13
Match length	49
% identity	71
NCBI Description	(Z72489) CP12 [Pisum sativum]

Seq. No.	398935
Seq. ID	LIB3431-020-P1-K1-D8
Method	BLASTX
NCBI GI	g320618
BLAST score	632
E value	5.0e-66
Match length	137
% identity	88
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398936

Seq. ID	LIB3431-020-P1-K1-D9
Method	BLASTX
NCBI GI	g2582822
BLAST score	458
E value	1.0e-45
Match length	108
% identity	80
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	398937
Seq. ID	LIB3431-020-P1-K1-E1
Method	BLASTX
NCBI GI	g4886307
BLAST score	543
E value	1.0e-55
Match length	123
% identity	87
NCBI Description	(AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]

Seq. No.	398938
Seq. ID	LIB3431-020-P1-K1-E10
Method	BLASTX
NCBI GI	g2570515
BLAST score	219
E value	1.0e-17
Match length	47
% identity	91
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	398939
Seq. ID	LIB3431-020-P1-K1-E11
Method	BLASTX
NCBI GI	g320618
BLAST score	607
E value	4.0e-63
Match length	133
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	398940
Seq. ID	LIB3431-020-P1-K1-E12
Method	BLASTX
NCBI GI	g132105
BLAST score	759
E value	6.0e-81
Match length	139
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

	(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	398941
Seq. ID	LIB3431-020-P1-K1-E2
Method	BLASTX
NCBI GI	g3345477
BLAST score	491
E value	2.0e-49
Match length	140
% identity	69
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.	398942
Seq. ID	LIB3431-020-P1-K1-E3
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	398943
Seq. ID	LIB3431-020-P1-K1-E5
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	1.0e-19
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	398944
Seq. ID	LIB3431-020-P1-K1-E6
Method	BLASTX
NCBI GI	g115787
BLAST score	417
E value	7.0e-41
Match length	121
% identity	74
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]
Seq. No.	398945
Seq. ID	LIB3431-020-P1-K1-E7
Method	BLASTX
NCBI GI	g1835731
BLAST score	559

E value	2.0e-57
Match length	106
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	398946
Seq. ID	LIB3431-020-P1-K1-E8
Method	BLASTX
NCBI GI	g2407281
BLAST score	625
E value	3.0e-65
Match length	117
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398947
Seq. ID	LIB3431-020-P1-K1-E9
Method	BLASTX
NCBI GI	g2565305
BLAST score	605
E value	5.0e-63
Match length	119
% identity	96
NCBI Description	(AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No.	398948
Seq. ID	LIB3431-020-P1-K1-F1
Method	BLASTN
NCBI GI	g3789951
BLAST score	188
E value	1.0e-101
Match length	380
% identity	96
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398949
Seq. ID	LIB3431-020-P1-K1-F11
Method	BLASTX
NCBI GI	g1661160
BLAST score	523
E value	3.0e-53
Match length	115
% identity	85
NCBI Description	(U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	398950
Seq. ID	LIB3431-020-P1-K1-F12
Method	BLASTX
NCBI GI	g728744
BLAST score	338
E value	1.0e-54
Match length	152
% identity	76

NCBI Description	AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir__S16390 auxin-induced protein - common tobacco >gi_19799_emb_CAA39708_ (X56267) auxin-induced protein [Nicotiana tabacum]
Seq. No.	398951
Seq. ID	LIB3431-020-P1-K1-F2
Method	BLASTX
NCBI GI	g3789952
BLAST score	788
E value	2.0e-84
Match length	152
% identity	96
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]
Seq. No.	398952
Seq. ID	LIB3431-020-P1-K1-F3
Method	BLASTX
NCBI GI	g115772
BLAST score	211
E value	2.0e-17
Match length	57
% identity	77
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_ (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]
Seq. No.	398953
Seq. ID	LIB3431-020-P1-K1-F4
Method	BLASTX
NCBI GI	g6002055
BLAST score	634
E value	3.0e-66
Match length	151
% identity	77
NCBI Description	(AJ249794) lipoxygenase [Arabidopsis thaliana]
Seq. No.	398954
Seq. ID	LIB3431-020-P1-K1-F8
Method	BLASTX
NCBI GI	g3345477
BLAST score	316
E value	5.0e-29
Match length	59
% identity	100
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.	398955
Seq. ID	LIB3431-020-P1-K1-F9
Method	BLASTX
NCBI GI	g131225
BLAST score	570
E value	7.0e-59
Match length	119

% identity	93
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	398956
Seq. ID	LIB3431-020-P1-K1-G10
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398957
Seq. ID	LIB3431-020-P1-K1-G11
Method	BLASTX
NCBI GI	g2462763
BLAST score	322
E value	2.0e-44
Match length	124
% identity	79
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	398958
Seq. ID	LIB3431-020-P1-K1-G12
Method	BLASTX
NCBI GI	g871931
BLAST score	490
E value	2.0e-49
Match length	125
% identity	80
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	398959
Seq. ID	LIB3431-020-P1-K1-G6
Method	BLASTN
NCBI GI	g5670155
BLAST score	43
E value	4.0e-15
Match length	75
% identity	89
NCBI Description	Oryza sativa subsp. japonica BAC clone 34K24, complete sequence

Seq. No.	398960
Seq. ID	LIB3431-020-P1-K1-G7
Method	BLASTN
NCBI GI	g21810
BLAST score	38
E value	9.0e-12
Match length	38

% identity	100
NCBI Description	T.aestivum mRNA for heat shock protein 26.6B

Seq. No.	398961
Seq. ID	LIB3431-020-P1-K1-H1
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	6.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	398962
Seq. ID	LIB3431-020-P1-K1-H10
Method	BLASTX
NCBI GI	g3915131
BLAST score	592
E value	2.0e-61
Match length	114
% identity	100
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza sativa]

Seq. No.	398963
Seq. ID	LIB3431-020-P1-K1-H11
Method	BLASTX
NCBI GI	g115787
BLAST score	529
E value	5.0e-54
Match length	121
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398964
Seq. ID	LIB3431-020-P1-K1-H2
Method	BLASTX
NCBI GI	g132105
BLAST score	185
E value	9.0e-14
Match length	105
% identity	48
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

	ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	398965
Seq. ID	LIB3431-020-P1-K1-H3
Method	BLASTX
NCBI GI	g4583546
BLAST score	145
E value	6.0e-09
Match length	70
% identity	40
NCBI Description	(AJ010819) GrpE protein [Arabidopsis thaliana]
Seq. No.	398966
Seq. ID	LIB3431-020-P1-K1-H4
Method	BLASTX
NCBI GI	g2270994
BLAST score	231
E value	4.0e-19
Match length	125
% identity	42
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]
Seq. No.	398967
Seq. ID	LIB3431-020-P1-K1-H5
Method	BLASTX
NCBI GI	g4097587
BLAST score	250
E value	3.0e-21
Match length	69
% identity	72
NCBI Description	(U64926) NTGP5 [Nicotiana tabacum]
Seq. No.	398968
Seq. ID	LIB3431-020-P1-K1-H7
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	398969
Seq. ID	LIB3431-020-P1-N1-A2
Method	BLASTN
NCBI GI	g3342030
BLAST score	85
E value	7.0e-40
Match length	109
% identity	94
NCBI Description	Joinvillea ascendens 18S small subunit ribosomal RNA gene, complete sequence

Seq. No. 398970
Seq. ID LIB3431-020-P1-N1-A8
Method BLASTX
NCBI GI g5932555
BLAST score 287
E value 1.0e-25
Match length 87
% identity 66
NCBI Description (AC009465) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 398971
Seq. ID LIB3431-020-P1-N1-B10
Method BLASTX
NCBI GI g421916
BLAST score 190
E value 2.0e-14
Match length 35
% identity 100
NCBI Description chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No. 398972
Seq. ID LIB3431-020-P1-N1-B5
Method BLASTX
NCBI GI g417260
BLAST score 313
E value 7.0e-29
Match length 78
% identity 76
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No. 398973
Seq. ID LIB3431-020-P1-N1-B6
Method BLASTX
NCBI GI g4063821
BLAST score 192
E value 2.0e-14
Match length 67
% identity 65
NCBI Description (AB015204) plastidic ATP sulfurylase [Oryza sativa]

Seq. No. 398974
Seq. ID LIB3431-020-P1-N1-B8
Method BLASTX
NCBI GI g4138290
BLAST score 307
E value 4.0e-28
Match length 60
% identity 100
NCBI Description (AJ005841) thioredoxin M [Oryza sativa]

Seq. No. 398975
Seq. ID LIB3431-020-P1-N1-C11

Method	BLASTX
NCBI GI	g1346875
BLAST score	251
E value	2.0e-21
Match length	79
% identity	57
NCBI Description	PHOTOSYSTEM II REACTION CENTER W PROTEIN >gi_1185169_emb_CAA91652_ (Z67753) PSII, protein W, 13 kDa [Odontella sinensis]

Seq. No.	398976
Seq. ID	LIB3431-020-P1-N1-C2
Method	BLASTN
NCBI GI	g20181
BLAST score	63
E value	6.0e-27
Match length	91
% identity	92
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	398977
Seq. ID	LIB3431-020-P1-N1-C4
Method	BLASTN
NCBI GI	g3789951
BLAST score	223
E value	1.0e-122
Match length	358
% identity	90
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398978
Seq. ID	LIB3431-020-P1-N1-C8
Method	BLASTN
NCBI GI	g2072554
BLAST score	269
E value	1.0e-149
Match length	357
% identity	94
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398979
Seq. ID	LIB3431-020-P1-N1-C9
Method	BLASTN
NCBI GI	g1519250
BLAST score	212
E value	1.0e-115
Match length	323
% identity	91
NCBI Description	Oryza sativa GF14-c protein mRNA, complete cds

Seq. No.	398980
Seq. ID	LIB3431-020-P1-N1-D11
Method	BLASTX

NCBI GI	g3915131
BLAST score	360
E value	4.0e-34
Match length	74
% identity	96
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza sativa]

Seq. No.	398981
Seq. ID	LIB3431-020-P1-N1-D3
Method	BLASTN
NCBI GI	g3695004
BLAST score	38
E value	1.0e-11
Match length	54
% identity	93
NCBI Description	Zea mays pyruvate dehydrogenase kinase isoform 2 mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	398982
Seq. ID	LIB3431-020-P1-N1-D5
Method	BLASTX
NCBI GI	g2570511
BLAST score	163
E value	2.0e-21
Match length	63
% identity	80
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	398983
Seq. ID	LIB3431-020-P1-N1-D8
Method	BLASTX
NCBI GI	g1617197
BLAST score	160
E value	7.0e-11
Match length	31
% identity	90
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	398984
Seq. ID	LIB3431-020-P1-N1-D9
Method	BLASTX
NCBI GI	g115787
BLAST score	483
E value	1.0e-48
Match length	100
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	398985

Seq. ID	LIB3431-020-P1-N1-E1
Method	BLASTN
NCBI GI	g218171
BLAST score	69
E value	2.0e-30
Match length	167
% identity	86
NCBI Description	Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No.	398986
Seq. ID	LIB3431-020-P1-N1-E11
Method	BLASTN
NCBI GI	g2570514
BLAST score	266
E value	1.0e-148
Match length	326
% identity	98
NCBI Description	Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	398987
Seq. ID	LIB3431-020-P1-N1-E12
Method	BLASTX
NCBI GI	g3036946
BLAST score	319
E value	2.0e-29
Match length	61
% identity	100
NCBI Description	(AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	398988
Seq. ID	LIB3431-020-P1-N1-E2
Method	BLASTX
NCBI GI	g4886307
BLAST score	480
E value	3.0e-48
Match length	108
% identity	85
NCBI Description	(AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]

Seq. No.	398989
Seq. ID	LIB3431-020-P1-N1-E3
Method	BLASTN
NCBI GI	g3345476
BLAST score	310
E value	1.0e-174
Match length	362
% identity	96
NCBI Description	Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No.	398990
Seq. ID	LIB3431-020-P1-N1-E5
Method	BLASTX
NCBI GI	g5916444

BLAST score	289
E value	8.0e-26
Match length	89
% identity	57
NCBI Description	(AC007633) putative protein [Arabidopsis thaliana]

Seq. No.	398991
Seq. ID	LIB3431-020-P1-N1-E6
Method	BLASTN
NCBI GI	g6103440
BLAST score	54
E value	2.0e-21
Match length	94
% identity	89
NCBI Description	Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds

Seq. No.	398992
Seq. ID	LIB3431-020-P1-N1-E8
Method	BLASTX
NCBI GI	g1835731
BLAST score	402
E value	4.0e-39
Match length	92
% identity	85
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	398993
Seq. ID	LIB3431-020-P1-N1-E9
Method	BLASTX
NCBI GI	g671740
BLAST score	473
E value	1.0e-47
Match length	86
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	398994
Seq. ID	LIB3431-020-P1-N1-F10
Method	BLASTX
NCBI GI	g132105
BLAST score	360
E value	1.0e-48
Match length	98
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	398995

Seq. ID	LIB3431-020-P1-N1-F12
Method	BLASTX
NCBI GI	g115800
BLAST score	180
E value	3.0e-13
Match length	45
% identity	76
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 3 PRECURSOR (LHCII TYPE I CAB-3) (LHCP) >gi_81771_pir__S01962 chlorophyll a/b-binding protein 3 precursor - soybean >gi_18552_emb_CAA31419_ (X12981) chlorophyll a/b binding preprotein (AA - 32 to 231) [Glycine max]

Seq. No.	398996
Seq. ID	LIB3431-020-P1-N1-F2
Method	BLASTN
NCBI GI	g3789951
BLAST score	154
E value	4.0e-81
Match length	348
% identity	95
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398997
Seq. ID	LIB3431-020-P1-N1-F3
Method	BLASTN
NCBI GI	g3789951
BLAST score	69
E value	2.0e-30
Match length	121
% identity	89
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	398998
Seq. ID	LIB3431-020-P1-N1-F4
Method	BLASTX
NCBI GI	g3036951
BLAST score	211
E value	3.0e-32
Match length	78
% identity	90
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	398999
Seq. ID	LIB3431-020-P1-N1-F5
Method	BLASTX
NCBI GI	g1654140
BLAST score	355
E value	7.0e-35
Match length	119
% identity	66
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No.	399000
Seq. ID	LIB3431-020-P1-N1-F6
Method	BLASTX
NCBI GI	g4079798
BLAST score	153
E value	3.0e-10
Match length	32
% identity	94
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	399001
Seq. ID	LIB3431-020-P1-N1-F7
Method	BLASTX
NCBI GI	g710308
BLAST score	381
E value	1.0e-36
Match length	79
% identity	86
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	399002
Seq. ID	LIB3431-020-P1-N1-F9
Method	BLASTX
NCBI GI	g3345477
BLAST score	204
E value	7.0e-16
Match length	46
% identity	80
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399003
Seq. ID	LIB3431-020-P1-N1-G10
Method	BLASTX
NCBI GI	g2462750
BLAST score	269
E value	1.0e-23
Match length	71
% identity	70
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	399004
Seq. ID	LIB3431-020-P1-N1-G11
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	1.0e-19
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399005
Seq. ID	LIB3431-020-P1-N1-G12

Method	BLASTX
NCBI GI	g2462762
BLAST score	341
E value	6.0e-32
Match length	85
% identity	73
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	399006
Seq. ID	LIB3431-020-P1-N1-G7
Method	BLASTX
NCBI GI	g131225
BLAST score	187
E value	5.0e-14
Match length	49
% identity	71
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399007
Seq. ID	LIB3431-020-P1-N1-H10
Method	BLASTX
NCBI GI	g871931
BLAST score	220
E value	8.0e-18
Match length	55
% identity	80
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	399008
Seq. ID	LIB3431-020-P1-N1-H12
Method	BLASTN
NCBI GI	g20181
BLAST score	119
E value	3.0e-60
Match length	139
% identity	96
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	399009
Seq. ID	LIB3431-020-P1-N1-H5
Method	BLASTN
NCBI GI	g505134
BLAST score	185
E value	1.0e-100
Match length	217
% identity	97
NCBI Description	Rice mRNA for ferredoxin, complete cds

Seq. No.	399010
Seq. ID	LIB3431-020-P1-N1-H7
Method	BLASTX
NCBI GI	g1617197

BLAST score	213
E value	7.0e-19
Match length	67
% identity	73
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399011
Seq. ID	LIB3431-020-P1-N1-H8
Method	BLASTX
NCBI GI	g2072555
BLAST score	213
E value	7.0e-17
Match length	44
% identity	91
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399012
Seq. ID	LIB3431-021-P1-K1-A1
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399013
Seq. ID	LIB3431-021-P1-K1-A10
Method	BLASTX
NCBI GI	g1709846
BLAST score	235
E value	2.0e-19
Match length	134
% identity	38
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) 22 kDa component of photosystem II [Lycopersicon esculentum]

Seq. No.	399014
Seq. ID	LIB3431-021-P1-K1-A11
Method	BLASTX
NCBI GI	g1350742
BLAST score	176
E value	1.0e-12
Match length	46
% identity	61
NCBI Description	PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264) coded for by C. elegans cDNA yk64g10.5; coded for by C. elegans cDNA yk51f3.5; coded for by C. elegans cDNA yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA yk64g1

Seq. No.	399015
Seq. ID	LIB3431-021-P1-K1-A12

Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	1.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399016
Seq. ID	LIB3431-021-P1-K1-A2
Method	BLASTX
NCBI GI	g4455169
BLAST score	180
E value	4.0e-13
Match length	71
% identity	45
NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	399017
Seq. ID	LIB3431-021-P1-K1-A3
Method	BLASTX
NCBI GI	g6016678
BLAST score	324
E value	6.0e-30
Match length	77
% identity	75
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	399018
Seq. ID	LIB3431-021-P1-K1-A5
Method	BLASTX
NCBI GI	g131388
BLAST score	417
E value	6.0e-41
Match length	137
% identity	65
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No.	399019
Seq. ID	LIB3431-021-P1-K1-A7
Method	BLASTX
NCBI GI	g4455169
BLAST score	235
E value	2.0e-19
Match length	71
% identity	58
NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	399020

Seq. ID	LIB3431-021-P1-K1-A8
Method	BLASTX
NCBI GI	g1632831
BLAST score	315
E value	7.0e-36
Match length	139
% identity	58
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	399021
Seq. ID	LIB3431-021-P1-K1-A9
Method	BLASTX
NCBI GI	g6016678
BLAST score	184
E value	1.0e-13
Match length	63
% identity	54
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	399022
Seq. ID	LIB3431-021-P1-K1-B1
Method	BLASTX
NCBI GI	g4689380
BLAST score	424
E value	8.0e-42
Match length	121
% identity	70
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]

Seq. No.	399023
Seq. ID	LIB3431-021-P1-K1-B10
Method	BLASTX
NCBI GI	g3377805
BLAST score	406
E value	1.0e-39
Match length	154
% identity	54
NCBI Description	(AF075597) contains similarity to several apoptosis or programmed cell death proteins such as rat apoptosis protein RP-8 (GB:M80601) [Arabidopsis thaliana] >gi_3912928_gb_AAC78712.1_ (AF001308) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	399024
Seq. ID	LIB3431-021-P1-K1-B11
Method	BLASTX
NCBI GI	g132105
BLAST score	657
E value	5.0e-69
Match length	140
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399025
Seq. ID	LIB3431-021-P1-K1-B12
Method	BLASTX
NCBI GI	g2306981
BLAST score	467
E value	1.0e-46
Match length	84
% identity	96
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No.	399026
Seq. ID	LIB3431-021-P1-K1-B2
Method	BLASTX
NCBI GI	g5762457
BLAST score	652
E value	2.0e-68
Match length	123
% identity	98
NCBI Description	(AF176040) ubiquitin-conjugating enzyme UBC2 [Mesembryanthemum crystallinum]

Seq. No.	399027
Seq. ID	LIB3431-021-P1-K1-B4
Method	BLASTX
NCBI GI	g131225
BLAST score	404
E value	1.0e-48
Match length	116
% identity	81
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399028
Seq. ID	LIB3431-021-P1-K1-B6
Method	BLASTX
NCBI GI	g4689380
BLAST score	678
E value	2.0e-71
Match length	137
% identity	90
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]

Seq. No.	399029
Seq. ID	LIB3431-021-P1-K1-B7
Method	BLASTX
NCBI GI	g115794
BLAST score	724
E value	7.0e-77
Match length	142

% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]
Seq. No.	399030
Seq. ID	LIB3431-021-P1-K1-B8
Method	BLASTN
NCBI GI	g20181
BLAST score	192
E value	1.0e-104
Match length	196
% identity	99
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein
Seq. No.	399031
Seq. ID	LIB3431-021-P1-K1-B9
Method	BLASTN
NCBI GI	g218209
BLAST score	117
E value	3.0e-59
Match length	157
% identity	95
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106
Seq. No.	399032
Seq. ID	LIB3431-021-P1-K1-C1
Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.	399033
Seq. ID	LIB3431-021-P1-K1-C10
Method	BLASTX
NCBI GI	g5106775
BLAST score	545
E value	5.0e-56
Match length	109
% identity	94
NCBI Description	(AF067732) ribosomal protein S12 [Hordeum vulgare]
Seq. No.	399034
Seq. ID	LIB3431-021-P1-K1-C11
Method	BLASTX
NCBI GI	g2289907
BLAST score	229
E value	8.0e-19
Match length	104

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% identity	45
NCBI Description	(AC002397) C2F [Mus musculus]

Seq. No.	399035
Seq. ID	LIB3431-021-P1-K1-C12
Method	BLASTX
NCBI GI	g129916
BLAST score	481
E value	2.0e-48
Match length	152
% identity	67
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]

Seq. No.	399036
Seq. ID	LIB3431-021-P1-K1-C2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399037
Seq. ID	LIB3431-021-P1-K1-C3
Method	BLASTX
NCBI GI	g115787
BLAST score	666
E value	5.0e-70
Match length	146
% identity	90
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399038
Seq. ID	LIB3431-021-P1-K1-C4
Method	BLASTX
NCBI GI	g3885882
BLAST score	492
E value	9.0e-50
Match length	94
% identity	99
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No.	399039
Seq. ID	LIB3431-021-P1-K1-C5
Method	BLASTX
NCBI GI	g417260
BLAST score	425

E value	7.0e-42
Match length	122
% identity	70
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	399040
Seq. ID	LIB3431-021-P1-K1-C7
Method	BLASTN
NCBI GI	g6015437
BLAST score	38
E value	9.0e-12
Match length	38
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399041
Seq. ID	LIB3431-021-P1-K1-C8
Method	BLASTX
NCBI GI	g2407281
BLAST score	423
E value	1.0e-41
Match length	129
% identity	66
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399042
Seq. ID	LIB3431-021-P1-K1-D1
Method	BLASTX
NCBI GI	g132105
BLAST score	623
E value	5.0e-65
Match length	134
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399043
Seq. ID	LIB3431-021-P1-K1-D10
Method	BLASTX
NCBI GI	g4336608
BLAST score	190
E value	9.0e-28
Match length	109
% identity	71
NCBI Description	(AF099111) sigma factor; Sig2 [Zea mays]

Seq. No.	399044

Seq. ID	LIB3431-021-P1-K1-D11
Method	BLASTX
NCBI GI	g4980489
BLAST score	174
E value	2.0e-12
Match length	100
% identity	38
NCBI Description	(AE001689) muconate cycloisomerase [Thermotoga maritima]

Seq. No.	399045
Seq. ID	LIB3431-021-P1-K1-D2
Method	BLASTX
NCBI GI	g6015065
BLAST score	704
E value	1.0e-74
Match length	144
% identity	91
NCBI Description	ELONGATION FACTOR 2 (EF-2) >gi_2369714_emb_CAB09900_ (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	399046
Seq. ID	LIB3431-021-P1-K1-D3
Method	BLASTX
NCBI GI	g3885886
BLAST score	666
E value	4.0e-70
Match length	130
% identity	100
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.	399047
Seq. ID	LIB3431-021-P1-K1-D4
Method	BLASTX
NCBI GI	g125580
BLAST score	611
E value	1.0e-63
Match length	137
% identity	87
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608) phosphoribulokinase [Triticum aestivum]

Seq. No.	399048
Seq. ID	LIB3431-021-P1-K1-D5
Method	BLASTX
NCBI GI	g2494320
BLAST score	252
E value	2.0e-21
Match length	58
% identity	78
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation factor-5 [Zea mays]

Seq. No.	399049
Seq. ID	LIB3431-021-P1-K1-D6

Method	BLASTX
NCBI GI	g482311
BLAST score	571
E value	4.0e-59
Match length	115
% identity	97
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	399050
Seq. ID	LIB3431-021-P1-K1-D7
Method	BLASTX
NCBI GI	g1346109
BLAST score	318
E value	3.0e-29
Match length	59
% identity	100
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231) RWD [Oryza sativa]

Seq. No.	399051
Seq. ID	LIB3431-021-P1-K1-D8
Method	BLASTX
NCBI GI	g131225
BLAST score	578
E value	1.0e-59
Match length	124
% identity	90
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399052
Seq. ID	LIB3431-021-P1-K1-D9
Method	BLASTX
NCBI GI	g4467099
BLAST score	482
E value	2.0e-48
Match length	119
% identity	85
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	399053
Seq. ID	LIB3431-021-P1-K1-E1
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399054
Seq. ID	LIB3431-021-P1-K1-E10
Method	BLASTX
NCBI GI	g1835731
BLAST score	484
E value	1.0e-48
Match length	93
% identity	99
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399055
Seq. ID	LIB3431-021-P1-K1-E11
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399056
Seq. ID	LIB3431-021-P1-K1-E12
Method	BLASTX
NCBI GI	g2499497
BLAST score	689
E value	9.0e-73
Match length	144
% identity	97
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_1161600_emb_CAA88841_ (Z48977) phosphoglycerate kinase [Nicotiana tabacum]

Seq. No.	399057
Seq. ID	LIB3431-021-P1-K1-E3
Method	BLASTX
NCBI GI	g3063453
BLAST score	207
E value	1.0e-18
Match length	61
% identity	82
NCBI Description	(AC003981) F22O13.15 [Arabidopsis thaliana]

Seq. No.	399058
Seq. ID	LIB3431-021-P1-K1-E4
Method	BLASTX
NCBI GI	g1835731
BLAST score	580
E value	5.0e-60
Match length	123
% identity	91
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399059
Seq. ID	LIB3431-021-P1-K1-E5

Method	BLASTN
NCBI GI	g2072554
BLAST score	330
E value	0.0e+00
Match length	330
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399060
Seq. ID	LIB3431-021-P1-K1-E8
Method	BLASTX
NCBI GI	g3914603
BLAST score	671
E value	1.0e-70
Match length	131
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	399061
Seq. ID	LIB3431-021-P1-K1-E9
Method	BLASTX
NCBI GI	g2582822
BLAST score	462
E value	3.0e-46
Match length	128
% identity	70
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	399062
Seq. ID	LIB3431-021-P1-K1-F1
Method	BLASTX
NCBI GI	g3789952
BLAST score	177
E value	7.0e-13
Match length	32
% identity	100
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	399063
Seq. ID	LIB3431-021-P1-K1-F11
Method	BLASTX
NCBI GI	g551047
BLAST score	222
E value	4.0e-18
Match length	43
% identity	95
NCBI Description	(X79277) type II LHCI [Lolium temulentum]

Seq. No.	399064
Seq. ID	LIB3431-021-P1-K1-F3
Method	BLASTX

NCBI GI	g2130069
BLAST score	750
E value	6.0e-80
Match length	136
% identity	99
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No.	399065
Seq. ID	LIB3431-021-P1-K1-F4
Method	BLASTX
NCBI GI	g4539423
BLAST score	487
E value	3.0e-49
Match length	126
% identity	75
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	399066
Seq. ID	LIB3431-021-P1-K1-F6
Method	BLASTX
NCBI GI	g2570515
BLAST score	447
E value	2.0e-68
Match length	146
% identity	96
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	399067
Seq. ID	LIB3431-021-P1-K1-F7
Method	BLASTX
NCBI GI	g3789954
BLAST score	387
E value	2.0e-37
Match length	98
% identity	80
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399068
Seq. ID	LIB3431-021-P1-K1-F8
Method	BLASTX
NCBI GI	g1835731
BLAST score	448
E value	2.0e-44
Match length	96
% identity	89
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399069
Seq. ID	LIB3431-021-P1-K1-F9
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36

% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399070
Seq. ID	LIB3431-021-P1-K1-G1
Method	BLASTN
NCBI GI	g304219
BLAST score	53
E value	6.0e-21
Match length	129
% identity	85
NCBI Description	Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No.	399071
Seq. ID	LIB3431-021-P1-K1-G10
Method	BLASTN
NCBI GI	g20262
BLAST score	95
E value	9.0e-46
Match length	190
% identity	88
NCBI Description	O.sativa light-induced mRNA

Seq. No.	399072
Seq. ID	LIB3431-021-P1-K1-G12
Method	BLASTX
NCBI GI	g548605
BLAST score	489
E value	2.0e-54
Match length	131
% identity	81
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	399073
Seq. ID	LIB3431-021-P1-K1-G2
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399074
Seq. ID	LIB3431-021-P1-K1-G3
Method	BLASTX
NCBI GI	g3800878
BLAST score	543
E value	1.0e-55
Match length	150
% identity	71
NCBI Description	(AF096281) threonine dehydratase/deaminase [Arabidopsis

thaliana]

Seq. No.	399075
Seq. ID	LIB3431-021-P1-K1-G4
Method	BLASTX
NCBI GI	g115787
BLAST score	404
E value	3.0e-42
Match length	117
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399076
Seq. ID	LIB3431-021-P1-K1-G5
Method	BLASTX
NCBI GI	g4585882
BLAST score	459
E value	4.0e-46
Match length	97
% identity	81
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	399077
Seq. ID	LIB3431-021-P1-K1-G6
Method	BLASTX
NCBI GI	g4581114
BLAST score	295
E value	1.0e-26
Match length	63
% identity	83
NCBI Description	(AC005825) putative HesB-like protein;required for efficient nitrogen fixation in Cyanobacteria [Arabidopsis thaliana]

Seq. No.	399078
Seq. ID	LIB3431-021-P1-K1-G8
Method	BLASTX
NCBI GI	g5881940
BLAST score	259
E value	2.0e-22
Match length	143
% identity	44
NCBI Description	(AL117387) putative secreted protein [Streptomyces coelicolor A3(2)]

Seq. No.	399079
Seq. ID	LIB3431-021-P1-K1-H1
Method	BLASTN
NCBI GI	g11957
BLAST score	198
E value	1.0e-107
Match length	202

% identity	50
NCBI Description	Rice complete chloroplast genome

Seq. No.	399080
Seq. ID	LIB3431-021-P1-K1-H11
Method	BLASTX
NCBI GI	g4973254
BLAST score	446
E value	3.0e-44
Match length	103
% identity	80
NCBI Description	(AF144386) thioredoxin f2 [Arabidopsis thaliana]

Seq. No.	399081
Seq. ID	LIB3431-021-P1-K1-H12
Method	BLASTX
NCBI GI	g320617
BLAST score	509
E value	8.0e-52
Match length	97
% identity	99
NCBI Description	chlorophyll a/b-binding protein II precursor - rice >gi_227612_prf__1707316B chlorophyll a/b binding protein 2 [Oryza sativa]

Seq. No.	399082
Seq. ID	LIB3431-021-P1-K1-H3
Method	BLASTX
NCBI GI	g2501190
BLAST score	655
E value	8.0e-69
Match length	136
% identity	92
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	399083
Seq. ID	LIB3431-021-P1-K1-H4
Method	BLASTX
NCBI GI	g3914603
BLAST score	607
E value	3.0e-63
Match length	117
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	399084
Seq. ID	LIB3431-021-P1-K1-H5
Method	BLASTX
NCBI GI	g1352468
BLAST score	296
E value	8.0e-27

Match length	67
% identity	81
NCBI Description	BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) >gi_1122439 (U16123) invertase [Zea mays]

Seq. No.	399085
Seq. ID	LIB3431-021-P1-K1-H7
Method	BLASTX
NCBI GI	g131225
BLAST score	570
E value	8.0e-59
Match length	124
% identity	90
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399086
Seq. ID	LIB3431-021-P1-K1-H9
Method	BLASTX
NCBI GI	g82080
BLAST score	425
E value	8.0e-42
Match length	121
% identity	68
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	399087
Seq. ID	LIB3431-021-P1-N1-A10
Method	BLASTX
NCBI GI	g6103011
BLAST score	220
E value	6.0e-18
Match length	58
% identity	72
NCBI Description	(X84225) precursor of photosystem II subunit (22KDa) [Nicotiana tabacum]

Seq. No.	399088
Seq. ID	LIB3431-021-P1-N1-A11
Method	BLASTX
NCBI GI	g1350742
BLAST score	159
E value	1.0e-10
Match length	43
% identity	58
NCBI Description	PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264) coded for by C. elegans cDNA yk64g10.5; coded for by C. elegans cDNA yk51f3.5; coded for by C. elegans cDNA yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA yk64g1

Seq. No.	399089
Seq. ID	LIB3431-021-P1-N1-A3
Method	BLASTX
NCBI GI	g6016678
BLAST score	221
E value	7.0e-18
Match length	58
% identity	66
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	399090
Seq. ID	LIB3431-021-P1-N1-A4
Method	BLASTX
NCBI GI	g6016678
BLAST score	186
E value	1.0e-13
Match length	63
% identity	54
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	399091
Seq. ID	LIB3431-021-P1-N1-A5
Method	BLASTX
NCBI GI	g482311
BLAST score	404
E value	3.0e-39
Match length	85
% identity	95
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	399092
Seq. ID	LIB3431-021-P1-N1-A8
Method	BLASTX
NCBI GI	g1632831
BLAST score	257
E value	4.0e-22
Match length	67
% identity	76
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	399093
Seq. ID	LIB3431-021-P1-N1-B11
Method	BLASTX
NCBI GI	g671740
BLAST score	415
E value	1.0e-40
Match length	76
% identity	99
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399094
Seq. ID	LIB3431-021-P1-N1-B12
Method	BLASTN
NCBI GI	g2306980

BLAST score	59
E value	2.0e-24
Match length	79
% identity	94
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	399095
Seq. ID	LIB3431-021-P1-N1-B2
Method	BLASTX
NCBI GI	g464986
BLAST score	341
E value	6.0e-32
Match length	67
% identity	93
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	399096
Seq. ID	LIB3431-021-P1-N1-B4
Method	BLASTX
NCBI GI	g131225
BLAST score	301
E value	3.0e-27
Match length	73
% identity	78
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399097
Seq. ID	LIB3431-021-P1-N1-B6
Method	BLASTX
NCBI GI	g115794
BLAST score	411
E value	4.0e-40
Match length	87
% identity	89
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No.	399098
Seq. ID	LIB3431-021-P1-N1-B7
Method	BLASTX

NCBI GI	g115794
BLAST score	546
E value	6.0e-56
Match length	111
% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No.	399099
Seq. ID	LIB3431-021-P1-N1-B8
Method	BLASTN
NCBI GI	g20181
BLAST score	188
E value	1.0e-101
Match length	196
% identity	99
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	399100
Seq. ID	LIB3431-021-P1-N1-C12
Method	BLASTX
NCBI GI	g129916
BLAST score	240
E value	4.0e-20
Match length	79
% identity	70
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]

Seq. No.	399101
Seq. ID	LIB3431-021-P1-N1-C2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399102
Seq. ID	LIB3431-021-P1-N1-C3
Method	BLASTX
NCBI GI	g693920
BLAST score	347
E value	1.0e-32
Match length	66
% identity	100
NCBI Description	(U21113) chlorophyll a/b binding protein [Solanum tuberosum]

Seq. No.	399103
Seq. ID	LIB3431-021-P1-N1-C4
Method	BLASTX
NCBI GI	g3885882
BLAST score	266
E value	4.0e-23
Match length	58
% identity	93
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No.	399104
Seq. ID	LIB3431-021-P1-N1-C5
Method	BLASTX
NCBI GI	g417260
BLAST score	313
E value	1.0e-28
Match length	78
% identity	76
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	399105
Seq. ID	LIB3431-021-P1-N1-C8
Method	BLASTX
NCBI GI	g132105
BLAST score	507
E value	2.0e-51
Match length	99
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399106
Seq. ID	LIB3431-021-P1-N1-D10
Method	BLASTX
NCBI GI	g4336608
BLAST score	243
E value	1.0e-20
Match length	61
% identity	75
NCBI Description	(AF099111) sigma factor; Sig2 [Zea mays]

Seq. No.	399107
Seq. ID	LIB3431-021-P1-N1-D3
Method	BLASTX
NCBI GI	g3885886
BLAST score	221
E value	7.0e-18

Match length	39
% identity	100
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.	399108
Seq. ID	LIB3431-021-P1-N1-D4
Method	BLASTX
NCBI GI	g21839
BLAST score	355
E value	1.0e-33
Match length	74
% identity	95
NCBI Description	(X57952) phosphoribulokinase [Triticum aestivum]

Seq. No.	399109
Seq. ID	LIB3431-021-P1-N1-D5
Method	BLASTX
NCBI GI	g2494320
BLAST score	252
E value	2.0e-21
Match length	58
% identity	78
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation factor-5 [Zea mays]

Seq. No.	399110
Seq. ID	LIB3431-021-P1-N1-D6
Method	BLASTX
NCBI GI	g482311
BLAST score	508
E value	1.0e-51
Match length	99
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	399111
Seq. ID	LIB3431-021-P1-N1-D7
Method	BLASTX
NCBI GI	g1346109
BLAST score	286
E value	1.0e-25
Match length	55
% identity	98
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231) RWD [Oryza sativa]

Seq. No.	399112
Seq. ID	LIB3431-021-P1-N1-D8
Method	BLASTX
NCBI GI	g131225
BLAST score	257
E value	2.0e-22
Match length	56

% identity	82
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399113
Seq. ID	LIB3431-021-P1-N1-D9
Method	BLASTN
NCBI GI	g438246
BLAST score	56
E value	1.0e-22
Match length	92
% identity	90
NCBI Description	S.tuberosum mRNA for glycine hydroxymethyltransferase

Seq. No.	399114
Seq. ID	LIB3431-021-P1-N1-E10
Method	BLASTN
NCBI GI	g1835730
BLAST score	144
E value	2.0e-75
Match length	156
% identity	98
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No.	399115
Seq. ID	LIB3431-021-P1-N1-E11
Method	BLASTX
NCBI GI	g2072555
BLAST score	233
E value	3.0e-19
Match length	44
% identity	98
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399116
Seq. ID	LIB3431-021-P1-N1-E12
Method	BLASTX
NCBI GI	g3738261
BLAST score	368
E value	4.0e-35
Match length	83
% identity	92
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	399117
Seq. ID	LIB3431-021-P1-N1-E4
Method	BLASTX
NCBI GI	g1835731
BLAST score	252
E value	1.0e-21
Match length	65

% identity	77
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399118
Seq. ID	LIB3431-021-P1-N1-E8
Method	BLASTX
NCBI GI	g132166
BLAST score	159
E value	8.0e-11
Match length	31
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	399119
Seq. ID	LIB3431-021-P1-N1-F1
Method	BLASTN
NCBI GI	g3789951
BLAST score	77
E value	4.0e-35
Match length	161
% identity	87
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	399120
Seq. ID	LIB3431-021-P1-N1-F11
Method	BLASTX
NCBI GI	g551047
BLAST score	222
E value	4.0e-18
Match length	43
% identity	95
NCBI Description	(X79277) type II LHCI [Lolium temulentum]

Seq. No.	399121
Seq. ID	LIB3431-021-P1-N1-F3
Method	BLASTX
NCBI GI	g2130069
BLAST score	200
E value	2.0e-15
Match length	39
% identity	97
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No.	399122
Seq. ID	LIB3431-021-P1-N1-F4
Method	BLASTX
NCBI GI	g2688822
BLAST score	284
E value	3.0e-25

Match length	98
% identity	63
NCBI Description	(U93272) pyrophosphate-dependent phosphofructo-1-kinase [Prunus armeniaca]

Seq. No.	399123
Seq. ID	LIB3431-021-P1-N1-F6
Method	BLASTX
NCBI GI	g2570515
BLAST score	196
E value	6.0e-15
Match length	41
% identity	93
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	399124
Seq. ID	LIB3431-021-P1-N1-F7
Method	BLASTX
NCBI GI	g3789954
BLAST score	390
E value	1.0e-37
Match length	72
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399125
Seq. ID	LIB3431-021-P1-N1-F8
Method	BLASTX
NCBI GI	g1835731
BLAST score	173
E value	2.0e-12
Match length	49
% identity	71
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399126
Seq. ID	LIB3431-021-P1-N1-G10
Method	BLASTN
NCBI GI	g20262
BLAST score	105
E value	3.0e-52
Match length	169
% identity	91
NCBI Description	O.sativa light-induced mRNA

Seq. No.	399127
Seq. ID	LIB3431-021-P1-N1-G3
Method	BLASTX
NCBI GI	g3800878
BLAST score	206
E value	4.0e-16
Match length	58
% identity	62
NCBI Description	(AF096281) threonine dehydratase/deaminase [Arabidopsis thaliana]

Seq. No.	399128
Seq. ID	LIB3431-021-P1-N1-G4
Method	BLASTX
NCBI GI	g421916
BLAST score	243
E value	1.0e-20
Match length	45
% identity	100
NCBI Description	chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No.	399129
Seq. ID	LIB3431-021-P1-N1-G5
Method	BLASTX
NCBI GI	g115813
BLAST score	229
E value	7.0e-19
Match length	54
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	399130
Seq. ID	LIB3431-021-P1-N1-G6
Method	BLASTX
NCBI GI	g1698548
BLAST score	254
E value	1.0e-21
Match length	68
% identity	69
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	399131
Seq. ID	LIB3431-021-P1-N1-G7
Method	BLASTX
NCBI GI	g2582822
BLAST score	268
E value	2.0e-23
Match length	75
% identity	71
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	399132
Seq. ID	LIB3431-021-P1-N1-H2
Method	BLASTN
NCBI GI	g3868755
BLAST score	98
E value	4.0e-48
Match length	134
% identity	93
NCBI Description	Oryza sativa CatC gene for catalase, complete cds

Seq. No.	399133
Seq. ID	LIB3431-021-P1-N1-H3

Method	BLASTX
NCBI GI	g2501190
BLAST score	240
E value	4.0e-20
Match length	68
% identity	75
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	399134
Seq. ID	LIB3431-021-P1-N1-H6
Method	BLASTX
NCBI GI	g131176
BLAST score	161
E value	4.0e-11
Match length	32
% identity	97
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No.	399135
Seq. ID	LIB3431-021-P1-N1-H7
Method	BLASTX
NCBI GI	g131225
BLAST score	304
E value	1.0e-27
Match length	75
% identity	77
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399136
Seq. ID	LIB3431-021-P1-N1-H8
Method	BLASTX
NCBI GI	g5738542
BLAST score	234
E value	1.0e-19
Match length	56
% identity	77
NCBI Description	(AJ245867) photosystem I subunit XI precursor [Arabidopsis thaliana]

Seq. No.	399137
Seq. ID	LIB3431-021-P1-N1-H9
Method	BLASTX
NCBI GI	g115813
BLAST score	200
E value	2.0e-15

Match length	51
% identity	76
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	399138
Seq. ID	LIB3431-022-P1-K1-A1
Method	BLASTX
NCBI GI	g2407281
BLAST score	632
E value	4.0e-66
Match length	121
% identity	98
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399139
Seq. ID	LIB3431-022-P1-K1-A12
Method	BLASTX
NCBI GI	g3212865
BLAST score	409
E value	6.0e-40
Match length	145
% identity	56
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	399140
Seq. ID	LIB3431-022-P1-K1-A3
Method	BLASTX
NCBI GI	g5640111
BLAST score	296
E value	1.0e-26
Match length	97
% identity	63
NCBI Description	(AJ243875) RAD23 protein [Lycopersicon esculentum]

Seq. No.	399141
Seq. ID	LIB3431-022-P1-K1-A4
Method	BLASTN
NCBI GI	g3885891
BLAST score	44
E value	1.0e-15
Match length	109
% identity	95
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	399142
Seq. ID	LIB3431-022-P1-K1-A5
Method	BLASTX
NCBI GI	g132105
BLAST score	637
E value	1.0e-66
Match length	137
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399143
Seq. ID	LIB3431-022-P1-K1-A6
Method	BLASTX
NCBI GI	g1173347
BLAST score	736
E value	3.0e-78
Match length	148
% identity	96
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	399144
Seq. ID	LIB3431-022-P1-K1-A7
Method	BLASTX
NCBI GI	g3345477
BLAST score	544
E value	9.0e-56
Match length	142
% identity	75
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399145
Seq. ID	LIB3431-022-P1-K1-A9
Method	BLASTX
NCBI GI	g2245086
BLAST score	373
E value	1.0e-35
Match length	104
% identity	68
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399146
Seq. ID	LIB3431-022-P1-K1-B1
Method	BLASTX
NCBI GI	g132105
BLAST score	609
E value	2.0e-63
Match length	131
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399147
Seq. ID	LIB3431-022-P1-K1-B10
Method	BLASTX
NCBI GI	g3929924
BLAST score	298
E value	6.0e-27
Match length	56
% identity	100
NCBI Description	(AB020502) catalase [Oryza sativa]

Seq. No.	399148
Seq. ID	LIB3431-022-P1-K1-B2
Method	BLASTN
NCBI GI	g218209
BLAST score	159
E value	5.0e-84
Match length	303
% identity	97
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	399149
Seq. ID	LIB3431-022-P1-K1-B3
Method	BLASTX
NCBI GI	g4982498
BLAST score	333
E value	5.0e-31
Match length	83
% identity	76
NCBI Description	(AC000107) F17F8.4 [Arabidopsis thaliana]

Seq. No.	399150
Seq. ID	LIB3431-022-P1-K1-B5
Method	BLASTX
NCBI GI	g3789952
BLAST score	557
E value	2.0e-57
Match length	114
% identity	96
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	399151
Seq. ID	LIB3431-022-P1-K1-B6
Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	1.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399152
Seq. ID	LIB3431-022-P1-K1-B9
Method	BLASTX
NCBI GI	g5802244
BLAST score	282
E value	5.0e-25
Match length	62
% identity	84
NCBI Description	(AF169022) seed maturation protein PM37 [Glycine max]

Seq. No.	399153
Seq. ID	LIB3431-022-P1-K1-C10
Method	BLASTX
NCBI GI	g6006363
BLAST score	245
E value	1.0e-20
Match length	45
% identity	100
NCBI Description	(AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No.	399154
Seq. ID	LIB3431-022-P1-K1-C12
Method	BLASTX
NCBI GI	g1661160
BLAST score	437
E value	3.0e-43
Match length	97
% identity	84
NCBI Description	(U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399155
Seq. ID	LIB3431-022-P1-K1-C3
Method	BLASTX
NCBI GI	g3273243
BLAST score	365
E value	7.0e-35
Match length	117
% identity	61
NCBI Description	(AB004660) NLS receptor [Oryza sativa] >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza sativa]

Seq. No.	399156
Seq. ID	LIB3431-022-P1-K1-C5
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399157
Seq. ID	LIB3431-022-P1-K1-C6

Method	BLASTX
NCBI GI	g5295988
BLAST score	656
E value	7.0e-69
Match length	148
% identity	90
NCBI Description	(AB003327) MADS box-like protein [Oryza sativa]

Seq. No.	399158
Seq. ID	LIB3431-022-P1-K1-C7
Method	BLASTX
NCBI GI	g6006363
BLAST score	370
E value	2.0e-35
Match length	71
% identity	100
NCBI Description	(AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No.	399159
Seq. ID	LIB3431-022-P1-K1-C8
Method	BLASTX
NCBI GI	g4512613
BLAST score	295
E value	1.0e-26
Match length	66
% identity	80
NCBI Description	(AC004793) F28K20.12 [Arabidopsis thaliana]

Seq. No.	399160
Seq. ID	LIB3431-022-P1-K1-D1
Method	BLASTX
NCBI GI	g4371296
BLAST score	307
E value	5.0e-28
Match length	134
% identity	51
NCBI Description	(AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	399161
Seq. ID	LIB3431-022-P1-K1-D10
Method	BLASTX
NCBI GI	g448445
BLAST score	263
E value	8.0e-23
Match length	72
% identity	69
NCBI Description	CF0 ATP synthase:SUBUNIT=9 [Spinacia oleracea]

Seq. No.	399162
Seq. ID	LIB3431-022-P1-K1-D11
Method	BLASTX
NCBI GI	g3935175
BLAST score	277
E value	2.0e-24

Match length	84
% identity	67
NCBI Description	(AC004557) F17L21.18 [Arabidopsis thaliana]

Seq. No.	399163
Seq. ID	LIB3431-022-P1-K1-D12
Method	BLASTX
NCBI GI	g3789954
BLAST score	661
E value	2.0e-69
Match length	125
% identity	98
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399164
Seq. ID	LIB3431-022-P1-K1-D4
Method	BLASTX
NCBI GI	g320618
BLAST score	593
E value	2.0e-61
Match length	130
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399165
Seq. ID	LIB3431-022-P1-K1-D5
Method	BLASTX
NCBI GI	g4099148
BLAST score	582
E value	3.0e-60
Match length	147
% identity	82
NCBI Description	(U84268) YLP [Hordeum vulgare]

Seq. No.	399166
Seq. ID	LIB3431-022-P1-K1-D6
Method	BLASTX
NCBI GI	g2293288
BLAST score	175
E value	2.0e-12
Match length	152
% identity	33
NCBI Description	(AF008220) YtcB [Bacillus subtilis] >gi_2635571_emb_CAB15065_ (Z99119) similar to NDP-sugar epimerase [Bacillus subtilis]

Seq. No.	399167
Seq. ID	LIB3431-022-P1-K1-D7
Method	BLASTX
NCBI GI	g5106775
BLAST score	488
E value	3.0e-49

Match length	96
% identity	98
NCBI Description	(AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No.	399168
Seq. ID	LIB3431-022-P1-K1-D8
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399169
Seq. ID	LIB3431-022-P1-K1-E10
Method	BLASTX
NCBI GI	g6063542
BLAST score	259
E value	2.0e-22
Match length	47
% identity	100
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No.	399170
Seq. ID	LIB3431-022-P1-K1-E11
Method	BLASTX
NCBI GI	g4469021
BLAST score	312
E value	1.0e-28
Match length	85
% identity	71
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399171
Seq. ID	LIB3431-022-P1-K1-E12
Method	BLASTX
NCBI GI	g115787
BLAST score	592
E value	2.0e-61
Match length	134
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399172
Seq. ID	LIB3431-022-P1-K1-E2
Method	BLASTX
NCBI GI	g1835731
BLAST score	546

E value	5.0e-56
Match length	103
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399173
Seq. ID	LIB3431-022-P1-K1-E3
Method	BLASTX
NCBI GI	g81601
BLAST score	159
E value	1.0e-10
Match length	43
% identity	70
NCBI Description	chaperonin 60 beta - Arabidopsis thaliana

Seq. No.	399174
Seq. ID	LIB3431-022-P1-K1-E4
Method	BLASTX
NCBI GI	g3789954
BLAST score	546
E value	5.0e-56
Match length	106
% identity	96
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399175
Seq. ID	LIB3431-022-P1-K1-E6
Method	BLASTN
NCBI GI	g1245938
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	399176
Seq. ID	LIB3431-022-P1-K1-E7
Method	BLASTX
NCBI GI	g1661160
BLAST score	636
E value	1.0e-66
Match length	142
% identity	87
NCBI Description	(U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399177
Seq. ID	LIB3431-022-P1-K1-E8
Method	BLASTX
NCBI GI	g4557093
BLAST score	215
E value	3.0e-17
Match length	65
% identity	66
NCBI Description	(AF001136) zinc finger protein [Pinus radiata]

Seq. No.	399178
Seq. ID	LIB3431-022-P1-K1-E9
Method	BLASTN
NCBI GI	g3075487
BLAST score	322
E value	0.0e+00
Match length	322
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	399179
Seq. ID	LIB3431-022-P1-K1-F10
Method	BLASTX
NCBI GI	g2493494
BLAST score	547
E value	4.0e-56
Match length	112
% identity	89
NCBI Description	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase II-2 [Hordeum vulgare]

Seq. No.	399180
Seq. ID	LIB3431-022-P1-K1-F11
Method	BLASTX
NCBI GI	g115787
BLAST score	584
E value	2.0e-60
Match length	133
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399181
Seq. ID	LIB3431-022-P1-K1-F12
Method	BLASTX
NCBI GI	g3618310
BLAST score	473
E value	2.0e-47
Match length	123
% identity	74
NCBI Description	(AB001883) zinc finger protein [Oryza sativa]

Seq. No.	399182
Seq. ID	LIB3431-022-P1-K1-F2
Method	BLASTX
NCBI GI	g710626
BLAST score	188
E value	5.0e-14
Match length	45
% identity	69

NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	399183
Seq. ID	LIB3431-022-P1-K1-F3
Method	BLASTX
NCBI GI	g5541681
BLAST score	327
E value	2.0e-30
Match length	124
% identity	56
NCBI Description	(AL096859) putative protein [Arabidopsis thaliana]

Seq. No.	399184
Seq. ID	LIB3431-022-P1-K1-F4
Method	BLASTX
NCBI GI	g5230790
BLAST score	162
E value	6.0e-11
Match length	46
% identity	70
NCBI Description	(AF107027) histone H1 WH1A.4 [Triticum aestivum]

Seq. No.	399185
Seq. ID	LIB3431-022-P1-K1-F5
Method	BLASTX
NCBI GI	g6016736
BLAST score	253
E value	1.0e-21
Match length	86
% identity	60
NCBI Description	(AC009325) unknown protein [Arabidopsis thaliana]

Seq. No.	399186
Seq. ID	LIB3431-022-P1-K1-F6
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399187
Seq. ID	LIB3431-022-P1-K1-F8
Method	BLASTX
NCBI GI	g320618
BLAST score	576
E value	2.0e-59
Match length	125
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399188
Seq. ID	LIB3431-022-P1-K1-F9
Method	BLASTX
NCBI GI	g5295954
BLAST score	363
E value	2.0e-34
Match length	72
% identity	97
NCBI Description	(AB026295) hypothetical protein [Oryza sativa]

Seq. No.	399189
Seq. ID	LIB3431-022-P1-K1-G10
Method	BLASTX
NCBI GI	g320618
BLAST score	622
E value	7.0e-65
Match length	135
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399190
Seq. ID	LIB3431-022-P1-K1-G12
Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	399191
Seq. ID	LIB3431-022-P1-K1-G4
Method	BLASTX
NCBI GI	g120657
BLAST score	528
E value	6.0e-54
Match length	132
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_66024_pir__DEZMG3 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No.	399192
Seq. ID	LIB3431-022-P1-K1-G5
Method	BLASTX

NCBI GI	g629775
BLAST score	740
E value	1.0e-78
Match length	149
% identity	92
NCBI Description	beta-ketoacyl-ACP synthase - barley (fragment)

Seq. No.	399193
Seq. ID	LIB3431-022-P1-K1-G6
Method	BLASTX
NCBI GI	g132105
BLAST score	614
E value	6.0e-64
Match length	132
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399194
Seq. ID	LIB3431-022-P1-K1-G8
Method	BLASTX
NCBI GI	g5816998
BLAST score	276
E value	2.0e-24
Match length	121
% identity	47
NCBI Description	(AL110123) putative protein [Arabidopsis thaliana]

Seq. No.	399195
Seq. ID	LIB3431-022-P1-K1-G9
Method	BLASTN
NCBI GI	g4959460
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	399196
Seq. ID	LIB3431-022-P1-K1-H10
Method	BLASTX
NCBI GI	g2213600
BLAST score	364
E value	1.0e-34
Match length	131
% identity	56
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	399197
Seq. ID	LIB3431-022-P1-K1-H11

Method	BLASTX
NCBI GI	g1171978
BLAST score	418
E value	4.0e-45
Match length	128
% identity	63
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	399198
Seq. ID	LIB3431-022-P1-K1-H12
Method	BLASTX
NCBI GI	g3345477
BLAST score	317
E value	3.0e-29
Match length	115
% identity	57
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399199
Seq. ID	LIB3431-022-P1-K1-H2
Method	BLASTX
NCBI GI	g1707998
BLAST score	417
E value	6.0e-41
Match length	118
% identity	73
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir__S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No.	399200
Seq. ID	LIB3431-022-P1-K1-H4
Method	BLASTX
NCBI GI	g3184559
BLAST score	289
E value	7.0e-26
Match length	128
% identity	50
NCBI Description	(AF052290) putative c-type cytochrome biogenesis protein [Synechococcus PCC7002]

Seq. No.	399201
Seq. ID	LIB3431-022-P1-K1-H6
Method	BLASTX
NCBI GI	g3510256
BLAST score	180
E value	3.0e-13
Match length	41
% identity	78
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	399202
Seq. ID	LIB3431-022-P1-K1-H7
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399203
Seq. ID	LIB3431-022-P1-K1-H8
Method	BLASTX
NCBI GI	g3126854
BLAST score	730
E value	1.0e-77
Match length	139
% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399204
Seq. ID	LIB3431-022-P1-N1-A1
Method	BLASTX
NCBI GI	g671740
BLAST score	202
E value	1.0e-15
Match length	51
% identity	80
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399205
Seq. ID	LIB3431-022-P1-N1-A4
Method	BLASTX
NCBI GI	g3885892
BLAST score	235
E value	1.0e-19
Match length	47
% identity	98
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	399206
Seq. ID	LIB3431-022-P1-N1-A5
Method	BLASTX
NCBI GI	g671740
BLAST score	197
E value	3.0e-15
Match length	37
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399207
Seq. ID	LIB3431-022-P1-N1-A6
Method	BLASTN

NCBI GI	g14264
BLAST score	51
E value	1.0e-19
Match length	115
% identity	86
NCBI Description	T.aestivum gene for sedoheptulose-1,7-bisphoshatase

Seq. No.	399208
Seq. ID	LIB3431-022-P1-N1-A7
Method	BLASTX
NCBI GI	g3345477
BLAST score	183
E value	2.0e-13
Match length	33
% identity	100
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399209
Seq. ID	LIB3431-022-P1-N1-A9
Method	BLASTX
NCBI GI	g2245086
BLAST score	224
E value	3.0e-18
Match length	65
% identity	66
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399210
Seq. ID	LIB3431-022-P1-N1-B1
Method	BLASTX
NCBI GI	g132105
BLAST score	364
E value	1.0e-34
Match length	73
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399211
Seq. ID	LIB3431-022-P1-N1-B10
Method	BLASTX
NCBI GI	g3929924
BLAST score	221
E value	5.0e-18
Match length	43
% identity	98
NCBI Description	(AB020502) catalase [Oryza sativa]

Seq. No.	399212
Seq. ID	LIB3431-022-P1-N1-B12

Method	BLASTN
NCBI GI	g3075487
BLAST score	42
E value	3.0e-14
Match length	82
% identity	88
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	399213
Seq. ID	LIB3431-022-P1-N1-B2
Method	BLASTN
NCBI GI	g218209
BLAST score	159
E value	5.0e-84
Match length	304
% identity	97
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	399214
Seq. ID	LIB3431-022-P1-N1-B3
Method	BLASTX
NCBI GI	g4982498
BLAST score	187
E value	5.0e-14
Match length	59
% identity	59
NCBI Description	(AC000107) F17F8.4 [Arabidopsis thaliana]

Seq. No.	399215
Seq. ID	LIB3431-022-P1-N1-B5
Method	BLASTN
NCBI GI	g3789951
BLAST score	168
E value	2.0e-89
Match length	374
% identity	93
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	399216
Seq. ID	LIB3431-022-P1-N1-B7
Method	BLASTX
NCBI GI	g132105
BLAST score	402
E value	4.0e-39
Match length	73
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399217
Seq. ID	LIB3431-022-P1-N1-B9
Method	BLASTX
NCBI GI	g1125691
BLAST score	180
E value	4.0e-13
Match length	62
% identity	65
NCBI Description	(X94301) DnaJ protein [Solanum tuberosum]

Seq. No.	399218
Seq. ID	LIB3431-022-P1-N1-C1
Method	BLASTX
NCBI GI	g4929312
BLAST score	328
E value	2.0e-30
Match length	112
% identity	63
NCBI Description	(AF145045) TATC [Arabidopsis thaliana]

Seq. No.	399219
Seq. ID	LIB3431-022-P1-N1-C10
Method	BLASTN
NCBI GI	g6006355
BLAST score	384
E value	0.0e+00
Match length	388
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	399220
Seq. ID	LIB3431-022-P1-N1-C12
Method	BLASTX
NCBI GI	g3036951
BLAST score	431
E value	1.0e-42
Match length	81
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399221
Seq. ID	LIB3431-022-P1-N1-C2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399222
Seq. ID	LIB3431-022-P1-N1-C6
Method	BLASTN
NCBI GI	g5295987
BLAST score	362
E value	0.0e+00
Match length	435
% identity	95
NCBI Description	Oryza sativa mRNA for MADS box-like protein, complete cds, clone:S10304

Seq. No.	399223
Seq. ID	LIB3431-022-P1-N1-C7
Method	BLASTN
NCBI GI	g6006355
BLAST score	249
E value	1.0e-138
Match length	310
% identity	95
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	399224
Seq. ID	LIB3431-022-P1-N1-C8
Method	BLASTX
NCBI GI	g4512613
BLAST score	305
E value	7.0e-28
Match length	67
% identity	82
NCBI Description	(AC004793) F28K20.12 [Arabidopsis thaliana]

Seq. No.	399225
Seq. ID	LIB3431-022-P1-N1-D12
Method	BLASTX
NCBI GI	g3789954
BLAST score	361
E value	3.0e-34
Match length	67
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399226
Seq. ID	LIB3431-022-P1-N1-D4
Method	BLASTX
NCBI GI	g115787
BLAST score	396
E value	2.0e-38
Match length	75
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399227

Seq. ID	LIB3431-022-P1-N1-D5
Method	BLASTX
NCBI GI	g3334409
BLAST score	204
E value	5.0e-16
Match length	52
% identity	79
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2129765_pir__S71261 V-type proton-ATPase - Arabidopsis thaliana >gi_1143394_emb_CAA63086_ (X92117) V-type proton-ATPase [Arabidopsis thaliana]

Seq. No.	399228
Seq. ID	LIB3431-022-P1-N1-D7
Method	BLASTX
NCBI GI	g5106775
BLAST score	342
E value	4.0e-32
Match length	71
% identity	92
NCBI Description	(AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No.	399229
Seq. ID	LIB3431-022-P1-N1-D8
Method	BLASTX
NCBI GI	g2072555
BLAST score	226
E value	2.0e-18
Match length	46
% identity	91
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399230
Seq. ID	LIB3431-022-P1-N1-E11
Method	BLASTX
NCBI GI	g4469021
BLAST score	310
E value	2.0e-28
Match length	72
% identity	81
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399231
Seq. ID	LIB3431-022-P1-N1-E12
Method	BLASTX
NCBI GI	g3036946
BLAST score	277
E value	2.0e-24
Match length	52
% identity	100
NCBI Description	(AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399232
Seq. ID	LIB3431-022-P1-N1-E2

Method	BLASTX
NCBI GI	g1835731
BLAST score	283
E value	3.0e-25
Match length	67
% identity	82
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399233
Seq. ID	LIB3431-022-P1-N1-E4
Method	BLASTX
NCBI GI	g3789954
BLAST score	357
E value	7.0e-34
Match length	66
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399234
Seq. ID	LIB3431-022-P1-N1-E5
Method	BLASTX
NCBI GI	g3789954
BLAST score	163
E value	3.0e-11
Match length	54
% identity	63
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399235
Seq. ID	LIB3431-022-P1-N1-E7
Method	BLASTX
NCBI GI	g4512125
BLAST score	178
E value	5.0e-13
Match length	32
% identity	100
NCBI Description	(AF133340) putative chlorophyll a/b-binding protein [Phalaenopsis sp. 'KCbutterfly']

Seq. No.	399236
Seq. ID	LIB3431-022-P1-N1-E8
Method	BLASTN
NCBI GI	g20181
BLAST score	100
E value	7.0e-49
Match length	176
% identity	89
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	399237
Seq. ID	LIB3431-022-P1-N1-E9
Method	BLASTN
NCBI GI	g3075487
BLAST score	275

E value	1.0e-153
Match length	279
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	399238
Seq. ID	LIB3431-022-P1-N1-F10
Method	BLASTX
NCBI GI	g2493494
BLAST score	199
E value	3.0e-15
Match length	48
% identity	81
NCBI Description	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase II-2 [Hordeum vulgare]

Seq. No.	399239
Seq. ID	LIB3431-022-P1-N1-F11
Method	BLASTX
NCBI GI	g3036942
BLAST score	251
E value	2.0e-21
Match length	47
% identity	100
NCBI Description	(AB012636) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399240
Seq. ID	LIB3431-022-P1-N1-F12
Method	BLASTX
NCBI GI	g3618310
BLAST score	366
E value	6.0e-35
Match length	77
% identity	92
NCBI Description	(AB001883) zinc finger protein [Oryza sativa]

Seq. No.	399241
Seq. ID	LIB3431-022-P1-N1-F6
Method	BLASTN
NCBI GI	g6103440
BLAST score	45
E value	3.0e-16
Match length	85
% identity	88
NCBI Description	Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds

Seq. No.	399242
Seq. ID	LIB3431-022-P1-N1-F8
Method	BLASTX
NCBI GI	g3036951
BLAST score	276

E value	2.0e-24
Match length	54
% identity	98
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399243
Seq. ID	LIB3431-022-P1-N1-F9
Method	BLASTN
NCBI GI	g5295936
BLAST score	310
E value	1.0e-174
Match length	411
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	399244
Seq. ID	LIB3431-022-P1-N1-G10
Method	BLASTX
NCBI GI	g3928150
BLAST score	412
E value	3.0e-40
Match length	110
% identity	72
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	399245
Seq. ID	LIB3431-022-P1-N1-G4
Method	BLASTX
NCBI GI	g120661
BLAST score	178
E value	6.0e-13
Match length	32
% identity	100
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	399246
Seq. ID	LIB3431-022-P1-N1-G6
Method	BLASTX
NCBI GI	g347451
BLAST score	263
E value	7.0e-23
Match length	51
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	399247
Seq. ID	LIB3431-022-P1-N1-H11
Method	BLASTX
NCBI GI	g2213871
BLAST score	195
E value	7.0e-15
Match length	53

% identity	83
NCBI Description	(AF003126) poly(A)-binding protein [Mesembryanthemum crystallinum]

Seq. No.	399248
Seq. ID	LIB3431-022-P1-N1-H12
Method	BLASTX
NCBI GI	g3345477
BLAST score	156
E value	2.0e-10
Match length	30
% identity	97
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399249
Seq. ID	LIB3431-022-P1-N1-H2
Method	BLASTX
NCBI GI	g1707998
BLAST score	153
E value	5.0e-10
Match length	29
% identity	100
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir__S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No.	399250
Seq. ID	LIB3431-022-P1-N1-H6
Method	BLASTX
NCBI GI	g3510256
BLAST score	167
E value	1.0e-11
Match length	41
% identity	73
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	399251
Seq. ID	LIB3431-022-P1-N1-H7
Method	BLASTN
NCBI GI	g2072554
BLAST score	310
E value	1.0e-174
Match length	322
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399252
Seq. ID	LIB3431-022-P1-N1-H8
Method	BLASTX
NCBI GI	g115802
BLAST score	190
E value	2.0e-14
Match length	35

% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No.	399253
Seq. ID	LIB3431-023-P1-K1-A1
Method	BLASTX
NCBI GI	g5430769
BLAST score	349
E value	6.0e-33
Match length	130
% identity	55
NCBI Description	(AC007504) Similar to somatic embryogenesis receptor-like kinase [Arabidopsis thaliana]

Seq. No.	399254
Seq. ID	LIB3431-023-P1-K1-A11
Method	BLASTX
NCBI GI	g1657621
BLAST score	212
E value	8.0e-17
Match length	109
% identity	54
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]

Seq. No.	399255
Seq. ID	LIB3431-023-P1-K1-A3
Method	BLASTX
NCBI GI	g1907270
BLAST score	485
E value	7.0e-49
Match length	122
% identity	74
NCBI Description	(X96761) sulphate transporter protein [Sporobolus stapfianus]

Seq. No.	399256
Seq. ID	LIB3431-023-P1-K1-A4
Method	BLASTX
NCBI GI	g5734618
BLAST score	244
E value	7.0e-27
Match length	154
% identity	44
NCBI Description	(AP000391) Similar to Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence; unknown protein (AC006234) [Oryza sativa]

Seq. No.	399257
Seq. ID	LIB3431-023-P1-K1-A5
Method	BLASTX

NCBI GI g1173327
BLAST score 227
E value 1.0e-18
Match length 107
% identity 50
NCBI Description U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') >gi_322619_pir__S30580 U2 snRNP protein A' - Arabidopsis thaliana >gi_17669_emb_CAA48890_ (X69137) U2 small nuclear ribonucleoprotein A' [Arabidopsis thaliana]

Seq. No. 399258
Seq. ID LIB3431-023-P1-K1-A6
Method BLASTX
NCBI GI g548605
BLAST score 519
E value 1.0e-57
Match length 132
% identity 91
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 399259
Seq. ID LIB3431-023-P1-K1-A8
Method BLASTN
NCBI GI g2586088
BLAST score 35
E value 5.0e-10
Match length 43
% identity 95
NCBI Description Oryza longistaminata receptor kinase-like protein, family member A2, pseudogene sequence

Seq. No. 399260
Seq. ID LIB3431-023-P1-K1-A9
Method BLASTX
NCBI GI g1052960
BLAST score 400
E value 7.0e-39
Match length 90
% identity 88
NCBI Description (U37437) PNIL34 [Ipomoea nil]

Seq. No. 399261
Seq. ID LIB3431-023-P1-K1-B1
Method BLASTX
NCBI GI g6006848
BLAST score 252
E value 2.0e-21
Match length 133
% identity 46
NCBI Description (AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No. 399262

Seq. ID	LIB3431-023-P1-K1-B10
Method	BLASTN
NCBI GI	g20153
BLAST score	157
E value	8.0e-83
Match length	157
% identity	100
NCBI Description	O.sativa random single-copy DNA fragment 12RG143R

Seq. No.	399263
Seq. ID	LIB3431-023-P1-K1-B11
Method	BLASTX
NCBI GI	g3913425
BLAST score	323
E value	7.0e-30
Match length	76
% identity	79
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	399264
Seq. ID	LIB3431-023-P1-K1-B2
Method	BLASTX
NCBI GI	g2407281
BLAST score	705
E value	1.0e-74
Match length	132
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399265
Seq. ID	LIB3431-023-P1-K1-B3
Method	BLASTX
NCBI GI	g6016732
BLAST score	203
E value	2.0e-18
Match length	86
% identity	57
NCBI Description	(AC009325) hypothetical protein [Arabidopsis thaliana] >gi_6091719_gb_AAF03431.1_AC010797_7 (AC010797) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399266
Seq. ID	LIB3431-023-P1-K1-B5
Method	BLASTN
NCBI GI	g3885887
BLAST score	419
E value	0.0e+00
Match length	442
% identity	99
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	399267
Seq. ID	LIB3431-023-P1-K1-B6

Method	BLASTX
NCBI GI	g2147484
BLAST score	592
E value	2.0e-61
Match length	137
% identity	81
NCBI Description	homeotic protein - Phalaenopsis sp >gi_1173622 (U34743) homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No.	399268
Seq. ID	LIB3431-023-P1-K1-B9
Method	BLASTX
NCBI GI	g2660676
BLAST score	614
E value	5.0e-64
Match length	134
% identity	81
NCBI Description	(AC002342) Dreg-2 like protein [Arabidopsis thaliana]

Seq. No.	399269
Seq. ID	LIB3431-023-P1-K1-C1
Method	BLASTX
NCBI GI	g6006848
BLAST score	405
E value	2.0e-45
Match length	141
% identity	67
NCBI Description	(AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	399270
Seq. ID	LIB3431-023-P1-K1-C11
Method	BLASTN
NCBI GI	g2306980
BLAST score	53
E value	7.0e-21
Match length	85
% identity	91
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	399271
Seq. ID	LIB3431-023-P1-K1-C12
Method	BLASTX
NCBI GI	g132105
BLAST score	607
E value	4.0e-63
Match length	132
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No.	399272
Seq. ID	LIB3431-023-P1-K1-C2
Method	BLASTX
NCBI GI	g461550
BLAST score	578
E value	1.0e-59
Match length	150
% identity	71
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana] >gi_5732056_gb_AAD48955.1_AF149414_4 (AF149414) Arabidopsis thaliana APC1-ATP synthase gamma chain 1 (GB:M61741); contains similarity to Pfam PF00231 -ATP synthase; score=658.6, E=3.1e-194n n+1

Seq. No.	399273
Seq. ID	LIB3431-023-P1-K1-C3
Method	BLASTX
NCBI GI	g3345477
BLAST score	550
E value	2.0e-56
Match length	121
% identity	88
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399274
Seq. ID	LIB3431-023-P1-K1-C4
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399275
Seq. ID	LIB3431-023-P1-K1-C5
Method	BLASTX
NCBI GI	g4995089
BLAST score	544
E value	4.0e-68
Match length	152
% identity	81
NCBI Description	(AJ242712) malate dehydrogenase 1 [Brassica napus]

Seq. No.	399276
Seq. ID	LIB3431-023-P1-K1-C6
Method	BLASTX
NCBI GI	g3643608
BLAST score	376

E value 5.0e-36
Match length 95
% identity 75
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana] >gi_4874312_gb_AAD31374.1_AC006053_16 (AC006053) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399277
Seq. ID LIB3431-023-P1-K1-C8
Method BLASTX
NCBI GI g4803952
BLAST score 284
E value 3.0e-25
Match length 69
% identity 77
NCBI Description (AC006202) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399278
Seq. ID LIB3431-023-P1-K1-C9
Method BLASTX
NCBI GI g4455350
BLAST score 322
E value 1.0e-29
Match length 79
% identity 81
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 399279
Seq. ID LIB3431-023-P1-K1-D1
Method BLASTX
NCBI GI g2052383
BLAST score 403
E value 3.0e-39
Match length 86
% identity 80
NCBI Description (U66345) calreticulin [Arabidopsis thaliana]

Seq. No. 399280
Seq. ID LIB3431-023-P1-K1-D10
Method BLASTX
NCBI GI g3885892
BLAST score 440
E value 1.0e-43
Match length 83
% identity 100
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 399281
Seq. ID LIB3431-023-P1-K1-D11
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 9.0e-20
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No.	399282
Seq. ID	LIB3431-023-P1-K1-D2
Method	BLASTX
NCBI GI	g5816996
BLAST score	406
E value	1.0e-39
Match length	85
% identity	91
NCBI Description	(AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No.	399283
Seq. ID	LIB3431-023-P1-K1-D3
Method	BLASTX
NCBI GI	g132105
BLAST score	560
E value	1.0e-57
Match length	122
% identity	86
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399284
Seq. ID	LIB3431-023-P1-K1-D5
Method	BLASTX
NCBI GI	g5816996
BLAST score	282
E value	5.0e-25
Match length	61
% identity	90
NCBI Description	(AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No.	399285
Seq. ID	LIB3431-023-P1-K1-D8
Method	BLASTX
NCBI GI	g4914457
BLAST score	392
E value	6.0e-38
Match length	122
% identity	55
NCBI Description	(AL050400) putative protein [Arabidopsis thaliana]

Seq. No.	399286
Seq. ID	LIB3431-023-P1-K1-E1
Method	BLASTX
NCBI GI	g3929924
BLAST score	620

E value	4.0e-74
Match length	135
% identity	99
NCBI Description	(AB020502) catalase [Oryza sativa]

Seq. No.	399287
Seq. ID	LIB3431-023-P1-K1-E11
Method	BLASTX
NCBI GI	g3789954
BLAST score	778
E value	3.0e-83
Match length	145
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399288
Seq. ID	LIB3431-023-P1-K1-E12
Method	BLASTX
NCBI GI	g517500
BLAST score	270
E value	7.0e-24
Match length	66
% identity	82
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	399289
Seq. ID	LIB3431-023-P1-K1-E3
Method	BLASTX
NCBI GI	g100849
BLAST score	365
E value	8.0e-49
Match length	128
% identity	75
NCBI Description	acetolactate synthase (EC 4.1.3.18) (clone pSOG108) - maize >gi_22139_emb_CAA45116_ (X63553) acetohydroxyacid synthase [Zea mays]

Seq. No.	399290
Seq. ID	LIB3431-023-P1-K1-E5
Method	BLASTX
NCBI GI	g131225
BLAST score	316
E value	1.0e-56
Match length	122
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399291
Seq. ID	LIB3431-023-P1-K1-E7
Method	BLASTN
NCBI GI	g6015437

BLAST score	39
E value	2.0e-12
Match length	39
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399292
Seq. ID	LIB3431-023-P1-K1-E8
Method	BLASTX
NCBI GI	g5922612
BLAST score	226
E value	2.0e-18
Match length	136
% identity	59
NCBI Description	(AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa]

Seq. No.	399293
Seq. ID	LIB3431-023-P1-K1-E9
Method	BLASTN
NCBI GI	g3023159
BLAST score	37
E value	3.0e-11
Match length	53
% identity	92
NCBI Description	Zantedeschia aethiopica geranylgeranyl reductase mRNA, partial cds

Seq. No.	399294
Seq. ID	LIB3431-023-P1-K1-F10
Method	BLASTX
NCBI GI	g4033838
BLAST score	505
E value	3.0e-51
Match length	150
% identity	61
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana] >gi_4972299_dbj_BAA78109.1_ (AB021120) RNA polymerase sigma subunit SigE [Arabidopsis thaliana]

Seq. No.	399295
Seq. ID	LIB3431-023-P1-K1-F11
Method	BLASTX
NCBI GI	g1304215
BLAST score	362
E value	2.0e-34
Match length	110
% identity	42
NCBI Description	(D84392) precursor of rice 22 kDa protein of photosystem II (PSII-S) [Oryza sativa]

Seq. No.	399296
Seq. ID	LIB3431-023-P1-K1-F12
Method	BLASTX
NCBI GI	g320618

BLAST score	435
E value	2.0e-70
Match length	133
% identity	100
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399297
Seq. ID	LIB3431-023-P1-K1-F5
Method	BLASTX
NCBI GI	g2570511
BLAST score	348
E value	8.0e-33
Match length	118
% identity	87
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	399298
Seq. ID	LIB3431-023-P1-K1-F6
Method	BLASTX
NCBI GI	g547712
BLAST score	510
E value	9.0e-52
Match length	103
% identity	98
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No.	399299
Seq. ID	LIB3431-023-P1-K1-F7
Method	BLASTX
NCBI GI	g2407281
BLAST score	784
E value	7.0e-84
Match length	148
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399300
Seq. ID	LIB3431-023-P1-K1-G10
Method	BLASTX
NCBI GI	g115787
BLAST score	664
E value	7.0e-70
Match length	130
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399301
Seq. ID	LIB3431-023-P1-K1-G12
Method	BLASTX
NCBI GI	g2501190
BLAST score	591
E value	3.0e-61
Match length	140
% identity	84
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	399302
Seq. ID	LIB3431-023-P1-K1-G2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399303
Seq. ID	LIB3431-023-P1-K1-G3
Method	BLASTX
NCBI GI	g4079798
BLAST score	558
E value	2.0e-57
Match length	143
% identity	78
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	399304
Seq. ID	LIB3431-023-P1-K1-G5
Method	BLASTX
NCBI GI	g66298
BLAST score	347
E value	9.0e-36
Match length	87
% identity	84
NCBI Description	catalase (EC 1.11.1.6) - rice >gi_20192_emb_CAA43814_ (X61626) catalase [Oryza sativa]

Seq. No.	399305
Seq. ID	LIB3431-023-P1-K1-G7
Method	BLASTX
NCBI GI	g4972093
BLAST score	263
E value	9.0e-23
Match length	116
% identity	47
NCBI Description	(AL078468) putative protein [Arabidopsis thaliana]

Seq. No.	399306
Seq. ID	LIB3431-023-P1-K1-G8
Method	BLASTX
NCBI GI	g3789954
BLAST score	639
E value	6.0e-67
Match length	119
% identity	99
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399307
Seq. ID	LIB3431-023-P1-K1-G9
Method	BLASTX
NCBI GI	g132105
BLAST score	582
E value	3.0e-60
Match length	125
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399308
Seq. ID	LIB3431-023-P1-K1-H10
Method	BLASTX
NCBI GI	g120510
BLAST score	380
E value	2.0e-36
Match length	86
% identity	84
NCBI Description	FERRITIN 2 PRECURSOR >gi_82688_pir__S24057 ferritin precursor (clone FM2) - maize >gi_22278_emb_CAA43664_ (X61392) ferritin [Zea mays]

Seq. No.	399309
Seq. ID	LIB3431-023-P1-K1-H11
Method	BLASTX
NCBI GI	g2072555
BLAST score	263
E value	2.0e-28
Match length	62
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399310
Seq. ID	LIB3431-023-P1-K1-H12
Method	BLASTX

NCBI GI	g1835731
BLAST score	283
E value	3.0e-25
Match length	64
% identity	83
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399311
Seq. ID	LIB3431-023-P1-K1-H3
Method	BLASTX
NCBI GI	g226263
BLAST score	177
E value	3.0e-13
Match length	78
% identity	53
NCBI Description	chlorophyll a/b binding protein [Glycine max]

Seq. No.	399312
Seq. ID	LIB3431-023-P1-K1-H4
Method	BLASTX
NCBI GI	g871931
BLAST score	356
E value	7.0e-34
Match length	72
% identity	99
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	399313
Seq. ID	LIB3431-023-P1-K1-H5
Method	BLASTX
NCBI GI	g4850400
BLAST score	145
E value	2.0e-19
Match length	93
% identity	68
NCBI Description	(AC007357) Similar to gb_M86917 oxysterol-binding protein from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	399314
Seq. ID	LIB3431-023-P1-K1-H6
Method	BLASTX
NCBI GI	g5123939
BLAST score	242
E value	5.0e-33
Match length	102
% identity	73
NCBI Description	(AL079349) putative protein [Arabidopsis thaliana]

Seq. No.	399315
Seq. ID	LIB3431-023-P1-K1-H8
Method	BLASTX
NCBI GI	g82080
BLAST score	494
E value	7.0e-50
Match length	136
% identity	69
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato

>gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	399316
Seq. ID	LIB3431-023-P1-K1-H9
Method	BLASTX
NCBI GI	g3914425
BLAST score	600
E value	2.0e-62
Match length	143
% identity	77
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana] >gi_4850389_gb_AAD31059.1_AC007357_8 (AC007357) Identical to gb_Y13695 multicatalytic endopeptidase complex, proteasome precursor, beta subunit (prce) from Arabidopsis thaliana. ESTs gb_Y09360, gb_F13852, gb_T20555, gb_T44620, gb_AI099779 and gb_AA5861

Seq. No.	399317
Seq. ID	LIB3431-023-P1-N1-A11
Method	BLASTX
NCBI GI	g1657621
BLAST score	146
E value	4.0e-09
Match length	36
% identity	81
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]

Seq. No.	399318
Seq. ID	LIB3431-023-P1-N1-A3
Method	BLASTN
NCBI GI	g5803242
BLAST score	228
E value	1.0e-125
Match length	365
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	399319
Seq. ID	LIB3431-023-P1-N1-A4
Method	BLASTX
NCBI GI	g5734618
BLAST score	154
E value	4.0e-10
Match length	93
% identity	38
NCBI Description	(AP000391) Similar to Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence; unknown protein (AC006234) [Oryza sativa]

Seq. No.	399320
Seq. ID	LIB3431-023-P1-N1-A6
Method	BLASTN
NCBI GI	g304219
BLAST score	36
E value	5.0e-11
Match length	68
% identity	88
NCBI Description	Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No.	399321
Seq. ID	LIB3431-023-P1-N1-B2
Method	BLASTX
NCBI GI	g347451
BLAST score	207
E value	3.0e-16
Match length	39
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	399322
Seq. ID	LIB3431-023-P1-N1-B5
Method	BLASTN
NCBI GI	g3885887
BLAST score	164
E value	4.0e-87
Match length	272
% identity	90
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	399323
Seq. ID	LIB3431-023-P1-N1-C11
Method	BLASTX
NCBI GI	g1076724
BLAST score	263
E value	7.0e-23
Match length	56
% identity	88
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No.	399324
Seq. ID	LIB3431-023-P1-N1-C12
Method	BLASTX
NCBI GI	g671740
BLAST score	546
E value	7.0e-56
Match length	99
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399325
Seq. ID	LIB3431-023-P1-N1-C2
Method	BLASTX
NCBI GI	g231610
BLAST score	215
E value	3.0e-17
Match length	65
% identity	74
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	399326
Seq. ID	LIB3431-023-P1-N1-C3
Method	BLASTN
NCBI GI	g606816
BLAST score	301
E value	1.0e-169
Match length	321
% identity	98
NCBI Description	Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds

Seq. No.	399327
Seq. ID	LIB3431-023-P1-N1-C4
Method	BLASTN
NCBI GI	g2072554
BLAST score	403
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399328
Seq. ID	LIB3431-023-P1-N1-C5
Method	BLASTX
NCBI GI	g3183079
BLAST score	629
E value	1.0e-65
Match length	147
% identity	82
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]

Seq. No.	399329
Seq. ID	LIB3431-023-P1-N1-C9
Method	BLASTX
NCBI GI	g731707
BLAST score	204
E value	2.0e-22
Match length	116
% identity	47
NCBI Description	SET1 PROTEIN >gi_626647_pir__S48961 hypothetical protein

YHR119w - yeast (Saccharomyces cerevisiae) >gi_529135 (U00059) Set1p [Saccharomyces cerevisiae]

Seq. No.	399330
Seq. ID	LIB3431-023-P1-N1-D11
Method	BLASTN
NCBI GI	g2072554
BLAST score	405
E value	0.0e+00
Match length	405
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399331
Seq. ID	LIB3431-023-P1-N1-D12
Method	BLASTX
NCBI GI	g671740
BLAST score	388
E value	3.0e-37
Match length	115
% identity	53
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399332
Seq. ID	LIB3431-023-P1-N1-D2
Method	BLASTX
NCBI GI	g5816996
BLAST score	333
E value	6.0e-31
Match length	86
% identity	79
NCBI Description	(AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No.	399333
Seq. ID	LIB3431-023-P1-N1-D3
Method	BLASTX
NCBI GI	g132105
BLAST score	402
E value	4.0e-39
Match length	73
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399334
Seq. ID	LIB3431-023-P1-N1-D5
Method	BLASTX

NCBI GI g3885519
BLAST score 164
E value 2.0e-11
Match length 35
% identity 94
NCBI Description (AF084204) similar to ribosomal protein L32 [Medicago sativa]

Seq. No. 399335
Seq. ID LIB3431-023-P1-N1-D9
Method BLASTX
NCBI GI g1070408
BLAST score 148
E value 2.0e-09
Match length 27
% identity 100
NCBI Description ferredoxin [2Fe-2S] I - rice

Seq. No. 399336
Seq. ID LIB3431-023-P1-N1-E1
Method BLASTX
NCBI GI g3929924
BLAST score 292
E value 3.0e-26
Match length 56
% identity 98
NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 399337
Seq. ID LIB3431-023-P1-N1-E11
Method BLASTX
NCBI GI g3789954
BLAST score 384
E value 5.0e-37
Match length 71
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399338
Seq. ID LIB3431-023-P1-N1-E3
Method BLASTX
NCBI GI g100849
BLAST score 367
E value 4.0e-35
Match length 85
% identity 86
NCBI Description acetolactate synthase (EC 4.1.3.18) (clone pSOG108) - maize >gi_22139_emb_CAA45116_ (X63553) acetohydroxyacid synthase [Zea mays]

Seq. No. 399339
Seq. ID LIB3431-023-P1-N1-E5
Method BLASTX
NCBI GI g131225
BLAST score 311
E value 2.0e-28

Match length	89
% identity	69
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399340
Seq. ID	LIB3431-023-P1-N1-F10
Method	BLASTX
NCBI GI	g4033838
BLAST score	251
E value	2.0e-21
Match length	60
% identity	80
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana] >gi_4972299_dbj_BAA78109.1_ (AB021120) RNA polymerase sigma subunit SigE [Arabidopsis thaliana]

Seq. No.	399341
Seq. ID	LIB3431-023-P1-N1-F11
Method	BLASTX
NCBI GI	g6103011
BLAST score	352
E value	2.0e-33
Match length	75
% identity	47
NCBI Description	(X84225) precursor of photosystem II subunit (22KDa) [Nicotiana tabacum]

Seq. No.	399342
Seq. ID	LIB3431-023-P1-N1-F12
Method	BLASTX
NCBI GI	g289920
BLAST score	300
E value	3.0e-27
Match length	57
% identity	100
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	399343
Seq. ID	LIB3431-023-P1-N1-F4
Method	BLASTX
NCBI GI	g118170
BLAST score	307
E value	6.0e-28
Match length	59
% identity	100
NCBI Description	CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I) >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784 (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259) oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967) oryzacystatin=cysteine protease inhibitor [Oryza=rice, Peptide, 102 aa] [Oryza] >gi_1280613 (U54702) oryzacystatin [Oryza sativa]

Seq. No.	399344
Seq. ID	LIB3431-023-P1-N1-F5
Method	BLASTX
NCBI GI	g115794
BLAST score	467
E value	9.0e-47
Match length	94
% identity	91
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No.	399345
Seq. ID	LIB3431-023-P1-N1-F6
Method	BLASTX
NCBI GI	g547712
BLAST score	219
E value	1.0e-17
Match length	43
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No.	399346
Seq. ID	LIB3431-023-P1-N1-F7
Method	BLASTX
NCBI GI	g347451
BLAST score	169
E value	8.0e-12
Match length	32
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	399347
Seq. ID	LIB3431-023-P1-N1-F9
Method	BLASTX
NCBI GI	g134034
BLAST score	238
E value	6.0e-20
Match length	66
% identity	68
NCBI Description	30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5) (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1) >gi_279640_pir__R3SPS5 ribosomal protein CS-S22 precursor, chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270) chloroplast ribosomal protein S22 [Spinacia oleracea] >gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein [Spinacia oleracea]

Seq. No.	399348
Seq. ID	LIB3431-023-P1-N1-G10
Method	BLASTX

NCBI GI	g421916
BLAST score	199
E value	2.0e-15
Match length	37
% identity	100
NCBI Description	chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No.	399349
Seq. ID	LIB3431-023-P1-N1-G2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399350
Seq. ID	LIB3431-023-P1-N1-G5
Method	BLASTX
NCBI GI	g2130069
BLAST score	192
E value	2.0e-14
Match length	39
% identity	95
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No.	399351
Seq. ID	LIB3431-023-P1-N1-G7
Method	BLASTX
NCBI GI	g4972093
BLAST score	236
E value	1.0e-19
Match length	59
% identity	76
NCBI Description	(AL078468) putative protein [Arabidopsis thaliana]

Seq. No.	399352
Seq. ID	LIB3431-023-P1-N1-G8
Method	BLASTX
NCBI GI	g3789954
BLAST score	329
E value	1.0e-30
Match length	62
% identity	98
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399353
Seq. ID	LIB3431-023-P1-N1-G9
Method	BLASTX
NCBI GI	g132105

BLAST score	507
E value	2.0e-51
Match length	93
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399354
Seq. ID	LIB3431-023-P1-N1-H10
Method	BLASTN
NCBI GI	g455510
BLAST score	100
E value	8.0e-49
Match length	104
% identity	99
NCBI Description	Rice mRNA for ferritin, partial sequence

Seq. No.	399355
Seq. ID	LIB3431-023-P1-N1-H11
Method	BLASTN
NCBI GI	g2072554
BLAST score	226
E value	1.0e-124
Match length	338
% identity	92
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399356
Seq. ID	LIB3431-023-P1-N1-H12
Method	BLASTX
NCBI GI	g1835731
BLAST score	284
E value	2.0e-25
Match length	71
% identity	80
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399357
Seq. ID	LIB3431-023-P1-N1-H4
Method	BLASTX
NCBI GI	g871931
BLAST score	204
E value	7.0e-16
Match length	38
% identity	100
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	399358
Seq. ID	LIB3431-023-P1-N1-H8

Method	BLASTX
NCBI GI	g115813
BLAST score	220
E value	8.0e-18
Match length	53
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	399359
Seq. ID	LIB3431-023-P1-N1-H9
Method	BLASTX
NCBI GI	g3914430
BLAST score	241
E value	3.0e-20
Match length	75
% identity	60
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No.	399360
Seq. ID	LIB3431-024-P1-K1-A1
Method	BLASTX
NCBI GI	g5902390
BLAST score	218
E value	1.0e-17
Match length	109
% identity	50
NCBI Description	(AC008148) Unknown protein [Arabidopsis thaliana]

Seq. No.	399361
Seq. ID	LIB3431-024-P1-K1-A11
Method	BLASTX
NCBI GI	g135535
BLAST score	377
E value	2.0e-36
Match length	93
% identity	81
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No.	399362
Seq. ID	LIB3431-024-P1-K1-A3
Method	BLASTX
NCBI GI	g3885894
BLAST score	565
E value	4.0e-58
Match length	139
% identity	81
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No.	399363
Seq. ID	LIB3431-024-P1-K1-A4
Method	BLASTN
NCBI GI	g487319
BLAST score	47
E value	3.0e-17
Match length	47
% identity	100
NCBI Description	Rice mRNA EN66, partial sequence

Seq. No.	399364
Seq. ID	LIB3431-024-P1-K1-A7
Method	BLASTX
NCBI GI	g5902390
BLAST score	174
E value	2.0e-12
Match length	119
% identity	40
NCBI Description	(AC008148) Unknown protein [Arabidopsis thaliana]

Seq. No.	399365
Seq. ID	LIB3431-024-P1-K1-A9
Method	BLASTX
NCBI GI	g2407281
BLAST score	673
E value	6.0e-71
Match length	125
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399366
Seq. ID	LIB3431-024-P1-K1-B1
Method	BLASTX
NCBI GI	g132105
BLAST score	530
E value	4.0e-54
Match length	96
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399367
Seq. ID	LIB3431-024-P1-K1-B10
Method	BLASTX
NCBI GI	g729478
BLAST score	343
E value	3.0e-32
Match length	119

% identity	55
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	399368
Seq. ID	LIB3431-024-P1-K1-B11
Method	BLASTX
NCBI GI	g1707998
BLAST score	227
E value	1.0e-18
Match length	83
% identity	59
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir__S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No.	399369
Seq. ID	LIB3431-024-P1-K1-B12
Method	BLASTX
NCBI GI	g167097
BLAST score	279
E value	3.0e-37
Match length	95
% identity	83
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	399370
Seq. ID	LIB3431-024-P1-K1-B2
Method	BLASTN
NCBI GI	g20262
BLAST score	139
E value	2.0e-72
Match length	159
% identity	97
NCBI Description	O.sativa light-induced mRNA

Seq. No.	399371
Seq. ID	LIB3431-024-P1-K1-B4
Method	BLASTX
NCBI GI	g3789954
BLAST score	623
E value	4.0e-65
Match length	115
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399372
Seq. ID	LIB3431-024-P1-K1-B5

Method	BLASTX
NCBI GI	g131225
BLAST score	350
E value	3.0e-33
Match length	76
% identity	89
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	399373
Seq. ID	LIB3431-024-P1-K1-B6
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	6.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399374
Seq. ID	LIB3431-024-P1-K1-B7
Method	BLASTX
NCBI GI	g1835731
BLAST score	479
E value	4.0e-48
Match length	102
% identity	89
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399375
Seq. ID	LIB3431-024-P1-K1-B9
Method	BLASTX
NCBI GI	g1835731
BLAST score	531
E value	2.0e-54
Match length	101
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399376
Seq. ID	LIB3431-024-P1-K1-C1
Method	BLASTX
NCBI GI	g4512616
BLAST score	497
E value	3.0e-50
Match length	120
% identity	79
NCBI Description	(AC004793) Contains similarity to gi_1653332 extragenic suppressor (SuhB) from Synechocystis sp. gb_D90912 and is a member of the Inositol monophophatase family PF_00459. EST gb_AA597395 comes from this gene. [Arabidopsis tha

Seq. No.	399377

Seq. ID	LIB3431-024-P1-K1-C10
Method	BLASTX
NCBI GI	g2407279
BLAST score	315
E value	7.0e-29
Match length	63
% identity	97
NCBI Description	(AF017362) aldolase [Oryza sativa]

Seq. No.	399378
Seq. ID	LIB3431-024-P1-K1-C11
Method	BLASTX
NCBI GI	g320618
BLAST score	458
E value	9.0e-46
Match length	106
% identity	83
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399379
Seq. ID	LIB3431-024-P1-K1-C12
Method	BLASTX
NCBI GI	g1835731
BLAST score	322
E value	9.0e-30
Match length	72
% identity	85
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399380
Seq. ID	LIB3431-024-P1-K1-C2
Method	BLASTX
NCBI GI	g4938486
BLAST score	327
E value	1.0e-30
Match length	78
% identity	78
NCBI Description	(AL078464) putative protein [Arabidopsis thaliana]

Seq. No.	399381
Seq. ID	LIB3431-024-P1-K1-C3
Method	BLASTX
NCBI GI	g482445
BLAST score	604
E value	6.0e-63
Match length	121
% identity	95
NCBI Description	chlorophyll a/b-binding protein precursor - swollen duckweed >gi_168296 (M29334) light-harvesting chlorophyll a/b protein precursor [Lemna gibba]

Seq. No.	399382
Seq. ID	LIB3431-024-P1-K1-C6

Method	BLASTX
NCBI GI	g4884866
BLAST score	275
E value	2.0e-24
Match length	96
% identity	57
NCBI Description	(AF133531) water channel protein MipI [Mesembryanthemum crystallinum]

Seq. No.	399383
Seq. ID	LIB3431-024-P1-K1-C7
Method	BLASTX
NCBI GI	g3402713
BLAST score	248
E value	5.0e-21
Match length	64
% identity	72
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399384
Seq. ID	LIB3431-024-P1-K1-C8
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399385
Seq. ID	LIB3431-024-P1-K1-C9
Method	BLASTN
NCBI GI	g20181
BLAST score	58
E value	5.0e-24
Match length	62
% identity	98
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	399386
Seq. ID	LIB3431-024-P1-K1-D1
Method	BLASTX
NCBI GI	g3913641
BLAST score	483
E value	6.0e-49
Match length	95
% identity	98
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041777_dbj_BAA25423_ (AB007194) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	399387
Seq. ID	LIB3431-024-P1-K1-D10

Method	BLASTX
NCBI GI	g4689380
BLAST score	620
E value	9.0e-65
Match length	125
% identity	88
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]

Seq. No.	399388
Seq. ID	LIB3431-024-P1-K1-D12
Method	BLASTX
NCBI GI	g320618
BLAST score	463
E value	2.0e-46
Match length	106
% identity	83
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399389
Seq. ID	LIB3431-024-P1-K1-D2
Method	BLASTN
NCBI GI	g2306980
BLAST score	150
E value	7.0e-79
Match length	174
% identity	97
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	399390
Seq. ID	LIB3431-024-P1-K1-D3
Method	BLASTX
NCBI GI	g871931
BLAST score	361
E value	1.0e-36
Match length	85
% identity	100
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	399391
Seq. ID	LIB3431-024-P1-K1-D4
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399392
Seq. ID	LIB3431-024-P1-K1-D6
Method	BLASTX

NCBI GI	g2342719
BLAST score	324
E value	6.0e-30
Match length	139
% identity	50
NCBI Description	(AC002341) SF16 protein isolog [Arabidopsis thaliana]

Seq. No.	399393
Seq. ID	LIB3431-024-P1-K1-D9
Method	BLASTX
NCBI GI	g4585882
BLAST score	399
E value	7.0e-39
Match length	127
% identity	62
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	399394
Seq. ID	LIB3431-024-P1-K1-E1
Method	BLASTX
NCBI GI	g2407281
BLAST score	547
E value	3.0e-56
Match length	108
% identity	96
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399395
Seq. ID	LIB3431-024-P1-K1-E10
Method	BLASTX
NCBI GI	g133936
BLAST score	685
E value	3.0e-72
Match length	132
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir__R3RZ3 ribosomal protein S3 - rice chloroplast >gi_12025_emb_CAA33934_ (X15901) ribosomal protein S3 [Oryza sativa] >gi_226646_prf__1603356BW ribosomal protein S3 [Oryza sativa]

Seq. No.	399396
Seq. ID	LIB3431-024-P1-K1-E12
Method	BLASTX
NCBI GI	g2130069
BLAST score	749
E value	8.0e-80
Match length	135
% identity	99
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No.	399397
Seq. ID	LIB3431-024-P1-K1-E2
Method	BLASTX

NCBI GI	g2827516
BLAST score	264
E value	5.0e-23
Match length	89
% identity	55
NCBI Description	(AL021633) DNA topoisomerase like-protein [Arabidopsis thaliana]

Seq. No.	399398
Seq. ID	LIB3431-024-P1-K1-E3
Method	BLASTN
NCBI GI	g20181
BLAST score	109
E value	4.0e-54
Match length	113
% identity	99
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	399399
Seq. ID	LIB3431-024-P1-K1-E4
Method	BLASTX
NCBI GI	g1835731
BLAST score	412
E value	2.0e-40
Match length	81
% identity	99
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399400
Seq. ID	LIB3431-024-P1-K1-E7
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399401
Seq. ID	LIB3431-024-P1-K1-E8
Method	BLASTX
NCBI GI	g320617
BLAST score	471
E value	2.0e-48
Match length	122
% identity	80
NCBI Description	chlorophyll a/b-binding protein II precursor - rice >gi_227612_prf__1707316B chlorophyll a/b binding protein 2 [Oryza sativa]

Seq. No.	399402
Seq. ID	LIB3431-024-P1-K1-F1
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20

Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399403
Seq. ID	LIB3431-024-P1-K1-F10
Method	BLASTX
NCBI GI	g3126854
BLAST score	606
E value	4.0e-63
Match length	114
% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399404
Seq. ID	LIB3431-024-P1-K1-F2
Method	BLASTX
NCBI GI	g5360230
BLAST score	500
E value	5.0e-51
Match length	88
% identity	99
NCBI Description	(AB015287) Ran [Oryza sativa]

Seq. No.	399405
Seq. ID	LIB3431-024-P1-K1-F3
Method	BLASTX
NCBI GI	g462195
BLAST score	309
E value	3.0e-28
Match length	74
% identity	81
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	399406
Seq. ID	LIB3431-024-P1-K1-F4
Method	BLASTX
NCBI GI	g4582436
BLAST score	388
E value	1.0e-37
Match length	94
% identity	77
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	399407
Seq. ID	LIB3431-024-P1-K1-F5
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36

% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399408
Seq. ID	LIB3431-024-P1-K1-F7
Method	BLASTX
NCBI GI	g4929312
BLAST score	233
E value	8.0e-29
Match length	123
% identity	59
NCBI Description	(AF145045) TATC [Arabidopsis thaliana]

Seq. No.	399409
Seq. ID	LIB3431-024-P1-K1-F8
Method	BLASTX
NCBI GI	g2564253
BLAST score	361
E value	2.0e-34
Match length	83
% identity	81
NCBI Description	(Z99996) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Hordeum vulgare]

Seq. No.	399410
Seq. ID	LIB3431-024-P1-K1-F9
Method	BLASTX
NCBI GI	g2245062
BLAST score	418
E value	5.0e-41
Match length	104
% identity	77
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399411
Seq. ID	LIB3431-024-P1-K1-G1
Method	BLASTX
NCBI GI	g2190543
BLAST score	145
E value	3.0e-09
Match length	98
% identity	39
NCBI Description	(AC001229) EST gb_N37484 comes from this gene. [Arabidopsis thaliana]

Seq. No.	399412
Seq. ID	LIB3431-024-P1-K1-G10
Method	BLASTX
NCBI GI	g4883530
BLAST score	235
E value	1.0e-19
Match length	110
% identity	48
NCBI Description	(AF123266) remorin 2 [Lycopersicon esculentum]

Seq. No.	399413
Seq. ID	LIB3431-024-P1-K1-G12

Method	BLASTX
NCBI GI	g5902158
BLAST score	246
E value	6.0e-21
Match length	75
% identity	56
NCBI Description	zinc finger protein 183 (RING finger, C3HC4 type) >gi_3123165_sp_O15541_Z183_HUMAN ZINC FINGER PROTEIN 183 >gi_2274982_emb_CAA66907_ (X98253) ZNF183 [Homo sapiens] >gi_2341022 (AC002477) zinc-finger protein [Homo sapiens]

Seq. No.	399414
Seq. ID	LIB3431-024-P1-K1-G2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	6.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399415
Seq. ID	LIB3431-024-P1-K1-G4
Method	BLASTX
NCBI GI	g115787
BLAST score	380
E value	1.0e-36
Match length	92
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399416
Seq. ID	LIB3431-024-P1-K1-G6
Method	BLASTX
NCBI GI	g1657859
BLAST score	155
E value	2.0e-10
Match length	60
% identity	55
NCBI Description	(U73218) chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]

Seq. No.	399417
Seq. ID	LIB3431-024-P1-K1-G7
Method	BLASTX
NCBI GI	g3386621
BLAST score	554
E value	6.0e-57
Match length	147
% identity	71
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	399418
Seq. ID	LIB3431-024-P1-K1-G8
Method	BLASTX
NCBI GI	g4538947
BLAST score	166
E value	1.0e-11
Match length	61
% identity	54
NCBI Description	(AL049483) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	399419
Seq. ID	LIB3431-024-P1-K1-G9
Method	BLASTX
NCBI GI	g132105
BLAST score	289
E value	4.0e-26
Match length	76
% identity	78
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399420
Seq. ID	LIB3431-024-P1-K1-H1
Method	BLASTX
NCBI GI	g3885886
BLAST score	327
E value	8.0e-31
Match length	65
% identity	100
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.	399421
Seq. ID	LIB3431-024-P1-K1-H11
Method	BLASTX
NCBI GI	g1931644
BLAST score	250
E value	3.0e-21
Match length	105
% identity	44
NCBI Description	(U95973) membrane protein PTM1 precursor isolog [Arabidopsis thaliana]

Seq. No.	399422
Seq. ID	LIB3431-024-P1-K1-H12
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20

Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399423
Seq. ID	LIB3431-024-P1-K1-H2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	6.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399424
Seq. ID	LIB3431-024-P1-K1-H3
Method	BLASTX
NCBI GI	g1835731
BLAST score	189
E value	3.0e-14
Match length	49
% identity	76
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399425
Seq. ID	LIB3431-024-P1-K1-H4
Method	BLASTX
NCBI GI	g1498315
BLAST score	250
E value	7.0e-25
Match length	121
% identity	50
NCBI Description	(U56419) IAP100 [Pisum sativum]

Seq. No.	399426
Seq. ID	LIB3431-024-P1-K1-H5
Method	BLASTX
NCBI GI	g1617197
BLAST score	290
E value	6.0e-26
Match length	76
% identity	74
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399427
Seq. ID	LIB3431-024-P1-K1-H6
Method	BLASTN
NCBI GI	g3821780
BLAST score	34
E value	9.0e-10
Match length	34
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	399428
Seq. ID	LIB3431-024-P1-K1-H8
Method	BLASTX
NCBI GI	g3288821
BLAST score	490
E value	2.0e-49
Match length	129
% identity	75
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	399429
Seq. ID	LIB3431-024-P1-N1-A2
Method	BLASTX
NCBI GI	g3345477
BLAST score	212
E value	7.0e-17
Match length	40
% identity	97
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399430
Seq. ID	LIB3431-024-P1-N1-A3
Method	BLASTN
NCBI GI	g3885893
BLAST score	99
E value	3.0e-48
Match length	131
% identity	94
NCBI Description	Oryza sativa photosystem-1 H subunit GOS5 (PSI-H) mRNA, complete cds

Seq. No.	399431
Seq. ID	LIB3431-024-P1-N1-A9
Method	BLASTX
NCBI GI	g132105
BLAST score	288
E value	4.0e-26
Match length	57
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399432
Seq. ID	LIB3431-024-P1-N1-B10
Method	BLASTX
NCBI GI	g729478

BLAST score	370
E value	2.0e-35
Match length	73
% identity	92
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	399433
Seq. ID	LIB3431-024-P1-N1-B12
Method	BLASTX
NCBI GI	g132166
BLAST score	156
E value	2.0e-10
Match length	31
% identity	84
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	399434
Seq. ID	LIB3431-024-P1-N1-B2
Method	BLASTX
NCBI GI	g417260
BLAST score	268
E value	2.0e-23
Match length	69
% identity	72
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	399435
Seq. ID	LIB3431-024-P1-N1-B4
Method	BLASTX
NCBI GI	g3789954
BLAST score	335
E value	3.0e-31
Match length	62
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399436
Seq. ID	LIB3431-024-P1-N1-B5
Method	BLASTX
NCBI GI	g131225
BLAST score	196
E value	5.0e-15
Match length	51
% identity	73

NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]
Seq. No.	399437
Seq. ID	LIB3431-024-P1-N1-B6
Method	BLASTX
NCBI GI	g2072555
BLAST score	196
E value	5.0e-15
Match length	37
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	399438
Seq. ID	LIB3431-024-P1-N1-B8
Method	BLASTX
NCBI GI	g131225
BLAST score	216
E value	2.0e-17
Match length	56
% identity	73
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]
Seq. No.	399439
Seq. ID	LIB3431-024-P1-N1-B9
Method	BLASTX
NCBI GI	g1835731
BLAST score	590
E value	4.0e-61
Match length	126
% identity	91
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.	399440
Seq. ID	LIB3431-024-P1-N1-C1
Method	BLASTX
NCBI GI	g4512616
BLAST score	334
E value	3.0e-31
Match length	80
% identity	81
NCBI Description	(AC004793) Contains similarity to gi_1653332 extragenic suppressor (SuhB) from Synechocystis sp. gb_D90912 and is a member of the Inositol monophophatase family PF_00459. EST gb_AA597395 comes from this gene. [Arabidopsis tha
Seq. No.	399441
Seq. ID	LIB3431-024-P1-N1-C10
Method	BLASTX
NCBI GI	g2407279

BLAST score	216
E value	2.0e-17
Match length	44
% identity	100
NCBI Description	(AF017362) aldolase [Oryza sativa]

Seq. No.	399442
Seq. ID	LIB3431-024-P1-N1-C11
Method	BLASTX
NCBI GI	g3036946
BLAST score	319
E value	2.0e-29
Match length	61
% identity	100
NCBI Description	(AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399443
Seq. ID	LIB3431-024-P1-N1-C12
Method	BLASTX
NCBI GI	g1835731
BLAST score	188
E value	3.0e-14
Match length	48
% identity	77
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399444
Seq. ID	LIB3431-024-P1-N1-C3
Method	BLASTX
NCBI GI	g3036942
BLAST score	243
E value	1.0e-20
Match length	45
% identity	100
NCBI Description	(AB012636) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399445
Seq. ID	LIB3431-024-P1-N1-C8
Method	BLASTN
NCBI GI	g2072554
BLAST score	246
E value	1.0e-136
Match length	282
% identity	97
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399446
Seq. ID	LIB3431-024-P1-N1-D1
Method	BLASTX
NCBI GI	g3913641
BLAST score	211
E value	4.0e-17
Match length	41
% identity	100

NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041777_dbj_BAA25423_ (AB007194) fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.	399447
Seq. ID	LIB3431-024-P1-N1-D10
Method	BLASTX
NCBI GI	g479406
BLAST score	396
E value	2.0e-38
Match length	78
% identity	95
NCBI Description	chlorophyll a/b-binding protein - garden pea >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding protein [Pisum sativum]
Seq. No.	399448
Seq. ID	LIB3431-024-P1-N1-D11
Method	BLASTX
NCBI GI	g3510256
BLAST score	194
E value	7.0e-15
Match length	48
% identity	67
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.	399449
Seq. ID	LIB3431-024-P1-N1-D12
Method	BLASTX
NCBI GI	g115787
BLAST score	432
E value	1.0e-42
Match length	82
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]
Seq. No.	399450
Seq. ID	LIB3431-024-P1-N1-D2
Method	BLASTX
NCBI GI	g551047
BLAST score	268
E value	2.0e-23
Match length	52
% identity	96
NCBI Description	(X79277) type II LHCI [Lolium temulentum]
Seq. No.	399451
Seq. ID	LIB3431-024-P1-N1-D3
Method	BLASTN
NCBI GI	g2305114
BLAST score	291
E value	1.0e-163

Match length	334
% identity	97
NCBI Description	Oryza sativa ferredoxin mRNA, complete cds

Seq. No.	399452
Seq. ID	LIB3431-024-P1-N1-D4
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399453
Seq. ID	LIB3431-024-P1-N1-D9
Method	BLASTX
NCBI GI	g115813
BLAST score	233
E value	2.0e-19
Match length	53
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	399454
Seq. ID	LIB3431-024-P1-N1-E1
Method	BLASTX
NCBI GI	g347451
BLAST score	224
E value	3.0e-18
Match length	46
% identity	91
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	399455
Seq. ID	LIB3431-024-P1-N1-E12
Method	BLASTX
NCBI GI	g2130069
BLAST score	194
E value	9.0e-15
Match length	39
% identity	95
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No.	399456
Seq. ID	LIB3431-024-P1-N1-E3
Method	BLASTN
NCBI GI	g20181
BLAST score	106
E value	2.0e-52
Match length	113
% identity	98
NCBI Description	Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein

Seq. No.	399457
Seq. ID	LIB3431-024-P1-N1-E4
Method	BLASTX
NCBI GI	g1835731
BLAST score	297
E value	7.0e-27
Match length	67
% identity	85
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399458
Seq. ID	LIB3431-024-P1-N1-E8
Method	BLASTX
NCBI GI	g3126854
BLAST score	240
E value	3.0e-20
Match length	65
% identity	74
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399459
Seq. ID	LIB3431-024-P1-N1-F1
Method	BLASTN
NCBI GI	g2072554
BLAST score	388
E value	0.0e+00
Match length	388
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399460
Seq. ID	LIB3431-024-P1-N1-F10
Method	BLASTX
NCBI GI	g3126854
BLAST score	261
E value	1.0e-22
Match length	52
% identity	94
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399461
Seq. ID	LIB3431-024-P1-N1-F12
Method	BLASTN
NCBI GI	g6069643
BLAST score	51
E value	1.0e-19
Match length	79
% identity	91
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0514G12

Seq. No.	399462
Seq. ID	LIB3431-024-P1-N1-F2
Method	BLASTN
NCBI GI	g5360229

BLAST score	394
E value	0.0e+00
Match length	419
% identity	98
NCBI Description	Oryza sativa mRNA for Ran, complete cds

Seq. No.	399463
Seq. ID	LIB3431-024-P1-N1-F3
Method	BLASTN
NCBI GI	g3789949
BLAST score	83
E value	1.0e-38
Match length	95
% identity	97
NCBI Description	Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No.	399464
Seq. ID	LIB3431-024-P1-N1-F4
Method	BLASTX
NCBI GI	g4582436
BLAST score	162
E value	7.0e-11
Match length	77
% identity	47
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	399465
Seq. ID	LIB3431-024-P1-N1-F7
Method	BLASTX
NCBI GI	g4929312
BLAST score	203
E value	7.0e-16
Match length	70
% identity	63
NCBI Description	(AF145045) TATC [Arabidopsis thaliana]

Seq. No.	399466
Seq. ID	LIB3431-024-P1-N1-G10
Method	BLASTX
NCBI GI	g4731573
BLAST score	201
E value	1.0e-15
Match length	48
% identity	77
NCBI Description	(AF123265) remorin 1 [Lycopersicon esculentum]

Seq. No.	399467
Seq. ID	LIB3431-024-P1-N1-G12
Method	BLASTX
NCBI GI	g5262156
BLAST score	226
E value	2.0e-18
Match length	65
% identity	52
NCBI Description	(AL080237) putative protein [Arabidopsis thaliana]

Seq. No.	399468
Seq. ID	LIB3431-024-P1-N1-G2
Method	BLASTX
NCBI GI	g2072555
BLAST score	227
E value	1.0e-18
Match length	44
% identity	98
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399469
Seq. ID	LIB3431-024-P1-N1-G4
Method	BLASTX
NCBI GI	g115784
BLAST score	182
E value	2.0e-13
Match length	33
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB) (LHCP) >gi_167525 (M16058) chlorophyll a/b-binding protein [Cucumis sativus]

Seq. No.	399470
Seq. ID	LIB3431-024-P1-N1-G5
Method	BLASTX
NCBI GI	g167097
BLAST score	151
E value	5.0e-17
Match length	52
% identity	88
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	399471
Seq. ID	LIB3431-024-P1-N1-G6
Method	BLASTX
NCBI GI	g115784
BLAST score	150
E value	1.0e-09
Match length	33
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB) (LHCP) >gi_167525 (M16058) chlorophyll a/b-binding protein [Cucumis sativus]

Seq. No.	399472
Seq. ID	LIB3431-024-P1-N1-G9
Method	BLASTX
NCBI GI	g132105
BLAST score	320
E value	1.0e-29
Match length	61
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399473
Seq. ID	LIB3431-024-P1-N1-H1
Method	BLASTX
NCBI GI	g3885886
BLAST score	317
E value	3.0e-29
Match length	56
% identity	98
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.	399474
Seq. ID	LIB3431-024-P1-N1-H12
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399475
Seq. ID	LIB3431-024-P1-N1-H2
Method	BLASTN
NCBI GI	g2072554
BLAST score	293
E value	1.0e-164
Match length	301
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399476
Seq. ID	LIB3431-024-P1-N1-H3
Method	BLASTX
NCBI GI	g1835731
BLAST score	189
E value	3.0e-14
Match length	49
% identity	78
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399477
Seq. ID	LIB3431-024-P1-N1-H5
Method	BLASTX
NCBI GI	g1617197
BLAST score	180
E value	3.0e-13

Match length	36
% identity	92
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399478
Seq. ID	LIB3431-024-P1-N1-H6
Method	BLASTX
NCBI GI	g4454458
BLAST score	208
E value	2.0e-16
Match length	69
% identity	62
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	399479
Seq. ID	LIB3431-024-P1-N1-H8
Method	BLASTX
NCBI GI	g226263
BLAST score	155
E value	3.0e-10
Match length	31
% identity	94
NCBI Description	chlorophyll a/b binding protein [Glycine max]

Seq. No.	399480
Seq. ID	LIB3431-025-P1-K1-A11
Method	BLASTX
NCBI GI	g4325041
BLAST score	573
E value	5.0e-59
Match length	128
% identity	89
NCBI Description	(AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No.	399481
Seq. ID	LIB3431-025-P1-K1-A12
Method	BLASTN
NCBI GI	g2072554
BLAST score	330
E value	0.0e+00
Match length	330
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399482
Seq. ID	LIB3431-025-P1-K1-A4
Method	BLASTX
NCBI GI	g5702231
BLAST score	161
E value	9.0e-11
Match length	44
% identity	68
NCBI Description	(AF145386) hypersensitive reaction associated Ca2+-binding protein [Phaseolus vulgaris]

Seq. No.	399483
Seq. ID	LIB3431-025-P1-K1-A8
Method	BLASTX
NCBI GI	g2501491
BLAST score	182
E value	1.0e-13
Match length	90
% identity	42
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 1 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 1) >gi_542014_pir__S41950 UTP-glucose glucosyltransferase - cassava >gi_453246_emb_CAA54609_ (X77459) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No.	399484
Seq. ID	LIB3431-025-P1-K1-B11
Method	BLASTX
NCBI GI	g671740
BLAST score	433
E value	1.0e-42
Match length	79
% identity	99
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399485
Seq. ID	LIB3431-025-P1-K1-B2
Method	BLASTX
NCBI GI	g1362184
BLAST score	447
E value	4.0e-44
Match length	91
% identity	100
NCBI Description	histone H2B-8 - wheat >gi_531058_dbj_BAA07157_ (D37943) protein H2B-8 [Triticum aestivum]

Seq. No.	399486
Seq. ID	LIB3431-025-P1-K1-B3
Method	BLASTX
NCBI GI	g1076800
BLAST score	681
E value	1.0e-71
Match length	148
% identity	86
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate peroxidase [Zea mays]

Seq. No.	399487
Seq. ID	LIB3431-025-P1-K1-B5
Method	BLASTX
NCBI GI	g3868756
BLAST score	842
E value	2.0e-90
Match length	154
% identity	100

NCBI Description	(D86611) catalase [Oryza sativa]

Seq. No.	399488
Seq. ID	LIB3431-025-P1-K1-B7
Method	BLASTX
NCBI GI	g4753659
BLAST score	199
E value	3.0e-15
Match length	117
% identity	39
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	399489
Seq. ID	LIB3431-025-P1-K1-B9
Method	BLASTX
NCBI GI	g4104220
BLAST score	656
E value	1.0e-68
Match length	184
% identity	73
NCBI Description	(AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium perenne]

Seq. No.	399490
Seq. ID	LIB3431-025-P1-K1-C10
Method	BLASTX
NCBI GI	g2245136
BLAST score	786
E value	6.0e-84
Match length	216
% identity	69
NCBI Description	(Z97344) trehalose-6-phosphate synthase like protein [Arabidopsis thaliana]

Seq. No.	399491
Seq. ID	LIB3431-025-P1-K1-C11
Method	BLASTX
NCBI GI	g629829
BLAST score	896
E value	8.0e-97
Match length	215
% identity	79
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) - wheat >gi_510677_emb_CAA54042_ (X76532) protochlorophyilide reductase [Triticum aestivum]

Seq. No.	399492
Seq. ID	LIB3431-025-P1-K1-C12
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	399493

Seq. ID	LIB3431-025-P1-K1-C9
Method	BLASTX
NCBI GI	g517500
BLAST score	281
E value	8.0e-25
Match length	156
% identity	44
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	399494
Seq. ID	LIB3431-025-P1-K1-D1
Method	BLASTX
NCBI GI	g1353352
BLAST score	238
E value	1.0e-37
Match length	130
% identity	72
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	399495
Seq. ID	LIB3431-025-P1-K1-D10
Method	BLASTX
NCBI GI	g2245136
BLAST score	416
E value	1.0e-40
Match length	176
% identity	51
NCBI Description	(Z97344) trehalose-6-phosphate synthase like protein [Arabidopsis thaliana]

Seq. No.	399496
Seq. ID	LIB3431-025-P1-K1-D12
Method	BLASTX
NCBI GI	g129233
BLAST score	615
E value	7.0e-64
Match length	118
% identity	97
NCBI Description	ORYZAIN GAMMA CHAIN PRECURSOR >gi_67646_pir__KHRZOG oryzain (EC 3.4.22.-) gamma precursor - rice >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor [Oryza sativa]

Seq. No.	399497
Seq. ID	LIB3431-025-P1-K1-D4
Method	BLASTX
NCBI GI	g1076725
BLAST score	419
E value	6.0e-41
Match length	92
% identity	89
NCBI Description	NADPH dehydrogenase (EC 1.6.99.1) - barley >gi_683476_emb_CAA59228_ (X84738) NADPH dehydrogenase [Hordeum vulgare]

Seq. No.	399498
Seq. ID	LIB3431-025-P1-K1-D8
Method	BLASTX
NCBI GI	g2055273
BLAST score	1024
E value	1.0e-112
Match length	236
% identity	83
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	399499
Seq. ID	LIB3431-025-P1-K1-D9
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	1.0e-19
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399500
Seq. ID	LIB3431-025-P1-K1-E11
Method	BLASTX
NCBI GI	g347451
BLAST score	459
E value	1.0e-57
Match length	165
% identity	74
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	399501
Seq. ID	LIB3431-025-P1-K1-E12
Method	BLASTX
NCBI GI	g2582822
BLAST score	606
E value	7.0e-63
Match length	168
% identity	71
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	399502
Seq. ID	LIB3431-025-P1-K1-E5
Method	BLASTX
NCBI GI	g462195
BLAST score	524
E value	4.0e-53
Match length	115
% identity	89
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza

sativa]

Seq. No.	399503
Seq. ID	LIB3431-025-P1-K1-E6
Method	BLASTX
NCBI GI	g2425101
BLAST score	798
E value	3.0e-85
Match length	215
% identity	64
NCBI Description	(AF019743) cationic peroxidase [Oryza sativa]

Seq. No.	399504
Seq. ID	LIB3431-025-P1-K1-E7
Method	BLASTN
NCBI GI	g1841354
BLAST score	66
E value	2.0e-29
Match length	66
% identity	100
NCBI Description	Oryza sativa mitochondrial DNA for cytochrome c oxidase subunit Vb precursor, complete cds

Seq. No.	399505
Seq. ID	LIB3431-025-P1-K1-E9
Method	BLASTX
NCBI GI	g3913239
BLAST score	406
E value	2.0e-39
Match length	146
% identity	58
NCBI Description	PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]

Seq. No.	399506
Seq. ID	LIB3431-025-P1-K1-F10
Method	BLASTX
NCBI GI	g1084455
BLAST score	503
E value	8.0e-51
Match length	118
% identity	81
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No.	399507
Seq. ID	LIB3431-025-P1-K1-F11
Method	BLASTX
NCBI GI	g1777961
BLAST score	958
E value	1.0e-104
Match length	233
% identity	76
NCBI Description	(U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No.	399508
Seq. ID	LIB3431-025-P1-K1-F12
Method	BLASTX
NCBI GI	g400803
BLAST score	509
E value	3.0e-64
Match length	154
% identity	82
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_283033_pir__A42807 phosphoglycerate mutase (EC 5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize >gi_168588 (M80912) 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Seq. No.	399509
Seq. ID	LIB3431-025-P1-K1-F2
Method	BLASTX
NCBI GI	g132105
BLAST score	423
E value	2.0e-41
Match length	81
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399510
Seq. ID	LIB3431-025-P1-K1-F3
Method	BLASTX
NCBI GI	g4467098
BLAST score	324
E value	1.0e-29
Match length	136
% identity	44
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	399511
Seq. ID	LIB3431-025-P1-K1-F5
Method	BLASTX
NCBI GI	g6093671
BLAST score	388
E value	2.0e-37
Match length	122
% identity	61
NCBI Description	CATIONIC PEROXIDASE 1 PRECURSOR >gi_1491776 (M37636) cationic peroxidase [Arachis hypogaea]

Seq. No.	399512
Seq. ID	LIB3431-025-P1-K1-F6
Method	BLASTX

NCBI GI	g1617197
BLAST score	304
E value	2.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399513
Seq. ID	LIB3431-025-P1-K1-F7
Method	BLASTX
NCBI GI	g4938484
BLAST score	326
E value	6.0e-30
Match length	205
% identity	45
NCBI Description	(AL078464) transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	399514
Seq. ID	LIB3431-025-P1-K1-F8
Method	BLASTX
NCBI GI	g1706260
BLAST score	355
E value	2.0e-33
Match length	68
% identity	94
NCBI Description	CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597 cysteine proteinase 1 precursor - maize >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No.	399515
Seq. ID	LIB3431-025-P1-K1-F9
Method	BLASTX
NCBI GI	g5815410
BLAST score	828
E value	4.0e-94
Match length	209
% identity	83
NCBI Description	(AF177392) blast and wounding induced mitogen-activated protein kinase [Oryza sativa]

Seq. No.	399516
Seq. ID	LIB3431-025-P1-K1-G10
Method	BLASTX
NCBI GI	g1653953
BLAST score	212
E value	6.0e-17
Match length	130
% identity	38
NCBI Description	(D90917) hypothetical protein [Synechocystis sp.]

Seq. No.	399517
Seq. ID	LIB3431-025-P1-K1-G9
Method	BLASTX
NCBI GI	g3789954
BLAST score	1065

E value	1.0e-116
Match length	199
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399518
Seq. ID	LIB3431-025-P1-K1-H10
Method	BLASTX
NCBI GI	g1737492
BLAST score	626
E value	4.0e-65
Match length	177
% identity	71
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	399519
Seq. ID	LIB3431-025-P1-K1-H3
Method	BLASTX
NCBI GI	g3913641
BLAST score	1185
E value	1.0e-130
Match length	227
% identity	100
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041777_dbj_BAA25423_ (AB007194) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	399520
Seq. ID	LIB3431-025-P1-K1-H4
Method	BLASTX
NCBI GI	g4678280
BLAST score	259
E value	5.0e-22
Match length	152
% identity	36
NCBI Description	(AL049660) zinc finger-like protein [Arabidopsis thaliana]

Seq. No.	399521
Seq. ID	LIB3431-025-P1-K1-H7
Method	BLASTX
NCBI GI	g115787
BLAST score	544
E value	1.0e-107
Match length	224
% identity	91
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399522
Seq. ID	LIB3431-025-P1-K1-H9
Method	BLASTX
NCBI GI	g3036951

BLAST score	611
E value	2.0e-63
Match length	117
% identity	98
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399523
Seq. ID	LIB3431-025-P1-N1-A1
Method	BLASTX
NCBI GI	g3885882
BLAST score	275
E value	3.0e-24
Match length	55
% identity	98
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No.	399524
Seq. ID	LIB3431-025-P1-N1-A11
Method	BLASTX
NCBI GI	g3808101
BLAST score	303
E value	1.0e-27
Match length	73
% identity	88
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	399525
Seq. ID	LIB3431-025-P1-N1-A12
Method	BLASTN
NCBI GI	g2072554
BLAST score	330
E value	0.0e+00
Match length	330
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	399526
Seq. ID	LIB3431-025-P1-N1-A5
Method	BLASTN
NCBI GI	g395929
BLAST score	82
E value	5.0e-38
Match length	145
% identity	90
NCBI Description	O.sativa retrotransposon Tos1-1

Seq. No.	399527
Seq. ID	LIB3431-025-P1-N1-A7
Method	BLASTX
NCBI GI	g693920
BLAST score	340
E value	6.0e-32
Match length	68
% identity	96
NCBI Description	(U21113) chlorophyll a/b binding protein [Solanum

tuberosum]

Seq. No.	399528
Seq. ID	LIB3431-025-P1-N1-A9
Method	BLASTX
NCBI GI	g4877984
BLAST score	274
E value	4.0e-24
Match length	61
% identity	90
NCBI Description	(AF145755) THA4 [Zea mays]

Seq. No.	399529
Seq. ID	LIB3431-025-P1-N1-B1
Method	BLASTN
NCBI GI	g5091597
BLAST score	132
E value	6.0e-68
Match length	219
% identity	26
NCBI Description	Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No.	399530
Seq. ID	LIB3431-025-P1-N1-B10
Method	BLASTX
NCBI GI	g2499966
BLAST score	249
E value	3.0e-21
Match length	66
% identity	77
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A) >gi_632722_bbs_151001 (S72356) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 141 aa] [Nicotiana sylvestris]

Seq. No.	399531
Seq. ID	LIB3431-025-P1-N1-B11
Method	BLASTX
NCBI GI	g671740
BLAST score	295
E value	1.0e-26
Match length	57
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399532
Seq. ID	LIB3431-025-P1-N1-B2
Method	BLASTX
NCBI GI	g1362184
BLAST score	342
E value	4.0e-32
Match length	71
% identity	100
NCBI Description	histone H2B-8 - wheat >gi_531058_dbj_BAA07157_ (D37943) protein H2B-8 [Triticum aestivum]

Seq. No.	399533
Seq. ID	LIB3431-025-P1-N1-B3
Method	BLASTN
NCBI GI	g433216
BLAST score	211
E value	1.0e-115
Match length	232
% identity	97
NCBI Description	Rice mRNA for ascorbate peroxidase (gene name SS622), partial cds

Seq. No.	399534
Seq. ID	LIB3431-025-P1-N1-B8
Method	BLASTX
NCBI GI	g1617197
BLAST score	300
E value	3.0e-27
Match length	71
% identity	77
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399535
Seq. ID	LIB3431-025-P1-N1-B9
Method	BLASTX
NCBI GI	g729135
BLAST score	267
E value	2.0e-23
Match length	55
% identity	89
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No.	399536
Seq. ID	LIB3431-025-P1-N1-C11
Method	BLASTX
NCBI GI	g129707
BLAST score	405
E value	2.0e-39
Match length	97
% identity	84
NCBI Description	PROTOCHLOROPHYLLIDE REDUCTASE (PCR) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi_100550_pir__S08406 protochlorophyllide reductase (EC 1.3.1.33) - oat (fragment) >gi_829253_emb_CAA34913_ (X17067) protochlorophyllide reductase (314 AA) [Avena sativa]

Seq. No.	399537
Seq. ID	LIB3431-025-P1-N1-C4
Method	BLASTX
NCBI GI	g3126854
BLAST score	523
E value	3.0e-53
Match length	99

% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399538
Seq. ID	LIB3431-025-P1-N1-C6
Method	BLASTX
NCBI GI	g2072555
BLAST score	228
E value	1.0e-18
Match length	42
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399539
Seq. ID	LIB3431-025-P1-N1-C7
Method	BLASTX
NCBI GI	g3914466
BLAST score	395
E value	2.0e-38
Match length	72
% identity	99
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN subunit precursor [Zea mays]

Seq. No.	399540
Seq. ID	LIB3431-025-P1-N1-C9
Method	BLASTX
NCBI GI	g517500
BLAST score	374
E value	7.0e-36
Match length	90
% identity	81
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	399541
Seq. ID	LIB3431-025-P1-N1-D1
Method	BLASTX
NCBI GI	g1353352
BLAST score	227
E value	1.0e-18
Match length	59
% identity	75
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	399542
Seq. ID	LIB3431-025-P1-N1-D10
Method	BLASTX
NCBI GI	g3126854
BLAST score	392
E value	5.0e-38
Match length	74

% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399543
Seq. ID	LIB3431-025-P1-N1-D11
Method	BLASTX
NCBI GI	g5091556
BLAST score	194
E value	9.0e-15
Match length	55
% identity	58
NCBI Description	(AC007067) T10O24.25 [Arabidopsis thaliana]

Seq. No.	399544
Seq. ID	LIB3431-025-P1-N1-D12
Method	BLASTX
NCBI GI	g1841466
BLAST score	182
E value	2.0e-13
Match length	32
% identity	94
NCBI Description	(Y11003) putative pre-pro-cysteine proteinase [Nicotiana tabacum]

Seq. No.	399545
Seq. ID	LIB3431-025-P1-N1-D2
Method	BLASTX
NCBI GI	g4587990
BLAST score	250
E value	2.0e-21
Match length	88
% identity	50
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399546
Seq. ID	LIB3431-025-P1-N1-D4
Method	BLASTX
NCBI GI	g2598151
BLAST score	222
E value	5.0e-18
Match length	43
% identity	95
NCBI Description	(AF027350) NADPH:protochlorophyllide oxidoreductase porB [Pinus taeda]

Seq. No.	399547
Seq. ID	LIB3431-025-P1-N1-D7
Method	BLASTX
NCBI GI	g417260
BLAST score	300
E value	3.0e-27
Match length	76
% identity	75
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	399548
Seq. ID	LIB3431-025-P1-N1-D9
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399549
Seq. ID	LIB3431-025-P1-N1-E11
Method	BLASTX
NCBI GI	g671740
BLAST score	240
E value	3.0e-20
Match length	47
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399550
Seq. ID	LIB3431-025-P1-N1-E2
Method	BLASTX
NCBI GI	g167097
BLAST score	151
E value	1.0e-20
Match length	61
% identity	87
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	399551
Seq. ID	LIB3431-025-P1-N1-E3
Method	BLASTX
NCBI GI	g4567263
BLAST score	282
E value	5.0e-25
Match length	70
% identity	74
NCBI Description	(AC006841) putative cell division inhibitor [Arabidopsis thaliana]

Seq. No.	399552
Seq. ID	LIB3431-025-P1-N1-E5
Method	BLASTX
NCBI GI	g462195
BLAST score	372
E value	1.0e-35
Match length	72
% identity	100
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza

sativa]

Seq. No.	399553
Seq. ID	LIB3431-025-P1-N1-E6
Method	BLASTN
NCBI GI	g5777612
BLAST score	407
E value	0.0e+00
Match length	418
% identity	99
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No.	399554
Seq. ID	LIB3431-025-P1-N1-E7
Method	BLASTN
NCBI GI	g1841354
BLAST score	66
E value	2.0e-29
Match length	66
% identity	100
NCBI Description	Oryza sativa mitochondrial DNA for cytochrome c oxidase subunit Vb precursor, complete cds

Seq. No.	399555
Seq. ID	LIB3431-025-P1-N1-E8
Method	BLASTX
NCBI GI	g3036951
BLAST score	427
E value	4.0e-42
Match length	80
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399556
Seq. ID	LIB3431-025-P1-N1-E9
Method	BLASTX
NCBI GI	g3913239
BLAST score	256
E value	4.0e-40
Match length	132
% identity	75
NCBI Description	PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]

Seq. No.	399557
Seq. ID	LIB3431-025-P1-N1-F10
Method	BLASTN
NCBI GI	g600766
BLAST score	296
E value	1.0e-166
Match length	364
% identity	95
NCBI Description	Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds

Seq. No.	399558

Seq. ID	LIB3431-025-P1-N1-F11
Method	BLASTX
NCBI GI	g1777961
BLAST score	342
E value	4.0e-32
Match length	114
% identity	61
NCBI Description	(U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No.	399559
Seq. ID	LIB3431-025-P1-N1-F2
Method	BLASTX
NCBI GI	g347451
BLAST score	236
E value	1.0e-19
Match length	47
% identity	98
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	399560
Seq. ID	LIB3431-025-P1-N1-F5
Method	BLASTX
NCBI GI	g520568
BLAST score	262
E value	1.0e-22
Match length	87
% identity	63
NCBI Description	(U12314) peroxidase [Cenchrus ciliaris]

Seq. No.	399561
Seq. ID	LIB3431-025-P1-N1-F6
Method	BLASTX
NCBI GI	g1617197
BLAST score	287
E value	1.0e-25
Match length	71
% identity	73
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399562
Seq. ID	LIB3431-025-P1-N1-F8
Method	BLASTX
NCBI GI	g2118130
BLAST score	255
E value	7.0e-22
Match length	47
% identity	94
NCBI Description	cysteine proteinase (EC 3.4.22.-), glucose starvation-induced - maize (fragment) >gi_559532_emb_CAA57675_ (X82185) cysteine proteinase [Zea mays]

Seq. No.	399563
Seq. ID	LIB3431-025-P1-N1-F9
Method	BLASTN

NCBI GI	g5815409
BLAST score	420
E value	0.0e+00
Match length	449
% identity	98
NCBI Description	Oryza sativa blast and wounding induced mitogen-activated protein kinase (BWMK1) mRNA, complete cds

Seq. No.	399564
Seq. ID	LIB3431-025-P1-N1-G10
Method	BLASTX
NCBI GI	g1653953
BLAST score	190
E value	3.0e-14
Match length	91
% identity	42
NCBI Description	(D90917) hypothetical protein [Synechocystis sp.]

Seq. No.	399565
Seq. ID	LIB3431-025-P1-N1-G11
Method	BLASTX
NCBI GI	g2130073
BLAST score	308
E value	4.0e-28
Match length	60
% identity	100
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No.	399566
Seq. ID	LIB3431-025-P1-N1-G12
Method	BLASTN
NCBI GI	g786177
BLAST score	55
E value	4.0e-22
Match length	130
% identity	86
NCBI Description	Rice DNA for aldolase C-1, complete cds

Seq. No.	399567
Seq. ID	LIB3431-025-P1-N1-G3
Method	BLASTX
NCBI GI	g2708745
BLAST score	197
E value	3.0e-15
Match length	48
% identity	81
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	399568
Seq. ID	LIB3431-025-P1-N1-G5
Method	BLASTX
NCBI GI	g21839
BLAST score	229

E value	7.0e-19
Match length	47
% identity	96
NCBI Description	(X57952) phosphoribulokinase [Triticum aestivum]

Seq. No.	399569
Seq. ID	LIB3431-025-P1-N1-G9
Method	BLASTX
NCBI GI	g3789954
BLAST score	354
E value	2.0e-33
Match length	66
% identity	98
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399570
Seq. ID	LIB3431-025-P1-N1-H10
Method	BLASTX
NCBI GI	g1737492
BLAST score	280
E value	6.0e-25
Match length	70
% identity	80
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	399571
Seq. ID	LIB3431-025-P1-N1-H12
Method	BLASTX
NCBI GI	g517500
BLAST score	296
E value	8.0e-27
Match length	94
% identity	67
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	399572
Seq. ID	LIB3431-025-P1-N1-H2
Method	BLASTX
NCBI GI	g1651922
BLAST score	176
E value	1.0e-12
Match length	59
% identity	56
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	399573
Seq. ID	LIB3431-025-P1-N1-H3
Method	BLASTX
NCBI GI	g3913641
BLAST score	529
E value	5.0e-54
Match length	100
% identity	100
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041777_dbj_BAA25423_ (AB007194) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	399574
Seq. ID	LIB3431-025-P1-N1-H5
Method	BLASTX
NCBI GI	g129707
BLAST score	419
E value	4.0e-41
Match length	95
% identity	86
NCBI Description	PROTOCHLOROPHYLLIDE REDUCTASE (PCR) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi_100550_pir__S08406 protochlorophyllide reductase (EC 1.3.1.33) - oat (fragment) >gi_829253_emb_CAA34913_ (X17067) protochlorophyllide reductase (314 AA) [Avena sativa]

Seq. No.	399575
Seq. ID	LIB3431-025-P1-N1-H7
Method	BLASTX
NCBI GI	g4512125
BLAST score	243
E value	1.0e-20
Match length	45
% identity	100
NCBI Description	(AF133340) putative chlorophyll a/b-binding protein [Phalaenopsis sp. 'KCbutterfly']

Seq. No.	399576
Seq. ID	LIB3431-025-P1-N1-H8
Method	BLASTX
NCBI GI	g267120
BLAST score	284
E value	2.0e-25
Match length	71
% identity	77
NCBI Description	THIOREDOXIN F-TYPE, CHLOROPLAST PRECURSOR (TRX-F) >gi_100070_pir__S20929 thioredoxin f precursor - garden pea >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum sativum] >gi_1388086 (U35830) thioredoxin f [Pisum sativum]

Seq. No.	399577
Seq. ID	LIB3431-025-P1-N1-H9
Method	BLASTX
NCBI GI	g3036951
BLAST score	450
E value	9.0e-45
Match length	85
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399578
Seq. ID	LIB3431-026-P1-K1-A1
Method	BLASTX

NCBI GI	g2570511
BLAST score	213
E value	3.0e-17
Match length	79
% identity	59
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	399579
Seq. ID	LIB3431-026-P1-K1-A10
Method	BLASTX
NCBI GI	g170131
BLAST score	278
E value	9.0e-25
Match length	87
% identity	66
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	399580
Seq. ID	LIB3431-026-P1-K1-A11
Method	BLASTX
NCBI GI	g3345477
BLAST score	434
E value	6.0e-43
Match length	129
% identity	66
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399581
Seq. ID	LIB3431-026-P1-K1-A12
Method	BLASTX
NCBI GI	g115787
BLAST score	475
E value	1.0e-47
Match length	112
% identity	86
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399582
Seq. ID	LIB3431-026-P1-K1-A2
Method	BLASTX
NCBI GI	g2407281
BLAST score	658
E value	4.0e-69
Match length	125
% identity	98
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399583
Seq. ID	LIB3431-026-P1-K1-A3
Method	BLASTX
NCBI GI	g1352461
BLAST score	371

E value	8.0e-39
Match length	98
% identity	77
NCBI Description	IN2-2 PROTEIN

Seq. No.	399584
Seq. ID	LIB3431-026-P1-K1-A4
Method	BLASTX
NCBI GI	g132105
BLAST score	672
E value	7.0e-71
Match length	124
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399585
Seq. ID	LIB3431-026-P1-K1-A5
Method	BLASTX
NCBI GI	g3345477
BLAST score	269
E value	1.0e-23
Match length	98
% identity	58
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399586
Seq. ID	LIB3431-026-P1-K1-A6
Method	BLASTX
NCBI GI	g4538920
BLAST score	150
E value	1.0e-09
Match length	57
% identity	60
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	399587
Seq. ID	LIB3431-026-P1-K1-A7
Method	BLASTN
NCBI GI	g218209
BLAST score	34
E value	1.0e-09
Match length	78
% identity	87
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	399588

Seq. ID	LIB3431-026-P1-K1-A8
Method	BLASTX
NCBI GI	g132105
BLAST score	614
E value	6.0e-64
Match length	132
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399589
Seq. ID	LIB3431-026-P1-K1-A9
Method	BLASTX
NCBI GI	g871931
BLAST score	420
E value	3.0e-41
Match length	116
% identity	74
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	399590
Seq. ID	LIB3431-026-P1-K1-B1
Method	BLASTX
NCBI GI	g5360230
BLAST score	631
E value	6.0e-66
Match length	120
% identity	97
NCBI Description	(AB015287) Ran [Oryza sativa]

Seq. No.	399591
Seq. ID	LIB3431-026-P1-K1-B10
Method	BLASTX
NCBI GI	g1617197
BLAST score	297
E value	9.0e-27
Match length	76
% identity	75
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399592
Seq. ID	LIB3431-026-P1-K1-B11
Method	BLASTX
NCBI GI	g4006881
BLAST score	356
E value	9.0e-34
Match length	105
% identity	68
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	399593
Seq. ID	LIB3431-026-P1-K1-B12
Method	BLASTX
NCBI GI	g4588906
BLAST score	409
E value	5.0e-40
Match length	90
% identity	87
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	399594
Seq. ID	LIB3431-026-P1-K1-B2
Method	BLASTX
NCBI GI	g5478797
BLAST score	822
E value	3.0e-88
Match length	159
% identity	94
NCBI Description	(AB021310) chlorophyll b synthase [Oryza sativa]

Seq. No.	399595
Seq. ID	LIB3431-026-P1-K1-B3
Method	BLASTX
NCBI GI	g1173347
BLAST score	322
E value	9.0e-43
Match length	108
% identity	89
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	399596
Seq. ID	LIB3431-026-P1-K1-B4
Method	BLASTX
NCBI GI	g1835731
BLAST score	387
E value	2.0e-37
Match length	85
% identity	87
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399597
Seq. ID	LIB3431-026-P1-K1-B5
Method	BLASTX
NCBI GI	g1835731
BLAST score	451
E value	4.0e-45
Match length	86
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399598
Seq. ID	LIB3431-026-P1-K1-B6

Method	BLASTX
NCBI GI	g3868756
BLAST score	494
E value	3.0e-50
Match length	88
% identity	100
NCBI Description	(D86611) catalase [Oryza sativa]

Seq. No.	399599
Seq. ID	LIB3431-026-P1-K1-C1
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399600
Seq. ID	LIB3431-026-P1-K1-C10
Method	BLASTX
NCBI GI	g5668640
BLAST score	515
E value	2.0e-52
Match length	148
% identity	61
NCBI Description	(AL109619) putative protein [Arabidopsis thaliana]

Seq. No.	399601
Seq. ID	LIB3431-026-P1-K1-C3
Method	BLASTX
NCBI GI	g132105
BLAST score	713
E value	2.0e-75
Match length	131
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399602
Seq. ID	LIB3431-026-P1-K1-C4
Method	BLASTX
NCBI GI	g125580
BLAST score	498
E value	2.0e-50
Match length	116
% identity	85
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

(PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608) phosphoribulokinase [Triticum aestivum]

Seq. No.	399603
Seq. ID	LIB3431-026-P1-K1-C6
Method	BLASTX
NCBI GI	g2072727
BLAST score	670
E value	2.0e-70
Match length	131
% identity	98
NCBI Description	(Y12595) Fd-GOGAT protein [Oryza sativa]

Seq. No.	399604
Seq. ID	LIB3431-026-P1-K1-C7
Method	BLASTX
NCBI GI	g115787
BLAST score	529
E value	4.0e-54
Match length	121
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399605
Seq. ID	LIB3431-026-P1-K1-C8
Method	BLASTX
NCBI GI	g3345477
BLAST score	544
E value	1.0e-55
Match length	149
% identity	71
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399606
Seq. ID	LIB3431-026-P1-K1-C9
Method	BLASTX
NCBI GI	g4490332
BLAST score	424
E value	1.0e-41
Match length	140
% identity	56
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	399607
Seq. ID	LIB3431-026-P1-K1-D1
Method	BLASTX
NCBI GI	g1362066
BLAST score	392
E value	6.0e-38
Match length	90
% identity	88
NCBI Description	small GTP-binding protein - garden pea

>gi_871510_emb_CAA90080_ (Z49900) small GTP-binding protein [Pisum sativum]

Seq. No.	399608
Seq. ID	LIB3431-026-P1-K1-D10
Method	BLASTX
NCBI GI	g115787
BLAST score	489
E value	2.0e-49
Match length	113
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399609
Seq. ID	LIB3431-026-P1-K1-D11
Method	BLASTX
NCBI GI	g2688839
BLAST score	531
E value	3.0e-54
Match length	136
% identity	69
NCBI Description	(AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]

Seq. No.	399610
Seq. ID	LIB3431-026-P1-K1-D12
Method	BLASTX
NCBI GI	g3176690
BLAST score	639
E value	6.0e-67
Match length	129
% identity	91
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	399611
Seq. ID	LIB3431-026-P1-K1-D4
Method	BLASTX
NCBI GI	g3004565
BLAST score	289
E value	8.0e-29
Match length	80
% identity	79
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	399612
Seq. ID	LIB3431-026-P1-K1-D5
Method	BLASTX
NCBI GI	g320618
BLAST score	558
E value	2.0e-57
Match length	124

% identity	85
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399613
Seq. ID	LIB3431-026-P1-K1-D6
Method	BLASTX
NCBI GI	g733458
BLAST score	145
E value	4.0e-09
Match length	77
% identity	51
NCBI Description	(U23190) chlorophyll a/b-binding apoprotein CP24 precursor [Zea mays]

Seq. No.	399614
Seq. ID	LIB3431-026-P1-K1-D8
Method	BLASTX
NCBI GI	g170131
BLAST score	391
E value	8.0e-38
Match length	116
% identity	65
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	399615
Seq. ID	LIB3431-026-P1-K1-D9
Method	BLASTX
NCBI GI	g2570511
BLAST score	561
E value	8.0e-58
Match length	107
% identity	97
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	399616
Seq. ID	LIB3431-026-P1-K1-E10
Method	BLASTX
NCBI GI	g2673913
BLAST score	244
E value	1.0e-20
Match length	66
% identity	64
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399617
Seq. ID	LIB3431-026-P1-K1-E11
Method	BLASTX
NCBI GI	g2055273
BLAST score	611
E value	1.0e-63
Match length	135
% identity	87
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	399618
Seq. ID	LIB3431-026-P1-K1-E12
Method	BLASTX
NCBI GI	g733454
BLAST score	548
E value	3.0e-56
Match length	126
% identity	83
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	399619
Seq. ID	LIB3431-026-P1-K1-E6
Method	BLASTX
NCBI GI	g3345477
BLAST score	598
E value	5.0e-62
Match length	120
% identity	95
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399620
Seq. ID	LIB3431-026-P1-K1-E7
Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	1.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399621
Seq. ID	LIB3431-026-P1-K1-E8
Method	BLASTX
NCBI GI	g3288821
BLAST score	528
E value	6.0e-54
Match length	137
% identity	74
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	399622
Seq. ID	LIB3431-026-P1-K1-F10
Method	BLASTX
NCBI GI	g2688824
BLAST score	146
E value	4.0e-09
Match length	76
% identity	45
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	399623

Seq. ID	LIB3431-026-P1-K1-F11
Method	BLASTX
NCBI GI	g115796
BLAST score	848
E value	2.0e-91
Match length	159
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	399624
Seq. ID	LIB3431-026-P1-K1-F12
Method	BLASTX
NCBI GI	g131388
BLAST score	257
E value	3.0e-22
Match length	102
% identity	61
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No.	399625
Seq. ID	LIB3431-026-P1-K1-F2
Method	BLASTX
NCBI GI	g2407281
BLAST score	632
E value	3.0e-66
Match length	116
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399626
Seq. ID	LIB3431-026-P1-K1-F4
Method	BLASTX
NCBI GI	g132105
BLAST score	567
E value	2.0e-58
Match length	122
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399627
Seq. ID	LIB3431-026-P1-K1-F7
Method	BLASTX
NCBI GI	g733454
BLAST score	431
E value	1.0e-42
Match length	103
% identity	81
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	399628
Seq. ID	LIB3431-026-P1-K1-F8
Method	BLASTX
NCBI GI	g3859597
BLAST score	275
E value	3.0e-24
Match length	96
% identity	54
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana]

Seq. No.	399629
Seq. ID	LIB3431-026-P1-K1-G1
Method	BLASTN
NCBI GI	g1619603
BLAST score	316
E value	1.0e-178
Match length	335
% identity	99
NCBI Description	O.sativa mRNA for lipid transfer protein >gi_1667589_gb_U77295_OSU77295 Oryza sativa lipid transfer protein (LTP) mRNA, complete cds

Seq. No.	399630
Seq. ID	LIB3431-026-P1-K1-G10
Method	BLASTX
NCBI GI	g3242708
BLAST score	414
E value	2.0e-40
Match length	144
% identity	56
NCBI Description	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	399631
Seq. ID	LIB3431-026-P1-K1-G11
Method	BLASTX
NCBI GI	g2624326
BLAST score	245
E value	8.0e-21
Match length	56
% identity	86
NCBI Description	(AJ002893) OsGRP1 [Oryza sativa]

Seq. No.	399632
Seq. ID	LIB3431-026-P1-K1-G2
Method	BLASTX

NCBI GI	g2306981
BLAST score	143
E value	4.0e-09
Match length	23
% identity	100
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No.	399633
Seq. ID	LIB3431-026-P1-K1-G3
Method	BLASTX
NCBI GI	g1617206
BLAST score	158
E value	1.0e-10
Match length	47
% identity	64
NCBI Description	(Z72489) CP12 [Pisum sativum]

Seq. No.	399634
Seq. ID	LIB3431-026-P1-K1-G4
Method	BLASTX
NCBI GI	g3885888
BLAST score	357
E value	8.0e-34
Match length	115
% identity	68
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	399635
Seq. ID	LIB3431-026-P1-K1-G5
Method	BLASTX
NCBI GI	g131192
BLAST score	441
E value	1.0e-43
Match length	128
% identity	70
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937 photosystem I chain V precursor - barley >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide PSI-G precursor [Hordeum vulgare]

Seq. No.	399636
Seq. ID	LIB3431-026-P1-K1-G7
Method	BLASTX
NCBI GI	g115787
BLAST score	668
E value	2.0e-70
Match length	134
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399637
Seq. ID	LIB3431-026-P1-K1-G8

Method	BLASTX
NCBI GI	g129915
BLAST score	492
E value	8.0e-50
Match length	104
% identity	92
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_66912_pir__TVWTGC phosphoglycerate kinase (EC 2.7.2.3) precursor, chloroplast - wheat >gi_21833_emb_CAA33303_ (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum aestivum] >gi_3293043_emb_CAA51931_ (X73528) phosphoglycerate kinase [Triticum aestivum]

Seq. No.	399638
Seq. ID	LIB3431-026-P1-K1-G9
Method	BLASTX
NCBI GI	g131176
BLAST score	299
E value	5.0e-27
Match length	58
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No.	399639
Seq. ID	LIB3431-026-P1-K1-H11
Method	BLASTX
NCBI GI	g3292814
BLAST score	298
E value	7.0e-27
Match length	80
% identity	68
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	399640
Seq. ID	LIB3431-026-P1-K1-H3
Method	BLASTX
NCBI GI	g3411227
BLAST score	402
E value	3.0e-39
Match length	84
% identity	90
NCBI Description	(AF078874) NBS-LRR type disease resistance protein O2 [Avena sativa]

Seq. No.	399641
Seq. ID	LIB3431-026-P1-K1-H4
Method	BLASTX
NCBI GI	g3913018
BLAST score	694
E value	2.0e-73
Match length	140

% identity	100
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	399642
Seq. ID	LIB3431-026-P1-K1-H5
Method	BLASTX
NCBI GI	g5007084
BLAST score	383
E value	3.0e-37
Match length	90
% identity	80
NCBI Description	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]

Seq. No.	399643
Seq. ID	LIB3431-026-P1-K1-H7
Method	BLASTX
NCBI GI	g3176725
BLAST score	200
E value	2.0e-15
Match length	98
% identity	41
NCBI Description	(AC002392) unknown protein [Arabidopsis thaliana]

Seq. No.	399644
Seq. ID	LIB3431-026-P1-K1-H8
Method	BLASTX
NCBI GI	g2754849
BLAST score	248
E value	5.0e-21
Match length	55
% identity	87
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	399645
Seq. ID	LIB3431-026-P1-K1-H9
Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	1.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399646
Seq. ID	LIB3431-026-P1-N1-A1
Method	BLASTN
NCBI GI	g3777599
BLAST score	44
E value	2.0e-15
Match length	155
% identity	88
NCBI Description	Oryza sativa clone LS101 50S ribosomal protein L5 (rpl5) mRNA, nuclear gene encoding chloroplast protein, partial

cds

Seq. No.	399647
Seq. ID	LIB3431-026-P1-N1-A10
Method	BLASTX
NCBI GI	g134034
BLAST score	220
E value	8.0e-18
Match length	61
% identity	67
NCBI Description	30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5) (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1) >gi_279640_pir__R3SPS5 ribosomal protein CS-S22 precursor, chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270) chloroplast ribosomal protein S22 [Spinacia oleracea] >gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein [Spinacia oleracea]

Seq. No.	399648
Seq. ID	LIB3431-026-P1-N1-A11
Method	BLASTX
NCBI GI	g3345477
BLAST score	226
E value	2.0e-18
Match length	42
% identity	100
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399649
Seq. ID	LIB3431-026-P1-N1-A12
Method	BLASTX
NCBI GI	g421916
BLAST score	167
E value	1.0e-11
Match length	30
% identity	100
NCBI Description	chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No.	399650
Seq. ID	LIB3431-026-P1-N1-A2
Method	BLASTX
NCBI GI	g671740
BLAST score	345
E value	2.0e-32
Match length	65
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399651
Seq. ID	LIB3431-026-P1-N1-A3
Method	BLASTX
NCBI GI	g2462750
BLAST score	240
E value	4.0e-20

Match length	65
% identity	69
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	399652
Seq. ID	LIB3431-026-P1-N1-A4
Method	BLASTX
NCBI GI	g132105
BLAST score	277
E value	2.0e-24
Match length	53
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399653
Seq. ID	LIB3431-026-P1-N1-A5
Method	BLASTX
NCBI GI	g3345477
BLAST score	210
E value	1.0e-16
Match length	40
% identity	97
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399654
Seq. ID	LIB3431-026-P1-N1-A6
Method	BLASTX
NCBI GI	g4538920
BLAST score	226
E value	2.0e-18
Match length	59
% identity	81
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	399655
Seq. ID	LIB3431-026-P1-N1-A7
Method	BLASTX
NCBI GI	g3913437
BLAST score	196
E value	2.0e-15
Match length	41
% identity	85
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970) RNA helicase [Arabidopsis thaliana]

Seq. No.	399656
Seq. ID	LIB3431-026-P1-N1-A8
Method	BLASTX
NCBI GI	g132105
BLAST score	301
E value	3.0e-27
Match length	57
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399657
Seq. ID	LIB3431-026-P1-N1-A9
Method	BLASTN
NCBI GI	g2305114
BLAST score	295
E value	1.0e-165
Match length	390
% identity	94
NCBI Description	Oryza sativa ferredoxin mRNA, complete cds

Seq. No.	399658
Seq. ID	LIB3431-026-P1-N1-B1
Method	BLASTN
NCBI GI	g5360229
BLAST score	393
E value	0.0e+00
Match length	393
% identity	100
NCBI Description	Oryza sativa mRNA for Ran, complete cds

Seq. No.	399659
Seq. ID	LIB3431-026-P1-N1-B10
Method	BLASTX
NCBI GI	g1617197
BLAST score	230
E value	5.0e-19
Match length	49
% identity	86
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399660
Seq. ID	LIB3431-026-P1-N1-B12
Method	BLASTX
NCBI GI	g4588906
BLAST score	465
E value	2.0e-46
Match length	100
% identity	88
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	399661
Seq. ID	LIB3431-026-P1-N1-B2
Method	BLASTN
NCBI GI	g5478796
BLAST score	349
E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Oryza sativa CAO mRNA for chlorophyll b synthase, partial cds

Seq. No.	399662
Seq. ID	LIB3431-026-P1-N1-B3
Method	BLASTX
NCBI GI	g1173347
BLAST score	250
E value	2.0e-21
Match length	54
% identity	94
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	399663
Seq. ID	LIB3431-026-P1-N1-B4
Method	BLASTX
NCBI GI	g1835731
BLAST score	359
E value	4.0e-34
Match length	80
% identity	88
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399664
Seq. ID	LIB3431-026-P1-N1-B5
Method	BLASTX
NCBI GI	g1835731
BLAST score	359
E value	4.0e-34
Match length	80
% identity	88
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399665
Seq. ID	LIB3431-026-P1-N1-B6
Method	BLASTX
NCBI GI	g3929924
BLAST score	292
E value	3.0e-26
Match length	56
% identity	98
NCBI Description	(AB020502) catalase [Oryza sativa]

Seq. No.	399666
Seq. ID	LIB3431-026-P1-N1-B8
Method	BLASTX
NCBI GI	g517500
BLAST score	401
E value	4.0e-39
Match length	97
% identity	81
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	399667
Seq. ID	LIB3431-026-P1-N1-C1
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399668
Seq. ID	LIB3431-026-P1-N1-C10
Method	BLASTX
NCBI GI	g5668640
BLAST score	332
E value	6.0e-31
Match length	97
% identity	57
NCBI Description	(AL109619) putative protein [Arabidopsis thaliana]

Seq. No.	399669
Seq. ID	LIB3431-026-P1-N1-C12
Method	BLASTX
NCBI GI	g4455296
BLAST score	241
E value	3.0e-20
Match length	44
% identity	89
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399670
Seq. ID	LIB3431-026-P1-N1-C3
Method	BLASTX
NCBI GI	g132105
BLAST score	301
E value	3.0e-27
Match length	57
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399671
Seq. ID	LIB3431-026-P1-N1-C4
Method	BLASTX
NCBI GI	g21839
BLAST score	229
E value	7.0e-19
Match length	47
% identity	96
NCBI Description	(X57952) phosphoribulokinase [Triticum aestivum]

Seq. No.	399672
Seq. ID	LIB3431-026-P1-N1-C6
Method	BLASTN
NCBI GI	g2072726
BLAST score	384
E value	0.0e+00
Match length	399
% identity	99
NCBI Description	O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No.	399673
Seq. ID	LIB3431-026-P1-N1-C7
Method	BLASTX
NCBI GI	g4512125
BLAST score	243
E value	2.0e-20
Match length	45
% identity	100
NCBI Description	(AF133340) putative chlorophyll a/b-binding protein [Phalaenopsis sp. 'KCbutterfly']

Seq. No.	399674
Seq. ID	LIB3431-026-P1-N1-C8
Method	BLASTX
NCBI GI	g606817
BLAST score	178
E value	6.0e-13
Match length	32
% identity	100
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]

Seq. No.	399675
Seq. ID	LIB3431-026-P1-N1-D10
Method	BLASTX
NCBI GI	g4512125
BLAST score	251
E value	2.0e-21
Match length	47
% identity	100
NCBI Description	(AF133340) putative chlorophyll a/b-binding protein

[Phalaenopsis sp. 'KCbutterfly']

Seq. No.	399676
Seq. ID	LIB3431-026-P1-N1-D3
Method	BLASTX
NCBI GI	g120661
BLAST score	181
E value	3.0e-13
Match length	45
% identity	76
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	399677
Seq. ID	LIB3431-026-P1-N1-D4
Method	BLASTX
NCBI GI	g3004565
BLAST score	337
E value	2.0e-31
Match length	94
% identity	67
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	399678
Seq. ID	LIB3431-026-P1-N1-D5
Method	BLASTX
NCBI GI	g115787
BLAST score	409
E value	6.0e-40
Match length	77
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	399679
Seq. ID	LIB3431-026-P1-N1-D6
Method	BLASTX
NCBI GI	g543939
BLAST score	160
E value	9.0e-11
Match length	39
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 PRECURSOR >gi_541819_pir__S40210 chlorophyll a/b-binding protein CP24 precursor - spinach >gi_437991_emb_CAA81105.1_ (Z25886) 20 kDa protein of CP24 precursor protein [Spinacia oleracea]

Seq. No.	399680
Seq. ID	LIB3431-026-P1-N1-D8
Method	BLASTX
NCBI GI	g170131
BLAST score	218
E value	1.0e-17

Match length	68
% identity	59
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	399681
Seq. ID	LIB3431-026-P1-N1-D9
Method	BLASTX
NCBI GI	g115794
BLAST score	501
E value	9.0e-51
Match length	100
% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No.	399682
Seq. ID	LIB3431-026-P1-N1-E10
Method	BLASTX
NCBI GI	g2673913
BLAST score	306
E value	7.0e-28
Match length	77
% identity	75
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399683
Seq. ID	LIB3431-026-P1-N1-E11
Method	BLASTX
NCBI GI	g2055273
BLAST score	201
E value	2.0e-15
Match length	52
% identity	71
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	399684
Seq. ID	LIB3431-026-P1-N1-E12
Method	BLASTX
NCBI GI	g733454
BLAST score	402
E value	4.0e-39
Match length	81
% identity	95
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	399685
Seq. ID	LIB3431-026-P1-N1-E6
Method	BLASTX
NCBI GI	g3345477
BLAST score	177
E value	9.0e-13
Match length	35
% identity	100

NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.	399686
Seq. ID	LIB3431-026-P1-N1-E7
Method	BLASTX
NCBI GI	g1617197
BLAST score	164
E value	3.0e-11
Match length	33
% identity	88
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]
Seq. No.	399687
Seq. ID	LIB3431-026-P1-N1-E8
Method	BLASTX
NCBI GI	g2754849
BLAST score	186
E value	8.0e-14
Match length	45
% identity	80
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]
Seq. No.	399688
Seq. ID	LIB3431-026-P1-N1-F11
Method	BLASTX
NCBI GI	g3126854
BLAST score	431
E value	1.0e-42
Match length	82
% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	399689
Seq. ID	LIB3431-026-P1-N1-F12
Method	BLASTX
NCBI GI	g482311
BLAST score	508
E value	1.0e-51
Match length	99
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	399690
Seq. ID	LIB3431-026-P1-N1-F2
Method	BLASTX
NCBI GI	g132105
BLAST score	301
E value	2.0e-27
Match length	57
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

	(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	399691
Seq. ID	LIB3431-026-P1-N1-F4
Method	BLASTX
NCBI GI	g132105
BLAST score	301
E value	2.0e-27
Match length	57
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	399692
Seq. ID	LIB3431-026-P1-N1-F7
Method	BLASTX
NCBI GI	g733454
BLAST score	232
E value	3.0e-19
Match length	48
% identity	94
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]
Seq. No.	399693
Seq. ID	LIB3431-026-P1-N1-G11
Method	BLASTN
NCBI GI	g2624325
BLAST score	140
E value	7.0e-73
Match length	168
% identity	96
NCBI Description	Oryza sativa mRNA for glycine-rich RNA-binding protein (OsGRP1)
Seq. No.	399694
Seq. ID	LIB3431-026-P1-N1-G12
Method	BLASTX
NCBI GI	g517500
BLAST score	272
E value	5.0e-24
Match length	72
% identity	79
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	399695
Seq. ID	LIB3431-026-P1-N1-G2
Method	BLASTX
NCBI GI	g1076724
BLAST score	364
E value	1.0e-34
Match length	70
% identity	94
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No.	399696
Seq. ID	LIB3431-026-P1-N1-G4
Method	BLASTN
NCBI GI	g3885887
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	399697
Seq. ID	LIB3431-026-P1-N1-G5
Method	BLASTN
NCBI GI	g2306980
BLAST score	112
E value	2.0e-56
Match length	125
% identity	98
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	399698
Seq. ID	LIB3431-026-P1-N1-G6
Method	BLASTX
NCBI GI	g2130089
BLAST score	222
E value	5.0e-18
Match length	42
% identity	93
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]

Seq. No.	399699
Seq. ID	LIB3431-026-P1-N1-G7
Method	BLASTX
NCBI GI	g3036946
BLAST score	300
E value	3.0e-27
Match length	57
% identity	100
NCBI Description	(AB012637) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No.	399700
Seq. ID	LIB3431-026-P1-N1-G8
Method	BLASTX
NCBI GI	g3738261
BLAST score	428
E value	3.0e-42
Match length	95
% identity	92
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	399701
Seq. ID	LIB3431-026-P1-N1-G9
Method	BLASTX
NCBI GI	g131176
BLAST score	187
E value	6.0e-14
Match length	37
% identity	97
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No.	399702
Seq. ID	LIB3431-026-P1-N1-H11
Method	BLASTX
NCBI GI	g3292814
BLAST score	232
E value	3.0e-19
Match length	57
% identity	72
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	399703
Seq. ID	LIB3431-026-P1-N1-H3
Method	BLASTX
NCBI GI	g4490715
BLAST score	147
E value	3.0e-09
Match length	99
% identity	34
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	399704
Seq. ID	LIB3431-026-P1-N1-H4
Method	BLASTX
NCBI GI	g3913018
BLAST score	166
E value	2.0e-11
Match length	33
% identity	100

NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	399705
Seq. ID	LIB3431-026-P1-N1-H5
Method	BLASTX
NCBI GI	g5007084
BLAST score	224
E value	3.0e-18
Match length	46
% identity	100
NCBI Description	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]

Seq. No.	399706
Seq. ID	LIB3431-026-P1-N1-H6
Method	BLASTX
NCBI GI	g132105
BLAST score	294
E value	2.0e-26
Match length	56
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399707
Seq. ID	LIB3431-026-P1-N1-H9
Method	BLASTX
NCBI GI	g1617197
BLAST score	212
E value	6.0e-17
Match length	44
% identity	89
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399708
Seq. ID	LIB3431-027-P1-K1-A1
Method	BLASTX
NCBI GI	g1173347
BLAST score	283
E value	3.0e-25
Match length	58
% identity	88
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	399709
Seq. ID	LIB3431-027-P1-K1-A11
Method	BLASTX
NCBI GI	g4557229
BLAST score	223
E value	4.0e-18
Match length	112
% identity	35
NCBI Description	angio-associated, migratory cell protein >gi_3121739_sp_Q13685_AAMP_HUMAN ANGIO-ASSOCIATED MIGRATORY CELL PROTEIN >gi_2134759_pir__I39383 angio-associated migratory cell protein - human >gi_870803 (M95627) angio-associated migratory cell protein [Homo sapiens]

Seq. No.	399710
Seq. ID	LIB3431-027-P1-K1-A12
Method	BLASTX
NCBI GI	g2493650
BLAST score	638
E value	7.0e-67
Match length	139
% identity	95
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale cereale]

Seq. No.	399711
Seq. ID	LIB3431-027-P1-K1-A3
Method	BLASTX
NCBI GI	g417103
BLAST score	541
E value	2.0e-55
Match length	124
% identity	88
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to

histone H3 (AB015760) [Oryza sativa]

Seq. No.	399712
Seq. ID	LIB3431-027-P1-K1-A4
Method	BLASTX
NCBI GI	g606817
BLAST score	378
E value	1.0e-39
Match length	128
% identity	70
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]

Seq. No.	399713
Seq. ID	LIB3431-027-P1-K1-A5
Method	BLASTX
NCBI GI	g2388689
BLAST score	270
E value	1.0e-23
Match length	67
% identity	76
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	399714
Seq. ID	LIB3431-027-P1-K1-A6
Method	BLASTX
NCBI GI	g320618
BLAST score	599
E value	3.0e-62
Match length	131
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399715
Seq. ID	LIB3431-027-P1-K1-A7
Method	BLASTX
NCBI GI	g1173347
BLAST score	802
E value	5.0e-86
Match length	153
% identity	95
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	399716
Seq. ID	LIB3431-027-P1-K1-A8
Method	BLASTX
NCBI GI	g733454

BLAST score	476
E value	5.0e-70
Match length	137
% identity	93
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	399717
Seq. ID	LIB3431-027-P1-K1-A9
Method	BLASTN
NCBI GI	g3885891
BLAST score	144
E value	3.0e-75
Match length	197
% identity	99
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	399718
Seq. ID	LIB3431-027-P1-K1-B1
Method	BLASTN
NCBI GI	g21843
BLAST score	195
E value	1.0e-105
Match length	412
% identity	87
NCBI Description	Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II

Seq. No.	399719
Seq. ID	LIB3431-027-P1-K1-B10
Method	BLASTX
NCBI GI	g2500959
BLAST score	424
E value	1.0e-41
Match length	133
% identity	62
NCBI Description	ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) >gi_1653611_dbj_BAA18523_ (D90915) alanyl-tRNA synthetase [Synechocystis sp.]

Seq. No.	399720
Seq. ID	LIB3431-027-P1-K1-B11
Method	BLASTX
NCBI GI	g3023816
BLAST score	474
E value	1.0e-47
Match length	90
% identity	100
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	399721
Seq. ID	LIB3431-027-P1-K1-B4
Method	BLASTX
NCBI GI	g2130127

BLAST score	447
E value	2.0e-44
Match length	99
% identity	90
NCBI Description	ferritin 1 precursor - maize >gi_1103628_emb_CAA58146_ (X83076) ferritin [Zea mays]

Seq. No.	399722
Seq. ID	LIB3431-027-P1-K1-B5
Method	BLASTX
NCBI GI	g132105
BLAST score	257
E value	3.0e-29
Match length	66
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399723
Seq. ID	LIB3431-027-P1-K1-B6
Method	BLASTX
NCBI GI	g132105
BLAST score	614
E value	6.0e-64
Match length	132
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399724
Seq. ID	LIB3431-027-P1-K1-B7
Method	BLASTX
NCBI GI	g131388
BLAST score	358
E value	6.0e-34
Match length	121
% identity	65
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No.	399725
Seq. ID	LIB3431-027-P1-K1-B8
Method	BLASTX
NCBI GI	g462195
BLAST score	325
E value	4.0e-30
Match length	62
% identity	100
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	399726
Seq. ID	LIB3431-027-P1-K1-C10
Method	BLASTX
NCBI GI	g1707998
BLAST score	297
E value	9.0e-27
Match length	92
% identity	66
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir__S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No.	399727
Seq. ID	LIB3431-027-P1-K1-C11
Method	BLASTX
NCBI GI	g3482977
BLAST score	273
E value	5.0e-24
Match length	138
% identity	46
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	399728
Seq. ID	LIB3431-027-P1-K1-C12
Method	BLASTX
NCBI GI	g100796
BLAST score	752
E value	4.0e-80
Match length	152
% identity	94
NCBI Description	phosphoribulokinase (EC 2.7.1.19) - wheat

Seq. No.	399729
Seq. ID	LIB3431-027-P1-K1-C3
Method	BLASTX
NCBI GI	g82080
BLAST score	336
E value	1.0e-35

Match length	118
% identity	68
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	399730
Seq. ID	LIB3431-027-P1-K1-C4
Method	BLASTX
NCBI GI	g1669341
BLAST score	219
E value	1.0e-17
Match length	133
% identity	41
NCBI Description	(D45066) AOBP (ascorbate oxidase promoter-binding protein) [Cucurbita maxima]

Seq. No.	399731
Seq. ID	LIB3431-027-P1-K1-C5
Method	BLASTX
NCBI GI	g4585882
BLAST score	498
E value	2.0e-50
Match length	150
% identity	64
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	399732
Seq. ID	LIB3431-027-P1-K1-C6
Method	BLASTX
NCBI GI	g5922612
BLAST score	282
E value	5.0e-25
Match length	127
% identity	46
NCBI Description	(AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa]

Seq. No.	399733
Seq. ID	LIB3431-027-P1-K1-C9
Method	BLASTX
NCBI GI	g671740
BLAST score	219
E value	1.0e-17
Match length	48
% identity	88
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399734
Seq. ID	LIB3431-027-P1-K1-D1
Method	BLASTX
NCBI GI	g2244926
BLAST score	292

E value	3.0e-26
Match length	98
% identity	58
NCBI Description	(Z97339) glutaredoxin homolog [Arabidopsis thaliana]

Seq. No.	399735
Seq. ID	LIB3431-027-P1-K1-D12
Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	1.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399736
Seq. ID	LIB3431-027-P1-K1-D2
Method	BLASTX
NCBI GI	g2306981
BLAST score	530
E value	4.0e-54
Match length	96
% identity	98
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No.	399737
Seq. ID	LIB3431-027-P1-K1-D4
Method	BLASTN
NCBI GI	g304219
BLAST score	78
E value	1.0e-35
Match length	161
% identity	87
NCBI Description	Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No.	399738
Seq. ID	LIB3431-027-P1-K1-D7
Method	BLASTX
NCBI GI	g1661160
BLAST score	458
E value	1.0e-45
Match length	101
% identity	84
NCBI Description	(U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399739
Seq. ID	LIB3431-027-P1-K1-D8
Method	BLASTX
NCBI GI	g3036951
BLAST score	343
E value	1.0e-36
Match length	80
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399740
Seq. ID	LIB3431-027-P1-K1-E1
Method	BLASTX
NCBI GI	g2570511
BLAST score	163
E value	3.0e-22
Match length	67
% identity	78
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	399741
Seq. ID	LIB3431-027-P1-K1-E10
Method	BLASTX
NCBI GI	g4678948
BLAST score	192
E value	2.0e-14
Match length	117
% identity	41
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	399742
Seq. ID	LIB3431-027-P1-K1-E11
Method	BLASTX
NCBI GI	g170131
BLAST score	260
E value	2.0e-22
Match length	66
% identity	68
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	399743
Seq. ID	LIB3431-027-P1-K1-E12
Method	BLASTX
NCBI GI	g132105
BLAST score	702
E value	3.0e-74
Match length	136
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399744
Seq. ID	LIB3431-027-P1-K1-E4
Method	BLASTX
NCBI GI	g2570515
BLAST score	569
E value	1.0e-58
Match length	130
% identity	86
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	399745
Seq. ID	LIB3431-027-P1-K1-E6
Method	BLASTX
NCBI GI	g5354158
BLAST score	384
E value	3.0e-43
Match length	140
% identity	64
NCBI Description	(AF149841) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_6041825_gb_AAF02140.1_AC009918_12 (AC009918) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No.	399746
Seq. ID	LIB3431-027-P1-K1-E7
Method	BLASTX
NCBI GI	g729668
BLAST score	241
E value	3.0e-20
Match length	68
% identity	63
NCBI Description	HISTONE H1 >gi_2147479_pir__S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No.	399747
Seq. ID	LIB3431-027-P1-K1-E8
Method	BLASTX
NCBI GI	g1835731
BLAST score	412
E value	3.0e-40
Match length	89
% identity	88
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399748
Seq. ID	LIB3431-027-P1-K1-E9
Method	BLASTX
NCBI GI	g3885894
BLAST score	464
E value	2.0e-46
Match length	110
% identity	82
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No.	399749
Seq. ID	LIB3431-027-P1-K1-F1
Method	BLASTX
NCBI GI	g1076722
BLAST score	667
E value	4.0e-70
Match length	144
% identity	90
NCBI Description	hypothetical protein - barley (fragment)

Seq. No.	399750
Seq. ID	LIB3431-027-P1-K1-F10
Method	BLASTX
NCBI GI	g1777961
BLAST score	504
E value	5.0e-51
Match length	154
% identity	58
NCBI Description	(U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No.	399751
Seq. ID	LIB3431-027-P1-K1-F11
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399752
Seq. ID	LIB3431-027-P1-K1-F12
Method	BLASTX
NCBI GI	g3510256
BLAST score	157
E value	2.0e-10
Match length	106
% identity	32
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	399753
Seq. ID	LIB3431-027-P1-K1-F2
Method	BLASTX
NCBI GI	g3204108
BLAST score	570
E value	8.0e-59
Match length	118
% identity	87
NCBI Description	(AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]

Seq. No.	399754
Seq. ID	LIB3431-027-P1-K1-F3
Method	BLASTX
NCBI GI	g132105
BLAST score	666
E value	5.0e-70
Match length	142
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399755
Seq. ID	LIB3431-027-P1-K1-F4
Method	BLASTX
NCBI GI	g3789952
BLAST score	307
E value	6.0e-28
Match length	66
% identity	88
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	399756
Seq. ID	LIB3431-027-P1-K1-F5
Method	BLASTX
NCBI GI	g1076800
BLAST score	717
E value	5.0e-76
Match length	155
% identity	87
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate peroxidase [Zea mays]

Seq. No.	399757
Seq. ID	LIB3431-027-P1-K1-F6
Method	BLASTX
NCBI GI	g1835731
BLAST score	531
E value	3.0e-54
Match length	101
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399758
Seq. ID	LIB3431-027-P1-K1-F8
Method	BLASTX
NCBI GI	g3126854
BLAST score	671
E value	1.0e-70
Match length	126
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399759
Seq. ID	LIB3431-027-P1-K1-F9
Method	BLASTX
NCBI GI	g6066383
BLAST score	236
E value	5.0e-20
Match length	49
% identity	98

NCBI Description	(AJ011926) Mg-protoporphyrin IX [Hordeum vulgare]

Seq. No.	399760
Seq. ID	LIB3431-027-P1-K1-G1
Method	BLASTX
NCBI GI	g2624328
BLAST score	542
E value	2.0e-55
Match length	118
% identity	90
NCBI Description	(AJ002894) OsGRP2 [Oryza sativa]

Seq. No.	399761
Seq. ID	LIB3431-027-P1-K1-G10
Method	BLASTX
NCBI GI	g3935168
BLAST score	292
E value	3.0e-26
Match length	125
% identity	53
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	399762
Seq. ID	LIB3431-027-P1-K1-G11
Method	BLASTX
NCBI GI	g3789952
BLAST score	698
E value	8.0e-74
Match length	139
% identity	98
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	399763
Seq. ID	LIB3431-027-P1-K1-G12
Method	BLASTX
NCBI GI	g3789954
BLAST score	840
E value	2.0e-90
Match length	154
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399764
Seq. ID	LIB3431-027-P1-K1-G4
Method	BLASTX
NCBI GI	g2832672
BLAST score	263
E value	9.0e-23
Match length	55
% identity	95
NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No.	399765
Seq. ID	LIB3431-027-P1-K1-G5
Method	BLASTX

NCBI GI	g5103831
BLAST score	281
E value	5.0e-25
Match length	94
% identity	60
NCBI Description	(AC007591) ESTs gb_H37032, gb_R6425, gb_Z34651, gb_N37268, gb_AA713172 and gb_Z34241 come from this gene. [Arabidopsis thaliana]

Seq. No.	399766
Seq. ID	LIB3431-027-P1-K1-G6
Method	BLASTN
NCBI GI	g3075487
BLAST score	157
E value	5.0e-83
Match length	157
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	399767
Seq. ID	LIB3431-027-P1-K1-G7
Method	BLASTX
NCBI GI	g5815133
BLAST score	183
E value	2.0e-13
Match length	99
% identity	37
NCBI Description	(AF169386) SPO11 [Mus musculus]

Seq. No.	399768
Seq. ID	LIB3431-027-P1-K1-G8
Method	BLASTX
NCBI GI	g3763918
BLAST score	236
E value	1.0e-19
Match length	67
% identity	70
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	399769
Seq. ID	LIB3431-027-P1-K1-H1
Method	BLASTX
NCBI GI	g1169544
BLAST score	540
E value	3.0e-55
Match length	154
% identity	67
NCBI Description	ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) ERD1 protein [Arabidopsis thaliana]

Seq. No.	399770
Seq. ID	LIB3431-027-P1-K1-H11
Method	BLASTX
NCBI GI	g3075488

BLAST score	572
E value	1.0e-65
Match length	139
% identity	91
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	399771
Seq. ID	LIB3431-027-P1-K1-H12
Method	BLASTX
NCBI GI	g3789954
BLAST score	148
E value	2.0e-19
Match length	118
% identity	53
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399772
Seq. ID	LIB3431-027-P1-K1-H3
Method	BLASTX
NCBI GI	g4587571
BLAST score	425
E value	8.0e-42
Match length	104
% identity	75
NCBI Description	(AC006550) Belongs to the PF_01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana]

Seq. No.	399773
Seq. ID	LIB3431-027-P1-K1-H5
Method	BLASTX
NCBI GI	g115796
BLAST score	721
E value	2.0e-76
Match length	138
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	399774
Seq. ID	LIB3431-027-P1-K1-H6
Method	BLASTX
NCBI GI	g3789954
BLAST score	186
E value	2.0e-14
Match length	64
% identity	61
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399775
Seq. ID	LIB3431-027-P1-K1-H7
Method	BLASTX
NCBI GI	g3881189

BLAST score	489
E value	3.0e-49
Match length	144
% identity	61
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y

Seq. No.	399776
Seq. ID	LIB3431-027-P1-K1-H8
Method	BLASTX
NCBI GI	g320618
BLAST score	489
E value	2.0e-49
Match length	109
% identity	85
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399777
Seq. ID	LIB3431-027-P1-K1-H9
Method	BLASTX
NCBI GI	g482311
BLAST score	731
E value	1.0e-77
Match length	142
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	399778
Seq. ID	LIB3431-027-P1-N1-A1
Method	BLASTX
NCBI GI	g687677
BLAST score	230
E value	4.0e-19
Match length	51
% identity	86
NCBI Description	(U19925) unknown [Arabidopsis thaliana]

Seq. No.	399779
Seq. ID	LIB3431-027-P1-N1-A11
Method	BLASTX
NCBI GI	g3413423
BLAST score	169
E value	7.0e-12
Match length	64
% identity	48
NCBI Description	(AJ006309) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399780
Seq. ID	LIB3431-027-P1-N1-A12

Method	BLASTX
NCBI GI	g2493650
BLAST score	299
E value	5.0e-36
Match length	90
% identity	77
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale cereale]

Seq. No.	399781
Seq. ID	LIB3431-027-P1-N1-A3
Method	BLASTX
NCBI GI	g4574208
BLAST score	265
E value	4.0e-23
Match length	53
% identity	100
NCBI Description	(AF093108) histone H3 [Tortula ruralis]

Seq. No.	399782
Seq. ID	LIB3431-027-P1-N1-A4
Method	BLASTX
NCBI GI	g3345477
BLAST score	177
E value	9.0e-13
Match length	41
% identity	85
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399783
Seq. ID	LIB3431-027-P1-N1-A6
Method	BLASTN
NCBI GI	g20177
BLAST score	399
E value	0.0e+00
Match length	433
% identity	99
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	399784
Seq. ID	LIB3431-027-P1-N1-A7
Method	BLASTX
NCBI GI	g1173347
BLAST score	284
E value	2.0e-25
Match length	61
% identity	95
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	399785
Seq. ID	LIB3431-027-P1-N1-A8
Method	BLASTX
NCBI GI	g733454
BLAST score	271
E value	8.0e-24
Match length	56
% identity	95
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	399786
Seq. ID	LIB3431-027-P1-N1-A9
Method	BLASTX
NCBI GI	g3885892
BLAST score	338
E value	1.0e-31
Match length	65
% identity	100
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	399787
Seq. ID	LIB3431-027-P1-N1-B1
Method	BLASTX
NCBI GI	g482311
BLAST score	186
E value	6.0e-14
Match length	36
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	399788
Seq. ID	LIB3431-027-P1-N1-B10
Method	BLASTN
NCBI GI	g169798
BLAST score	42
E value	3.0e-14
Match length	94
% identity	86
NCBI Description	Oryza sativa 16.9 kDa heat shock protein gene, complete cds

Seq. No.	399789
Seq. ID	LIB3431-027-P1-N1-B2
Method	BLASTX
NCBI GI	g482311
BLAST score	154
E value	4.0e-10
Match length	44
% identity	73
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	399790
Seq. ID	LIB3431-027-P1-N1-B3

Method	BLASTN
NCBI GI	g6006355
BLAST score	351
E value	0.0e+00
Match length	375
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	399791
Seq. ID	LIB3431-027-P1-N1-B4
Method	BLASTN
NCBI GI	g455510
BLAST score	173
E value	3.0e-92
Match length	201
% identity	97
NCBI Description	Rice mRNA for ferritin, partial sequence

Seq. No.	399792
Seq. ID	LIB3431-027-P1-N1-B5
Method	BLASTX
NCBI GI	g132105
BLAST score	734
E value	6.0e-78
Match length	160
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399793
Seq. ID	LIB3431-027-P1-N1-B6
Method	BLASTX
NCBI GI	g132105
BLAST score	339
E value	1.0e-42
Match length	89
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399794
Seq. ID	LIB3431-027-P1-N1-B7
Method	BLASTX

NCBI GI	g482311
BLAST score	345
E value	1.0e-32
Match length	75
% identity	91
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	399795
Seq. ID	LIB3431-027-P1-N1-B8
Method	BLASTN
NCBI GI	g3789949
BLAST score	288
E value	1.0e-161
Match length	292
% identity	100
NCBI Description	Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No.	399796
Seq. ID	LIB3431-027-P1-N1-C10
Method	BLASTX
NCBI GI	g1346155
BLAST score	168
E value	1.0e-11
Match length	33
% identity	97
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	399797
Seq. ID	LIB3431-027-P1-N1-C3
Method	BLASTX
NCBI GI	g115813
BLAST score	227
E value	1.0e-18
Match length	53
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	399798
Seq. ID	LIB3431-027-P1-N1-C5
Method	BLASTX
NCBI GI	g115813
BLAST score	243
E value	2.0e-20
Match length	55
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	399799
Seq. ID	LIB3431-027-P1-N1-C8
Method	BLASTX
NCBI GI	g6063542
BLAST score	225
E value	2.0e-18
Match length	41
% identity	98
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No.	399800
Seq. ID	LIB3431-027-P1-N1-C9
Method	BLASTN
NCBI GI	g218209
BLAST score	41
E value	1.0e-13
Match length	131
% identity	81
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	399801
Seq. ID	LIB3431-027-P1-N1-D1
Method	BLASTX
NCBI GI	g2244926
BLAST score	292
E value	3.0e-26
Match length	88
% identity	65
NCBI Description	(Z97339) glutaredoxin homolog [Arabidopsis thaliana]

Seq. No.	399802
Seq. ID	LIB3431-027-P1-N1-D10
Method	BLASTX
NCBI GI	g4115337
BLAST score	201
E value	1.0e-15
Match length	41
% identity	16
NCBI Description	(L81141) ubiquitin [Pisum sativum]

Seq. No.	399803
Seq. ID	LIB3431-027-P1-N1-D12
Method	BLASTX
NCBI GI	g1617197
BLAST score	212
E value	6.0e-17
Match length	44
% identity	89
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399804

Seq. ID	LIB3431-027-P1-N1-D2
Method	BLASTX
NCBI GI	g1076724
BLAST score	284
E value	2.0e-25
Match length	56
% identity	95
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No.	399805
Seq. ID	LIB3431-027-P1-N1-D4
Method	BLASTX
NCBI GI	g548605
BLAST score	484
E value	1.0e-48
Match length	126
% identity	79
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	399806
Seq. ID	LIB3431-027-P1-N1-D7
Method	BLASTX
NCBI GI	g3036951
BLAST score	343
E value	2.0e-32
Match length	65
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	399807
Seq. ID	LIB3431-027-P1-N1-D8
Method	BLASTX
NCBI GI	g421916
BLAST score	243
E value	1.0e-20
Match length	45
% identity	100
NCBI Description	chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No.	399808
Seq. ID	LIB3431-027-P1-N1-E1
Method	BLASTN
NCBI GI	g2570510
BLAST score	150
E value	8.0e-79
Match length	226
% identity	92
NCBI Description	Oryza sativa chlorophyll a-b binding protein mRNA, complete

cds

Seq. No.	399809
Seq. ID	LIB3431-027-P1-N1-E11
Method	BLASTX
NCBI GI	g170131
BLAST score	213
E value	5.0e-17
Match length	61
% identity	66
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	399810
Seq. ID	LIB3431-027-P1-N1-E12
Method	BLASTX
NCBI GI	g132105
BLAST score	169
E value	2.0e-20
Match length	55
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399811
Seq. ID	LIB3431-027-P1-N1-E4
Method	BLASTN
NCBI GI	g2570514
BLAST score	266
E value	1.0e-148
Match length	369
% identity	98
NCBI Description	Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	399812
Seq. ID	LIB3431-027-P1-N1-E5
Method	BLASTX
NCBI GI	g451193
BLAST score	284
E value	2.0e-25
Match length	87
% identity	66
NCBI Description	(L28008) wali7 [Triticum aestivum] >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]

Seq. No.	399813
Seq. ID	LIB3431-027-P1-N1-E6
Method	BLASTX
NCBI GI	g5354158
BLAST score	155
E value	3.0e-10

Match length	42
% identity	60
NCBI Description	(AF149841) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_6041825_gb_AAF02140.1_AC009918_12 (AC009918) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No.	399814
Seq. ID	LIB3431-027-P1-N1-E8
Method	BLASTX
NCBI GI	g1835731
BLAST score	359
E value	4.0e-34
Match length	80
% identity	88
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399815
Seq. ID	LIB3431-027-P1-N1-E9
Method	BLASTX
NCBI GI	g3885894
BLAST score	398
E value	1.0e-38
Match length	90
% identity	86
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No.	399816
Seq. ID	LIB3431-027-P1-N1-F1
Method	BLASTX
NCBI GI	g3328221
BLAST score	348
E value	7.0e-33
Match length	69
% identity	93
NCBI Description	(AF076920) thioredoxin peroxidase [Secale cereale]

Seq. No.	399817
Seq. ID	LIB3431-027-P1-N1-F10
Method	BLASTX
NCBI GI	g2826842
BLAST score	268
E value	2.0e-23
Match length	75
% identity	63
NCBI Description	(AJ002236) loxc homologue [Lycopersicon pimpinellifolium]

Seq. No.	399818
Seq. ID	LIB3431-027-P1-N1-F11
Method	BLASTN
NCBI GI	g2072554
BLAST score	361
E value	0.0e+00
Match length	389
% identity	98
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No.	399819
Seq. ID	LIB3431-027-P1-N1-F2
Method	BLASTX
NCBI GI	g3204108
BLAST score	344
E value	2.0e-32
Match length	94
% identity	70
NCBI Description	(AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]

Seq. No.	399820
Seq. ID	LIB3431-027-P1-N1-F3
Method	BLASTN
NCBI GI	g218207
BLAST score	195
E value	1.0e-105
Match length	315
% identity	90
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	399821
Seq. ID	LIB3431-027-P1-N1-F4
Method	BLASTN
NCBI GI	g3789951
BLAST score	134
E value	4.0e-69
Match length	318
% identity	86
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	399822
Seq. ID	LIB3431-027-P1-N1-F5
Method	BLASTN
NCBI GI	g433216
BLAST score	223
E value	1.0e-122
Match length	232
% identity	99
NCBI Description	Rice mRNA for ascorbate peroxidase (gene name SS622), partial cds

Seq. No.	399823
Seq. ID	LIB3431-027-P1-N1-F6
Method	BLASTX
NCBI GI	g1835731
BLAST score	326
E value	3.0e-30
Match length	73
% identity	86
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399824
Seq. ID	LIB3431-027-P1-N1-F8
Method	BLASTX
NCBI GI	g3126854
BLAST score	333
E value	5.0e-31
Match length	63
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399825
Seq. ID	LIB3431-027-P1-N1-F9
Method	BLASTX
NCBI GI	g6066383
BLAST score	236
E value	5.0e-20
Match length	49
% identity	98
NCBI Description	(AJ011926) Mg-protoporphyrin IX [Hordeum vulgare]

Seq. No.	399826
Seq. ID	LIB3431-027-P1-N1-G1
Method	BLASTN
NCBI GI	g2624327
BLAST score	319
E value	1.0e-179
Match length	322
% identity	100
NCBI Description	Oryza sativa mRNA for glycine rich RNA-binding protein 2 (OsGRP2)

Seq. No.	399827
Seq. ID	LIB3431-027-P1-N1-G11
Method	BLASTN
NCBI GI	g3789951
BLAST score	193
E value	1.0e-104
Match length	391
% identity	95
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	399828
Seq. ID	LIB3431-027-P1-N1-G12
Method	BLASTX
NCBI GI	g3789954
BLAST score	339
E value	9.0e-32
Match length	63
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399829
Seq. ID	LIB3431-027-P1-N1-G4

Method	BLASTX
NCBI GI	g2832672
BLAST score	183
E value	2.0e-13
Match length	37
% identity	97
NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No.	399830
Seq. ID	LIB3431-027-P1-N1-G6
Method	BLASTN
NCBI GI	g3075487
BLAST score	149
E value	3.0e-78
Match length	157
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	399831
Seq. ID	LIB3431-027-P1-N1-G8
Method	BLASTX
NCBI GI	g3763918
BLAST score	225
E value	3.0e-18
Match length	70
% identity	64
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	399832
Seq. ID	LIB3431-027-P1-N1-H1
Method	BLASTX
NCBI GI	g733454
BLAST score	383
E value	6.0e-37
Match length	80
% identity	93
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	399833
Seq. ID	LIB3431-027-P1-N1-H11
Method	BLASTN
NCBI GI	g3075487
BLAST score	310
E value	1.0e-174
Match length	314
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	399834
Seq. ID	LIB3431-027-P1-N1-H12
Method	BLASTX
NCBI GI	g517500
BLAST score	347

E value	9.0e-33
Match length	87
% identity	79
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	399835
Seq. ID	LIB3431-027-P1-N1-H5
Method	BLASTX
NCBI GI	g3126854
BLAST score	300
E value	2.0e-27
Match length	57
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399836
Seq. ID	LIB3431-027-P1-N1-H6
Method	BLASTN
NCBI GI	g3789953
BLAST score	227
E value	1.0e-125
Match length	291
% identity	95
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	399837
Seq. ID	LIB3431-027-P1-N1-H7
Method	BLASTX
NCBI GI	g3881189
BLAST score	292
E value	4.0e-26
Match length	107
% identity	48
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y

Seq. No.	399838
Seq. ID	LIB3431-027-P1-N1-H9
Method	BLASTX
NCBI GI	g482311
BLAST score	426
E value	6.0e-42
Match length	84
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	399839
Seq. ID	LIB3431-028-P1-K1-A1
Method	BLASTX

NCBI GI	g2570497
BLAST score	373
E value	7.0e-36
Match length	76
% identity	97
NCBI Description	(AF022731) H protein subunit of glycine decarboxylase [Oryza sativa]

Seq. No.	399840
Seq. ID	LIB3431-028-P1-K1-A10
Method	BLASTX
NCBI GI	g4680203
BLAST score	377
E value	4.0e-36
Match length	153
% identity	49
NCBI Description	(AF114171) TNP2-like protein [Sorghum bicolor]

Seq. No.	399841
Seq. ID	LIB3431-028-P1-K1-A11
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399842
Seq. ID	LIB3431-028-P1-K1-A4
Method	BLASTX
NCBI GI	g4325041
BLAST score	630
E value	7.0e-66
Match length	144
% identity	88
NCBI Description	(AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No.	399843
Seq. ID	LIB3431-028-P1-K1-A6
Method	BLASTX
NCBI GI	g1835731
BLAST score	594
E value	1.0e-61
Match length	126
% identity	91
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399844
Seq. ID	LIB3431-028-P1-K1-A7
Method	BLASTX
NCBI GI	g4127348
BLAST score	289
E value	6.0e-26
Match length	117
% identity	51

NCBI Description	(AJ010449) glutathione transferase [Alopecurus myosuroides]

Seq. No.	399845
Seq. ID	LIB3431-028-P1-K1-A9
Method	BLASTX
NCBI GI	g1698548
BLAST score	456
E value	2.0e-45
Match length	137
% identity	60
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	399846
Seq. ID	LIB3431-028-P1-K1-B1
Method	BLASTX
NCBI GI	g3345477
BLAST score	147
E value	3.0e-09
Match length	28
% identity	100
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399847
Seq. ID	LIB3431-028-P1-K1-B10
Method	BLASTX
NCBI GI	g5921189
BLAST score	364
E value	1.0e-34
Match length	153
% identity	49
NCBI Description	CYTOCHROME P450 71C4 >gi_550542_emb_CAA57425_ (X81831) cytochrome P450 [Zea mays] >gi_1850903_emb_CAA72196_ (Y11368) cytochrome p450 [Zea mays]

Seq. No.	399848
Seq. ID	LIB3431-028-P1-K1-B12
Method	BLASTX
NCBI GI	g320618
BLAST score	408
E value	7.0e-40
Match length	98
% identity	81
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	399849
Seq. ID	LIB3431-028-P1-K1-B2
Method	BLASTX
NCBI GI	g6002102
BLAST score	322
E value	1.0e-29
Match length	91
% identity	68
NCBI Description	(AJ249833) Acyl-CoA binding protein (ACBP) [Digitalis

lanata]

Seq. No.	399850
Seq. ID	LIB3431-028-P1-K1-B3
Method	BLASTN
NCBI GI	g20262
BLAST score	69
E value	3.0e-30
Match length	89
% identity	94
NCBI Description	O.sativa light-induced mRNA

Seq. No.	399851
Seq. ID	LIB3431-028-P1-K1-B5
Method	BLASTX
NCBI GI	g2499775
BLAST score	188
E value	5.0e-14
Match length	84
% identity	49
NCBI Description	51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) >gi_915280 (U16959) FKBP51 [Mus musculus] >gi_1020307 (U36220) FK506 binding protein 51 [Mus musculus]

Seq. No.	399852
Seq. ID	LIB3431-028-P1-K1-C1
Method	BLASTX
NCBI GI	g5802955
BLAST score	194
E value	8.0e-15
Match length	79
% identity	47
NCBI Description	(AF178990) stress related protein [Vitis riparia]

Seq. No.	399853
Seq. ID	LIB3431-028-P1-K1-C10
Method	BLASTX
NCBI GI	g2734085
BLAST score	154
E value	5.0e-10
Match length	107
% identity	28
NCBI Description	(AF003136) contains similarity to ATP synthase subunit B [Caenorhabditis elegans]

Seq. No.	399854
Seq. ID	LIB3431-028-P1-K1-C12
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399855

Seq. ID	LIB3431-028-P1-K1-C3
Method	BLASTN
NCBI GI	g5822826
BLAST score	265
E value	1.0e-147
Match length	265
% identity	100
NCBI Description	Oryza sativa D1 gene for alpha-subunit of GTP-binding protein, wild type, partial sequence

Seq. No.	399856
Seq. ID	LIB3431-028-P1-K1-C4
Method	BLASTN
NCBI GI	g218171
BLAST score	59
E value	1.0e-24
Match length	139
% identity	86
NCBI Description	Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No.	399857
Seq. ID	LIB3431-028-P1-K1-C5
Method	BLASTX
NCBI GI	g1835731
BLAST score	573
E value	3.0e-59
Match length	109
% identity	100
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399858
Seq. ID	LIB3431-028-P1-K1-C7
Method	BLASTX
NCBI GI	g167097
BLAST score	313
E value	3.0e-41
Match length	102
% identity	83
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	399859
Seq. ID	LIB3431-028-P1-K1-C8
Method	BLASTX
NCBI GI	g548770
BLAST score	755
E value	2.0e-80
Match length	145
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No.	399860
Seq. ID	LIB3431-028-P1-K1-D1

Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	399861
Seq. ID	LIB3431-028-P1-K1-D11
Method	BLASTX
NCBI GI	g5441889
BLAST score	661
E value	2.0e-69
Match length	148
% identity	89
NCBI Description	(AP000367) Similar to SEC7 protein, Saccharomyces cerevisiae, PIR2:S49764; Contains Immunoglobulins and major histocompatibility complex proteins signature. (AL022604) [Oryza sativa]

Seq. No.	399862
Seq. ID	LIB3431-028-P1-K1-D12
Method	BLASTX
NCBI GI	g82080
BLAST score	422
E value	1.0e-41
Match length	120
% identity	68
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	399863
Seq. ID	LIB3431-028-P1-K1-D2
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399864
Seq. ID	LIB3431-028-P1-K1-D4
Method	BLASTX
NCBI GI	g548605
BLAST score	435
E value	4.0e-43
Match length	112
% identity	80
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No.	399865
Seq. ID	LIB3431-028-P1-K1-D5
Method	BLASTN
NCBI GI	g3885891
BLAST score	119
E value	2.0e-60
Match length	156
% identity	100
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	399866
Seq. ID	LIB3431-028-P1-K1-D6
Method	BLASTX
NCBI GI	g2501189
BLAST score	164
E value	7.0e-12
Match length	33
% identity	91
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	399867
Seq. ID	LIB3431-028-P1-K1-D7
Method	BLASTX
NCBI GI	g3341692
BLAST score	324
E value	6.0e-30
Match length	141
% identity	54
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	399868
Seq. ID	LIB3431-028-P1-K1-D8
Method	BLASTX
NCBI GI	g2570511
BLAST score	660
E value	9.0e-72
Match length	138
% identity	97
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	399869
Seq. ID	LIB3431-028-P1-K1-D9
Method	BLASTX
NCBI GI	g1076800
BLAST score	561
E value	1.0e-57
Match length	121
% identity	85
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate

peroxidase [Zea mays]

Seq. No.	399870
Seq. ID	LIB3431-028-P1-K1-E1
Method	BLASTX
NCBI GI	g132105
BLAST score	699
E value	6.0e-74
Match length	149
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399871
Seq. ID	LIB3431-028-P1-K1-E2
Method	BLASTX
NCBI GI	g2633727
BLAST score	148
E value	2.0e-09
Match length	137
% identity	28
NCBI Description	(Z99111) ykrT [Bacillus subtilis]

Seq. No.	399872
Seq. ID	LIB3431-028-P1-K1-E3
Method	BLASTX
NCBI GI	g2570497
BLAST score	565
E value	3.0e-58
Match length	123
% identity	93
NCBI Description	(AF022731) H protein subunit of glycine decarboxylase [Oryza sativa]

Seq. No.	399873
Seq. ID	LIB3431-028-P1-K1-E4
Method	BLASTX
NCBI GI	g1661160
BLAST score	382
E value	8.0e-37
Match length	89
% identity	80
NCBI Description	(U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399874
Seq. ID	LIB3431-028-P1-K1-E5
Method	BLASTX
NCBI GI	g836954
BLAST score	452
E value	6.0e-45

Match length	154
% identity	60
NCBI Description	(U20948) receptor protein kinase [Ipomoea trifida]

Seq. No.	399875
Seq. ID	LIB3431-028-P1-K1-E6
Method	BLASTN
NCBI GI	g3789953
BLAST score	55
E value	5.0e-22
Match length	77
% identity	92
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	399876
Seq. ID	LIB3431-028-P1-K1-E7
Method	BLASTX
NCBI GI	g3560529
BLAST score	336
E value	2.0e-31
Match length	87
% identity	75
NCBI Description	(AF039598) light harvesting chlorophyll A/B binding protein [Prunus persica]

Seq. No.	399877
Seq. ID	LIB3431-028-P1-K1-E8
Method	BLASTX
NCBI GI	g2407281
BLAST score	349
E value	7.0e-33
Match length	65
% identity	100
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399878
Seq. ID	LIB3431-028-P1-K1-E9
Method	BLASTX
NCBI GI	g3329386
BLAST score	334
E value	4.0e-31
Match length	138
% identity	47
NCBI Description	(AF038958) synaptic glycoprotein SC2 spliced variant [Homo sapiens]

Seq. No.	399879
Seq. ID	LIB3431-028-P1-K1-F10
Method	BLASTX
NCBI GI	g2570511
BLAST score	644
E value	3.0e-67
Match length	136
% identity	95

NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	399880
Seq. ID	LIB3431-028-P1-K1-F11
Method	BLASTX
NCBI GI	g671740
BLAST score	547
E value	4.0e-56
Match length	101
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399881
Seq. ID	LIB3431-028-P1-K1-F2
Method	BLASTX
NCBI GI	g132672
BLAST score	459
E value	8.0e-46
Match length	97
% identity	95
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi_71224_pir__R5RZ14 ribosomal protein L14 - rice chloroplast >gi_12023_emb_CAA33932_ (X15901) ribosomal protein L14 [Oryza sativa] >gi_226644_prf__1603356BU ribosomal protein L14 [Oryza sativa]

Seq. No.	399882
Seq. ID	LIB3431-028-P1-K1-F3
Method	BLASTX
NCBI GI	g5442410
BLAST score	243
E value	2.0e-20
Match length	108
% identity	48
NCBI Description	(AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No.	399883
Seq. ID	LIB3431-028-P1-K1-F5
Method	BLASTX
NCBI GI	g548603
BLAST score	158
E value	1.0e-10
Match length	34
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	399884
Seq. ID	LIB3431-028-P1-K1-F6
Method	BLASTX
NCBI GI	g2673920
BLAST score	248
E value	5.0e-21
Match length	81

% identity	59
NCBI Description	(AC002561) similar to Drosophila couch potato protein [Arabidopsis thaliana]

Seq. No.	399885
Seq. ID	LIB3431-028-P1-K1-F8
Method	BLASTX
NCBI GI	g3033382
BLAST score	257
E value	4.0e-22
Match length	101
% identity	49
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	399886
Seq. ID	LIB3431-028-P1-K1-G1
Method	BLASTX
NCBI GI	g6006894
BLAST score	404
E value	2.0e-39
Match length	113
% identity	75
NCBI Description	(AC008153) unknown protein [Arabidopsis thaliana]

Seq. No.	399887
Seq. ID	LIB3431-028-P1-K1-G10
Method	BLASTX
NCBI GI	g168523
BLAST score	274
E value	3.0e-24
Match length	113
% identity	55
NCBI Description	(M31483) glyceraldehyde-3-phosphate dehydrogenase precursor [Zea mays]

Seq. No.	399888
Seq. ID	LIB3431-028-P1-K1-G12
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	7.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399889
Seq. ID	LIB3431-028-P1-K1-G2
Method	BLASTX
NCBI GI	g2293480
BLAST score	413
E value	1.0e-40
Match length	86
% identity	93
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	399890
Seq. ID	LIB3431-028-P1-K1-G3
Method	BLASTX
NCBI GI	g5902394
BLAST score	155
E value	3.0e-10
Match length	37
% identity	86
NCBI Description	(AC008148) Putative phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	399891
Seq. ID	LIB3431-028-P1-K1-G4
Method	BLASTX
NCBI GI	g3126854
BLAST score	645
E value	1.0e-67
Match length	121
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399892
Seq. ID	LIB3431-028-P1-K1-G5
Method	BLASTX
NCBI GI	g3668091
BLAST score	519
E value	8.0e-53
Match length	149
% identity	14
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399893
Seq. ID	LIB3431-028-P1-K1-G6
Method	BLASTX
NCBI GI	g2780746
BLAST score	717
E value	5.0e-76
Match length	138
% identity	100
NCBI Description	(AB005290) plastid RNA polymerase sigma factor [Oryza sativa]

Seq. No.	399894
Seq. ID	LIB3431-028-P1-K1-G8
Method	BLASTX
NCBI GI	g710308
BLAST score	699
E value	6.0e-74
Match length	153
% identity	88
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	399895
Seq. ID	LIB3431-028-P1-K1-G9
Method	BLASTX
NCBI GI	g4510406
BLAST score	174

E value	1.0e-12
Match length	104
% identity	48
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	399896
Seq. ID	LIB3431-028-P1-K1-H1
Method	BLASTX
NCBI GI	g586038
BLAST score	537
E value	6.0e-55
Match length	148
% identity	72
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN, CHLOROPLAST PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC) >gi_480296_pir__S36637 signal recognition particle 54CP protein precursor - Arabidopsis thaliana >gi_396701_emb_CAA79981.1_ (Z21970) 54CP [Arabidopsis thaliana]

Seq. No.	399897
Seq. ID	LIB3431-028-P1-K1-H10
Method	BLASTX
NCBI GI	g132105
BLAST score	609
E value	2.0e-63
Match length	131
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399898
Seq. ID	LIB3431-028-P1-K1-H11
Method	BLASTX
NCBI GI	g1170606
BLAST score	314
E value	8.0e-29
Match length	81
% identity	77
NCBI Description	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No.	399899
Seq. ID	LIB3431-028-P1-K1-H12

Method	BLASTN
NCBI GI	g20262
BLAST score	186
E value	1.0e-100
Match length	333
% identity	90
NCBI Description	O.sativa light-induced mRNA

Seq. No.	399900
Seq. ID	LIB3431-028-P1-K1-H2
Method	BLASTX
NCBI GI	g2499614
BLAST score	720
E value	2.0e-76
Match length	146
% identity	90
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43) >gi_481830_pir__S39559 mitogen-activated protein kinase 3 homolog ntf3 - common tobacco >gi_406751_emb_CAA49592_ (X69971) NTF3 [Nicotiana tabacum]

Seq. No.	399901
Seq. ID	LIB3431-028-P1-K1-H3
Method	BLASTX
NCBI GI	g4079798
BLAST score	565
E value	3.0e-58
Match length	109
% identity	100
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	399902
Seq. ID	LIB3431-028-P1-K1-H4
Method	BLASTX
NCBI GI	g1351270
BLAST score	542
E value	1.0e-55
Match length	113
% identity	93
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]

Seq. No.	399903
Seq. ID	LIB3431-028-P1-K1-H5
Method	BLASTX
NCBI GI	g871931
BLAST score	452
E value	6.0e-45
Match length	117
% identity	79
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	399904
Seq. ID	LIB3431-028-P1-K1-H6

Method	BLASTX
NCBI GI	g417260
BLAST score	323
E value	5.0e-30
Match length	106
% identity	64
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	399905
Seq. ID	LIB3431-028-P1-K1-H7
Method	BLASTX
NCBI GI	g1498315
BLAST score	364
E value	1.0e-34
Match length	135
% identity	54
NCBI Description	(U56419) IAP100 [Pisum sativum]

Seq. No.	399906
Seq. ID	LIB3431-028-P1-K1-H8
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	399907
Seq. ID	LIB3431-028-P1-K1-H9
Method	BLASTX
NCBI GI	g4079798
BLAST score	416
E value	7.0e-41
Match length	111
% identity	74
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	399908
Seq. ID	LIB3431-028-P1-N1-A1
Method	BLASTX
NCBI GI	g2887286
BLAST score	273
E value	3.0e-24
Match length	61
% identity	82
NCBI Description	(Z99530) H protein [Flaveria anomala]

Seq. No.	399909
Seq. ID	LIB3431-028-P1-N1-A10
Method	BLASTN
NCBI GI	g6041757
BLAST score	410
E value	0.0e+00

Match length	418
% identity	100
NCBI Description	Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence

Seq. No.	399910
Seq. ID	LIB3431-028-P1-N1-A11
Method	BLASTX
NCBI GI	g2462750
BLAST score	173
E value	2.0e-12
Match length	51
% identity	67
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	399911
Seq. ID	LIB3431-028-P1-N1-A12
Method	BLASTX
NCBI GI	g3643602
BLAST score	246
E value	7.0e-21
Match length	78
% identity	58
NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	399912
Seq. ID	LIB3431-028-P1-N1-A4
Method	BLASTX
NCBI GI	g3808101
BLAST score	344
E value	2.0e-32
Match length	79
% identity	90
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	399913
Seq. ID	LIB3431-028-P1-N1-A6
Method	BLASTX
NCBI GI	g1835731
BLAST score	286
E value	1.0e-25
Match length	65
% identity	85
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399914
Seq. ID	LIB3431-028-P1-N1-B1
Method	BLASTX
NCBI GI	g3345477
BLAST score	277
E value	1.0e-24
Match length	52
% identity	100
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	399915
Seq. ID	LIB3431-028-P1-N1-B12
Method	BLASTX
NCBI GI	g289920
BLAST score	298
E value	5.0e-27
Match length	58
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	399916
Seq. ID	LIB3431-028-P1-N1-B2
Method	BLASTX
NCBI GI	g6002102
BLAST score	213
E value	3.0e-17
Match length	47
% identity	83
NCBI Description	(AJ249833) Acyl-CoA binding protein (ACBP) [Digitalis lanata]

Seq. No.	399917
Seq. ID	LIB3431-028-P1-N1-B3
Method	BLASTN
NCBI GI	g20262
BLAST score	343
E value	0.0e+00
Match length	363
% identity	99
NCBI Description	O.sativa light-induced mRNA

Seq. No.	399918
Seq. ID	LIB3431-028-P1-N1-B4
Method	BLASTX
NCBI GI	g131176
BLAST score	275
E value	2.0e-24
Match length	57
% identity	93
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No.	399919
Seq. ID	LIB3431-028-P1-N1-C10
Method	BLASTX
NCBI GI	g1136416
BLAST score	144
E value	7.0e-09
Match length	51
% identity	57
NCBI Description	(D80000) similar to mitosis-specific chromosome segregation

protein SMC1 of S.cerevisiae. [Homo sapiens]

Seq. No.	399920
Seq. ID	LIB3431-028-P1-N1-C12
Method	BLASTX
NCBI GI	g134034
BLAST score	238
E value	5.0e-20
Match length	70
% identity	64
NCBI Description	30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5) (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1) >gi_279640_pir__R3SPS5 ribosomal protein CS-S22 precursor, chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270) chloroplast ribosomal protein S22 [Spinacia oleracea] >gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein [Spinacia oleracea]

Seq. No.	399921
Seq. ID	LIB3431-028-P1-N1-C4
Method	BLASTX
NCBI GI	g693920
BLAST score	327
E value	2.0e-30
Match length	64
% identity	98
NCBI Description	(U21113) chlorophyll a/b binding protein [Solanum tuberosum]

Seq. No.	399922
Seq. ID	LIB3431-028-P1-N1-C5
Method	BLASTX
NCBI GI	g1835731
BLAST score	330
E value	1.0e-30
Match length	74
% identity	86
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	399923
Seq. ID	LIB3431-028-P1-N1-C7
Method	BLASTX
NCBI GI	g132166
BLAST score	160
E value	6.0e-11
Match length	31
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	399924
Seq. ID	LIB3431-028-P1-N1-C8
Method	BLASTX

NCBI GI	g548770
BLAST score	321
E value	9.0e-30
Match length	63
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No.	399925
Seq. ID	LIB3431-028-P1-N1-D10
Method	BLASTN
NCBI GI	g433216
BLAST score	55
E value	4.0e-22
Match length	138
% identity	85
NCBI Description	Rice mRNA for ascorbate peroxidase (gene name SS622), partial cds

Seq. No.	399926
Seq. ID	LIB3431-028-P1-N1-D11
Method	BLASTN
NCBI GI	g5441876
BLAST score	357
E value	0.0e+00
Match length	439
% identity	97
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	399927
Seq. ID	LIB3431-028-P1-N1-D12
Method	BLASTX
NCBI GI	g115813
BLAST score	238
E value	5.0e-20
Match length	54
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	399928
Seq. ID	LIB3431-028-P1-N1-D2
Method	BLASTX
NCBI GI	g2072555
BLAST score	224
E value	3.0e-18
Match length	44
% identity	95
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399929
Seq. ID	LIB3431-028-P1-N1-D5

Method	BLASTX
NCBI GI	g3885892
BLAST score	261
E value	1.0e-22
Match length	53
% identity	98
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	399930
Seq. ID	LIB3431-028-P1-N1-D6
Method	BLASTX
NCBI GI	g2501190
BLAST score	198
E value	3.0e-15
Match length	57
% identity	74
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	399931
Seq. ID	LIB3431-028-P1-N1-D8
Method	BLASTX
NCBI GI	g115793
BLAST score	396
E value	2.0e-38
Match length	78
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]

Seq. No.	399932
Seq. ID	LIB3431-028-P1-N1-D9
Method	BLASTN
NCBI GI	g433216
BLAST score	165
E value	9.0e-88
Match length	171
% identity	99
NCBI Description	Rice mRNA for ascorbate peroxidase (gene name SS622), partial cds

Seq. No.	399933
Seq. ID	LIB3431-028-P1-N1-E1
Method	BLASTX
NCBI GI	g132105
BLAST score	301
E value	2.0e-27
Match length	57
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399934
Seq. ID	LIB3431-028-P1-N1-E3
Method	BLASTX
NCBI GI	g2499417
BLAST score	323
E value	5.0e-30
Match length	74
% identity	82
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1085826_pir__S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No.	399935
Seq. ID	LIB3431-028-P1-N1-E4
Method	BLASTX
NCBI GI	g289920
BLAST score	315
E value	5.0e-29
Match length	64
% identity	95
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	399936
Seq. ID	LIB3431-028-P1-N1-E5
Method	BLASTX
NCBI GI	g2129703
BLAST score	189
E value	3.0e-14
Match length	87
% identity	49
NCBI Description	receptor kinase - Arabidopsis thaliana >gi_2129704_pir__S71184 receptor kinase - Arabidopsis thaliana >gi_166692 (M80238) receptor kinase [Arabidopsis thaliana] >gi_445123_prf__1908429A receptor kinase [Arabidopsis thaliana]

Seq. No.	399937
Seq. ID	LIB3431-028-P1-N1-E6
Method	BLASTX
NCBI GI	g3789954
BLAST score	357
E value	7.0e-34
Match length	66
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399938

Seq. ID	LIB3431-028-P1-N1-E7
Method	BLASTN
NCBI GI	g3126853
BLAST score	171
E value	3.0e-91
Match length	209
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	399939
Seq. ID	LIB3431-028-P1-N1-E8
Method	BLASTN
NCBI GI	g218209
BLAST score	149
E value	4.0e-78
Match length	313
% identity	97
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	399940
Seq. ID	LIB3431-028-P1-N1-F10
Method	BLASTX
NCBI GI	g115794
BLAST score	611
E value	2.0e-63
Match length	127
% identity	91
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No.	399941
Seq. ID	LIB3431-028-P1-N1-F11
Method	BLASTX
NCBI GI	g132105
BLAST score	406
E value	1.0e-39
Match length	76
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399942
Seq. ID	LIB3431-028-P1-N1-F3

Method	BLASTX
NCBI GI	g5442410
BLAST score	182
E value	2.0e-13
Match length	78
% identity	50
NCBI Description	(AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No.	399943
Seq. ID	LIB3431-028-P1-N1-F5
Method	BLASTX
NCBI GI	g548603
BLAST score	158
E value	1.0e-10
Match length	34
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	399944
Seq. ID	LIB3431-028-P1-N1-F8
Method	BLASTX
NCBI GI	g3033382
BLAST score	359
E value	3.0e-34
Match length	76
% identity	86
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	399945
Seq. ID	LIB3431-028-P1-N1-F9
Method	BLASTX
NCBI GI	g1076724
BLAST score	374
E value	7.0e-36
Match length	72
% identity	94
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No.	399946
Seq. ID	LIB3431-028-P1-N1-G10
Method	BLASTX
NCBI GI	g120661
BLAST score	180
E value	4.0e-13
Match length	38
% identity	87
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	399947
Seq. ID	LIB3431-028-P1-N1-G12

Method	BLASTX
NCBI GI	g2072555
BLAST score	231
E value	5.0e-19
Match length	44
% identity	98
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	399948
Seq. ID	LIB3431-028-P1-N1-G2
Method	BLASTN
NCBI GI	g2331130
BLAST score	247
E value	1.0e-136
Match length	275
% identity	97
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No.	399949
Seq. ID	LIB3431-028-P1-N1-G3
Method	BLASTX
NCBI GI	g534982
BLAST score	340
E value	6.0e-32
Match length	100
% identity	68
NCBI Description	(X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No.	399950
Seq. ID	LIB3431-028-P1-N1-G4
Method	BLASTX
NCBI GI	g3126854
BLAST score	370
E value	2.0e-35
Match length	70
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	399951
Seq. ID	LIB3431-028-P1-N1-G5
Method	BLASTN
NCBI GI	g4680488
BLAST score	45
E value	5.0e-16
Match length	114
% identity	84
NCBI Description	Oryza sativa BAC clone 1.H19, complete sequence

Seq. No.	399952
Seq. ID	LIB3431-028-P1-N1-G6
Method	BLASTX
NCBI GI	g2780746
BLAST score	279
E value	8.0e-25

Match length	56
% identity	96
NCBI Description	(AB005290) plastid RNA polymerase sigma factor [Oryza sativa]

Seq. No.	399953
Seq. ID	LIB3431-028-P1-N1-G8
Method	BLASTX
NCBI GI	g710308
BLAST score	318
E value	2.0e-29
Match length	58
% identity	97
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	399954
Seq. ID	LIB3431-028-P1-N1-H10
Method	BLASTX
NCBI GI	g671740
BLAST score	508
E value	2.0e-51
Match length	91
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399955
Seq. ID	LIB3431-028-P1-N1-H11
Method	BLASTX
NCBI GI	g671740
BLAST score	256
E value	5.0e-22
Match length	55
% identity	89
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399956
Seq. ID	LIB3431-028-P1-N1-H12
Method	BLASTN
NCBI GI	g3063523
BLAST score	72
E value	2.0e-32
Match length	88
% identity	95
NCBI Description	Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	399957
Seq. ID	LIB3431-028-P1-N1-H2
Method	BLASTX
NCBI GI	g4914323
BLAST score	206
E value	4.0e-16
Match length	44
% identity	77
NCBI Description	(AC005489) F14N23.9 [Arabidopsis thaliana]

Seq. No.	399958
Seq. ID	LIB3431-028-P1-N1-H3
Method	BLASTX
NCBI GI	g4079798
BLAST score	183
E value	1.0e-13
Match length	34
% identity	100
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	399959
Seq. ID	LIB3431-028-P1-N1-H4
Method	BLASTX
NCBI GI	g1351270
BLAST score	149
E value	1.0e-09
Match length	30
% identity	100
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]

Seq. No.	399960
Seq. ID	LIB3431-028-P1-N1-H5
Method	BLASTX
NCBI GI	g871931
BLAST score	199
E value	2.0e-15
Match length	65
% identity	66
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	399961
Seq. ID	LIB3431-028-P1-N1-H6
Method	BLASTX
NCBI GI	g417260
BLAST score	247
E value	5.0e-21
Match length	65
% identity	71
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	399962
Seq. ID	LIB3431-028-P1-N1-H9
Method	BLASTX
NCBI GI	g4079798
BLAST score	268
E value	2.0e-23
Match length	52
% identity	98
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	399963
Seq. ID	LIB3431-029-P1-K1-A1
Method	BLASTN
NCBI GI	g2570516
BLAST score	55
E value	2.0e-22
Match length	125
% identity	87
NCBI Description	Oryza sativa thioredoxin F isoform mRNA, complete cds

Seq. No.	399964
Seq. ID	LIB3431-029-P1-K1-A10
Method	BLASTX
NCBI GI	g2982362
BLAST score	444
E value	4.0e-44
Match length	91
% identity	89
NCBI Description	(AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No.	399965
Seq. ID	LIB3431-029-P1-K1-A11
Method	BLASTN
NCBI GI	g473980
BLAST score	74
E value	1.0e-33
Match length	115
% identity	90
NCBI Description	Rice mRNA, partial homologous to glycine-rich protein gene

Seq. No.	399966
Seq. ID	LIB3431-029-P1-K1-A5
Method	BLASTX
NCBI GI	g2501189
BLAST score	383
E value	6.0e-37
Match length	111
% identity	69
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	399967
Seq. ID	LIB3431-029-P1-K1-A8
Method	BLASTX
NCBI GI	g3075488
BLAST score	270
E value	2.0e-47
Match length	117
% identity	82
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	399968
Seq. ID	LIB3431-029-P1-K1-B1
Method	BLASTX

NCBI GI	g3292814
BLAST score	540
E value	3.0e-55
Match length	144
% identity	72
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	399969
Seq. ID	LIB3431-029-P1-K1-B11
Method	BLASTX
NCBI GI	g2662343
BLAST score	639
E value	7.0e-67
Match length	124
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	399970
Seq. ID	LIB3431-029-P1-K1-B12
Method	BLASTX
NCBI GI	g5734634
BLAST score	286
E value	2.0e-25
Match length	83
% identity	60
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No.	399971
Seq. ID	LIB3431-029-P1-K1-B3
Method	BLASTX
NCBI GI	g1084455
BLAST score	527
E value	9.0e-54
Match length	115
% identity	88
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No.	399972
Seq. ID	LIB3431-029-P1-K1-B4
Method	BLASTX
NCBI GI	g132105
BLAST score	566
E value	2.0e-58
Match length	131
% identity	82
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399973
Seq. ID	LIB3431-029-P1-K1-B5
Method	BLASTX
NCBI GI	g3747044
BLAST score	157
E value	2.0e-10
Match length	51
% identity	59
NCBI Description	(AF093537) blue copper protein [Zea mays]

Seq. No.	399974
Seq. ID	LIB3431-029-P1-K1-B9
Method	BLASTX
NCBI GI	g115815
BLAST score	457
E value	8.0e-46
Match length	86
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN M9 PRECURSOR (LHCII TYPE I CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll a/b-binding protein precursor - maize >gi_22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]

Seq. No.	399975
Seq. ID	LIB3431-029-P1-K1-C2
Method	BLASTX
NCBI GI	g3288821
BLAST score	473
E value	2.0e-47
Match length	115
% identity	78
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	399976
Seq. ID	LIB3431-029-P1-K1-C7
Method	BLASTX
NCBI GI	g1001253
BLAST score	222
E value	5.0e-18
Match length	130
% identity	39
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	399977
Seq. ID	LIB3431-029-P1-K1-C8
Method	BLASTX
NCBI GI	g2407281
BLAST score	682
E value	6.0e-72
Match length	129
% identity	98
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399978
Seq. ID	LIB3431-029-P1-K1-C9
Method	BLASTX
NCBI GI	g2708741
BLAST score	391
E value	6.0e-38
Match length	122
% identity	61
NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399979
Seq. ID	LIB3431-029-P1-K1-D10
Method	BLASTX
NCBI GI	g5923674
BLAST score	468
E value	7.0e-47
Match length	135
% identity	65
NCBI Description	(AC009326) unknown protein [Arabidopsis thaliana]

Seq. No.	399980
Seq. ID	LIB3431-029-P1-K1-D12
Method	BLASTN
NCBI GI	g6063530
BLAST score	310
E value	1.0e-174
Match length	321
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	399981
Seq. ID	LIB3431-029-P1-K1-D2
Method	BLASTX
NCBI GI	g464986
BLAST score	491
E value	2.0e-49
Match length	95
% identity	92
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	399982
Seq. ID	LIB3431-029-P1-K1-D3
Method	BLASTX
NCBI GI	g482311
BLAST score	707
E value	8.0e-75

Match length	142
% identity	97
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	399983
Seq. ID	LIB3431-029-P1-K1-D8
Method	BLASTX
NCBI GI	g132105
BLAST score	565
E value	3.0e-58
Match length	124
% identity	85
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399984
Seq. ID	LIB3431-029-P1-K1-E10
Method	BLASTX
NCBI GI	g132105
BLAST score	609
E value	2.0e-63
Match length	131
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	399985
Seq. ID	LIB3431-029-P1-K1-E11
Method	BLASTX
NCBI GI	g1617206
BLAST score	190
E value	6.0e-23
Match length	74
% identity	76
NCBI Description	(Z72489) CP12 [Pisum sativum]

Seq. No.	399986
Seq. ID	LIB3431-029-P1-K1-E12
Method	BLASTX
NCBI GI	g2407281
BLAST score	497

E value	2.0e-50
Match length	98
% identity	98
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	399987
Seq. ID	LIB3431-029-P1-K1-E3
Method	BLASTX
NCBI GI	g5262204
BLAST score	288
E value	9.0e-26
Match length	75
% identity	77
NCBI Description	(AL080252) putative protein [Arabidopsis thaliana]

Seq. No.	399988
Seq. ID	LIB3431-029-P1-K1-E8
Method	BLASTX
NCBI GI	g2624328
BLAST score	489
E value	2.0e-49
Match length	115
% identity	88
NCBI Description	(AJ002894) OsGRP2 [Oryza sativa]

Seq. No.	399989
Seq. ID	LIB3431-029-P1-K1-F1
Method	BLASTX
NCBI GI	g2501190
BLAST score	606
E value	5.0e-63
Match length	142
% identity	85
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	399990
Seq. ID	LIB3431-029-P1-K1-F10
Method	BLASTX
NCBI GI	g2306981
BLAST score	277
E value	1.0e-24
Match length	54
% identity	89
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No.	399991
Seq. ID	LIB3431-029-P1-K1-F11
Method	BLASTX
NCBI GI	g4567279
BLAST score	412
E value	3.0e-40
Match length	138
% identity	60

NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	399992
Seq. ID	LIB3431-029-P1-K1-F12
Method	BLASTX
NCBI GI	g3063447
BLAST score	244
E value	2.0e-33
Match length	155
% identity	24
NCBI Description	(AC003981) F22O13.9 [Arabidopsis thaliana]

Seq. No.	399993
Seq. ID	LIB3431-029-P1-K1-F2
Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	1.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	399994
Seq. ID	LIB3431-029-P1-K1-F3
Method	BLASTN
NCBI GI	g2407266
BLAST score	102
E value	3.0e-50
Match length	158
% identity	91
NCBI Description	Oryza sativa low molecular early light-inducible protein mRNA, complete cds

Seq. No.	399995
Seq. ID	LIB3431-029-P1-K1-F4
Method	BLASTX
NCBI GI	g729478
BLAST score	230
E value	5.0e-19
Match length	120
% identity	42
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	399996
Seq. ID	LIB3431-029-P1-K1-F5
Method	BLASTX
NCBI GI	g3789954
BLAST score	654
E value	1.0e-68
Match length	121
% identity	100

NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	399997
Seq. ID	LIB3431-029-P1-K1-F6
Method	BLASTX
NCBI GI	g2570511
BLAST score	514
E value	2.0e-52
Match length	98
% identity	99
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	399998
Seq. ID	LIB3431-029-P1-K1-F8
Method	BLASTX
NCBI GI	g131176
BLAST score	322
E value	9.0e-30
Match length	62
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No.	399999
Seq. ID	LIB3431-029-P1-K1-F9
Method	BLASTX
NCBI GI	g3850621
BLAST score	450
E value	9.0e-45
Match length	127
% identity	69
NCBI Description	(Y15382) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	400000
Seq. ID	LIB3431-029-P1-K1-G10
Method	BLASTX
NCBI GI	g3075488
BLAST score	713
E value	1.0e-75
Match length	143
% identity	97
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	400001
Seq. ID	LIB3431-029-P1-K1-G11
Method	BLASTX
NCBI GI	g4406764
BLAST score	293
E value	3.0e-26
Match length	80

% identity	64
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No.	400002
Seq. ID	LIB3431-029-P1-K1-G12
Method	BLASTN
NCBI GI	g20262
BLAST score	166
E value	3.0e-88
Match length	274
% identity	91
NCBI Description	O.sativa light-induced mRNA

Seq. No.	400003
Seq. ID	LIB3431-029-P1-K1-G2
Method	BLASTX
NCBI GI	g115787
BLAST score	545
E value	7.0e-56
Match length	104
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	400004
Seq. ID	LIB3431-029-P1-K1-G6
Method	BLASTX
NCBI GI	g2982243
BLAST score	405
E value	2.0e-39
Match length	137
% identity	58
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	400005
Seq. ID	LIB3431-029-P1-K1-G7
Method	BLASTX
NCBI GI	g548604
BLAST score	158
E value	1.0e-10
Match length	59
% identity	59
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_1076728_pir__S51813 photosystem-I PSI-F chain precursor - barley >gi_469560 (U08135) photosystem-I PSI-F subunit precursor [Hordeum vulgare]

Seq. No.	400006
Seq. ID	LIB3431-029-P1-K1-G8
Method	BLASTX
NCBI GI	g1835731
BLAST score	391

E value	8.0e-38
Match length	86
% identity	86
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	400007
Seq. ID	LIB3431-029-P1-K1-G9
Method	BLASTX
NCBI GI	g3618310
BLAST score	461
E value	5.0e-46
Match length	123
% identity	72
NCBI Description	(AB001883) zinc finger protein [Oryza sativa]

Seq. No.	400008
Seq. ID	LIB3431-029-P1-K1-H1
Method	BLASTX
NCBI GI	g3980400
BLAST score	253
E value	1.0e-21
Match length	134
% identity	42
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	400009
Seq. ID	LIB3431-029-P1-K1-H10
Method	BLASTN
NCBI GI	g3885887
BLAST score	265
E value	1.0e-147
Match length	265
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	400010
Seq. ID	LIB3431-029-P1-K1-H11
Method	BLASTX
NCBI GI	g3126854
BLAST score	581
E value	3.0e-60
Match length	109
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	400011
Seq. ID	LIB3431-029-P1-K1-H2
Method	BLASTX
NCBI GI	g2191138
BLAST score	249
E value	3.0e-21
Match length	76
% identity	68
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No.	400012
Seq. ID	LIB3431-029-P1-K1-H3
Method	BLASTX
NCBI GI	g132105
BLAST score	546
E value	6.0e-56
Match length	122
% identity	84
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400013
Seq. ID	LIB3431-029-P1-K1-H5
Method	BLASTN
NCBI GI	g168500
BLAST score	62
E value	3.0e-26
Match length	118
% identity	88
NCBI Description	Maize (Zea mays) histone H4 gene (H4C14), complete cds

Seq. No.	400014
Seq. ID	LIB3431-029-P1-K1-H7
Method	BLASTX
NCBI GI	g5926740
BLAST score	455
E value	2.0e-45
Match length	89
% identity	98
NCBI Description	(AB025310) asparaginyl endopeptidase [Oryza sativa]

Seq. No.	400015
Seq. ID	LIB3431-029-P1-N1-A10
Method	BLASTX
NCBI GI	g2982362
BLAST score	306
E value	6.0e-28
Match length	63
% identity	89
NCBI Description	(AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No.	400016
Seq. ID	LIB3431-029-P1-N1-A2
Method	BLASTX
NCBI GI	g4469021
BLAST score	271
E value	6.0e-24
Match length	75
% identity	71

NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	400017
Seq. ID	LIB3431-029-P1-N1-A3
Method	BLASTX
NCBI GI	g4585992
BLAST score	195
E value	6.0e-15
Match length	49
% identity	78
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	400018
Seq. ID	LIB3431-029-P1-N1-A7
Method	BLASTX
NCBI GI	g82167
BLAST score	152
E value	6.0e-10
Match length	27
% identity	100
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A, chloroplast - common tobacco (fragment)

Seq. No.	400019
Seq. ID	LIB3431-029-P1-N1-A8
Method	BLASTX
NCBI GI	g3075488
BLAST score	143
E value	6.0e-09
Match length	29
% identity	90
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	400020
Seq. ID	LIB3431-029-P1-N1-A9
Method	BLASTN
NCBI GI	g3075487
BLAST score	37
E value	1.0e-11
Match length	133
% identity	82
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	400021
Seq. ID	LIB3431-029-P1-N1-B1
Method	BLASTX
NCBI GI	g3292814
BLAST score	174
E value	2.0e-12
Match length	43
% identity	79
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	400022
Seq. ID	LIB3431-029-P1-N1-B11

Method	BLASTN
NCBI GI	g2662344
BLAST score	319
E value	1.0e-179
Match length	323
% identity	100
NCBI Description	Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No.	400023
Seq. ID	LIB3431-029-P1-N1-B2
Method	BLASTX
NCBI GI	g3183079
BLAST score	180
E value	2.0e-15
Match length	62
% identity	66
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]

Seq. No.	400024
Seq. ID	LIB3431-029-P1-N1-B3
Method	BLASTN
NCBI GI	g600766
BLAST score	329
E value	0.0e+00
Match length	368
% identity	98
NCBI Description	Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds

Seq. No.	400025
Seq. ID	LIB3431-029-P1-N1-B4
Method	BLASTN
NCBI GI	g218207
BLAST score	135
E value	6.0e-70
Match length	199
% identity	92
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No.	400026
Seq. ID	LIB3431-029-P1-N1-B6
Method	BLASTX
NCBI GI	g1076308
BLAST score	156
E value	2.0e-10
Match length	74
% identity	45
NCBI Description	RNA-binding protein cp33 precursor - Arabidopsis thaliana >gi_681910_dbj_BAA06522_ (D31714) cp33 [Arabidopsis thaliana] >gi_4886289_emb_CAB43448.1_ (AL050300) RNA-binding protein cp33 precursor [Arabidopsis thaliana]

Seq. No.	400027
Seq. ID	LIB3431-029-P1-N1-B9

Method	BLASTN
NCBI GI	g20181
BLAST score	66
E value	1.0e-28
Match length	126
% identity	88
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	400028
Seq. ID	LIB3431-029-P1-N1-C3
Method	BLASTN
NCBI GI	g218171
BLAST score	166
E value	3.0e-88
Match length	242
% identity	93
NCBI Description	Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No.	400029
Seq. ID	LIB3431-029-P1-N1-C4
Method	BLASTN
NCBI GI	g218154
BLAST score	76
E value	1.0e-34
Match length	138
% identity	99
NCBI Description	Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No.	400030
Seq. ID	LIB3431-029-P1-N1-C5
Method	BLASTN
NCBI GI	g218154
BLAST score	84
E value	2.0e-39
Match length	124
% identity	92
NCBI Description	Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No.	400031
Seq. ID	LIB3431-029-P1-N1-C8
Method	BLASTN
NCBI GI	g218209
BLAST score	155
E value	1.0e-81
Match length	338
% identity	96
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	400032
Seq. ID	LIB3431-029-P1-N1-D1

Method	BLASTN
NCBI GI	g3789953
BLAST score	214
E value	1.0e-117
Match length	293
% identity	94
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	400033
Seq. ID	LIB3431-029-P1-N1-D12
Method	BLASTN
NCBI GI	g6063530
BLAST score	115
E value	7.0e-58
Match length	299
% identity	83
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No.	400034
Seq. ID	LIB3431-029-P1-N1-D2
Method	BLASTX
NCBI GI	g464986
BLAST score	351
E value	3.0e-33
Match length	70
% identity	91
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	400035
Seq. ID	LIB3431-029-P1-N1-D3
Method	BLASTX
NCBI GI	g482311
BLAST score	238
E value	5.0e-20
Match length	48
% identity	98
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oxyza sativa]

Seq. No.	400036
Seq. ID	LIB3431-029-P1-N1-D5
Method	BLASTN
NCBI GI	g4079797
BLAST score	125

E value	6.0e-64
Match length	243
% identity	100
NCBI Description	Oryza sativa 23 kDa polypeptide of photosystem II mRNA, complete cds

Seq. No.	400037
Seq. ID	LIB3431-029-P1-N1-D6
Method	BLASTX
NCBI GI	g2570511
BLAST score	163
E value	1.0e-20
Match length	62
% identity	79
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	400038
Seq. ID	LIB3431-029-P1-N1-D8
Method	BLASTX
NCBI GI	g132105
BLAST score	161
E value	5.0e-11
Match length	34
% identity	91
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400039
Seq. ID	LIB3431-029-P1-N1-D9
Method	BLASTX
NCBI GI	g4038034
BLAST score	142
E value	8.0e-09
Match length	42
% identity	67
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	400040
Seq. ID	LIB3431-029-P1-N1-E10
Method	BLASTX
NCBI GI	g671740
BLAST score	164
E value	2.0e-11
Match length	33
% identity	94
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	400041
Seq. ID	LIB3431-029-P1-N1-E4

Method	BLASTX
NCBI GI	g5733874
BLAST score	225
E value	2.0e-18
Match length	75
% identity	53
NCBI Description	(AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No.	400042
Seq. ID	LIB3431-029-P1-N1-E5
Method	BLASTX
NCBI GI	g2407279
BLAST score	182
E value	1.0e-13
Match length	37
% identity	100
NCBI Description	(AF017362) aldolase [Oryza sativa]

Seq. No.	400043
Seq. ID	LIB3431-029-P1-N1-E6
Method	BLASTN
NCBI GI	g218171
BLAST score	84
E value	2.0e-39
Match length	239
% identity	85
NCBI Description	Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No.	400044
Seq. ID	LIB3431-029-P1-N1-E7
Method	BLASTX
NCBI GI	g3980415
BLAST score	196
E value	4.0e-15
Match length	75
% identity	53
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	400045
Seq. ID	LIB3431-029-P1-N1-E8
Method	BLASTN
NCBI GI	g2624327
BLAST score	210
E value	1.0e-114
Match length	222
% identity	99
NCBI Description	Oryza sativa mRNA for glycine rich RNA-binding protein 2 (OsGRP2)

Seq. No.	400046
Seq. ID	LIB3431-029-P1-N1-F10
Method	BLASTX
NCBI GI	g1076724
BLAST score	163

E value	3.0e-11
Match length	34
% identity	82
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No.	400047
Seq. ID	LIB3431-029-P1-N1-F4
Method	BLASTX
NCBI GI	g729477
BLAST score	294
E value	1.0e-26
Match length	58
% identity	90
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_320548_pir__A44974 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - common ice plant >gi_167256 (M25528) ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1) [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A ferredoxin NADP reductase [Mesembryanthemum crystallinum]

Seq. No.	400048
Seq. ID	LIB3431-029-P1-N1-F5
Method	BLASTN
NCBI GI	g3789953
BLAST score	301
E value	1.0e-169
Match length	321
% identity	98
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	400049
Seq. ID	LIB3431-029-P1-N1-F6
Method	BLASTX
NCBI GI	g2570511
BLAST score	163
E value	8.0e-22
Match length	63
% identity	81
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	400050
Seq. ID	LIB3431-029-P1-N1-F8
Method	BLASTN
NCBI GI	g19086
BLAST score	51
E value	1.0e-19
Match length	75
% identity	92
NCBI Description	Hordeum vulgare pot. psaE mRNA

Seq. No.	400051
Seq. ID	LIB3431-029-P1-N1-F9
Method	BLASTX

NCBI GI	g3850621
BLAST score	177
E value	7.0e-13
Match length	39
% identity	87
NCBI Description	(Y15382) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	400052
Seq. ID	LIB3431-029-P1-N1-G1
Method	BLASTX
NCBI GI	g115813
BLAST score	233
E value	2.0e-19
Match length	53
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	400053
Seq. ID	LIB3431-029-P1-N1-G10
Method	BLASTN
NCBI GI	g3075487
BLAST score	75
E value	5.0e-34
Match length	94
% identity	97
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	400054
Seq. ID	LIB3431-029-P1-N1-G12
Method	BLASTN
NCBI GI	g20262
BLAST score	173
E value	2.0e-92
Match length	345
% identity	88
NCBI Description	O.sativa light-induced mRNA

Seq. No.	400055
Seq. ID	LIB3431-029-P1-N1-G2
Method	BLASTX
NCBI GI	g3036946
BLAST score	314
E value	6.0e-29
Match length	61
% identity	98
NCBI Description	(AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	400056
Seq. ID	LIB3431-029-P1-N1-G3
Method	BLASTN
NCBI GI	g2072554
BLAST score	142

E value	4.0e-74
Match length	194
% identity	93
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	400057
Seq. ID	LIB3431-029-P1-N1-G6
Method	BLASTX
NCBI GI	g2982243
BLAST score	294
E value	2.0e-26
Match length	83
% identity	66
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	400058
Seq. ID	LIB3431-029-P1-N1-G7
Method	BLASTX
NCBI GI	g3885892
BLAST score	242
E value	2.0e-20
Match length	53
% identity	92
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	400059
Seq. ID	LIB3431-029-P1-N1-G8
Method	BLASTX
NCBI GI	g1835731
BLAST score	280
E value	6.0e-25
Match length	64
% identity	84
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	400060
Seq. ID	LIB3431-029-P1-N1-G9
Method	BLASTN
NCBI GI	g3618309
BLAST score	270
E value	1.0e-150
Match length	306
% identity	97
NCBI Description	Oryza sativa mRNA for zinc finger protein, complete cds, clone:E10707

Seq. No.	400061
Seq. ID	LIB3431-029-P1-N1-H11
Method	BLASTN
NCBI GI	g3126853
BLAST score	155
E value	6.0e-82
Match length	197
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete

cds

Seq. No.	400062
Seq. ID	LIB3431-029-P1-N1-H2
Method	BLASTX
NCBI GI	g687677
BLAST score	234
E value	1.0e-19
Match length	58
% identity	76
NCBI Description	(U19925) unknown [Arabidopsis thaliana]

Seq. No.	400063
Seq. ID	LIB3431-029-P1-N1-H3
Method	BLASTX
NCBI GI	g347451
BLAST score	173
E value	2.0e-12
Match length	33
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	400064
Seq. ID	LIB3431-029-P1-N1-H5
Method	BLASTX
NCBI GI	g223793
BLAST score	190
E value	2.0e-14
Match length	37
% identity	100
NCBI Description	histone H4 [Physarum polycephalum]

Seq. No.	400065
Seq. ID	LIB3431-029-P1-N1-H6
Method	BLASTN
NCBI GI	g20177
BLAST score	137
E value	3.0e-71
Match length	172
% identity	95
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	400066
Seq. ID	LIB3431-029-P1-N1-H7
Method	BLASTN
NCBI GI	g5926739
BLAST score	369
E value	0.0e+00
Match length	393
% identity	98
NCBI Description	Oryza sativa mRNA for asparaginyl endopeptidase, complete cds

Seq. No.	400067
Seq. ID	LIB3431-029-P1-N1-H9

Method	BLASTX
NCBI GI	g5103833
BLAST score	156
E value	1.0e-10
Match length	43
% identity	70
NCBI Description	(AC007591) ESTs gb_R65145, gb_N96612 and gb_R90096 come from this gene. [Arabidopsis thaliana]

Seq. No.	400068
Seq. ID	LIB3431-030-P1-K2-A11
Method	BLASTX
NCBI GI	g4586039
BLAST score	419
E value	4.0e-41
Match length	130
% identity	62
NCBI Description	(AC007109) unknown protein [Arabidopsis thaliana]

Seq. No.	400069
Seq. ID	LIB3431-030-P1-K2-A3
Method	BLASTN
NCBI GI	g4206059
BLAST score	33
E value	3.0e-09
Match length	33
% identity	100
NCBI Description	Homo sapiens map 20q13.3; 51cR from D20S173 repeat region, complete sequence

Seq. No.	400070
Seq. ID	LIB3431-030-P1-K2-A5
Method	BLASTN
NCBI GI	g5922603
BLAST score	84
E value	3.0e-39
Match length	107
% identity	95
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No.	400071
Seq. ID	LIB3431-030-P1-K2-A6
Method	BLASTX
NCBI GI	g729479
BLAST score	473
E value	1.0e-47
Match length	105
% identity	84
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No.	400072
Seq. ID	LIB3431-030-P1-K2-A7
Method	BLASTX
NCBI GI	g871931
BLAST score	204
E value	3.0e-16

Match length	66
% identity	68
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	400073
Seq. ID	LIB3431-030-P1-K2-A9
Method	BLASTX
NCBI GI	g671740
BLAST score	638
E value	9.0e-67
Match length	119
% identity	99
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	400074
Seq. ID	LIB3431-030-P1-K2-B1
Method	BLASTN
NCBI GI	g2407280
BLAST score	43
E value	2.0e-15
Match length	90
% identity	88
NCBI Description	Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	400075
Seq. ID	LIB3431-030-P1-K2-B2
Method	BLASTX
NCBI GI	g2832681
BLAST score	414
E value	2.0e-40
Match length	89
% identity	82
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	400076
Seq. ID	LIB3431-030-P1-K2-B3
Method	BLASTN
NCBI GI	g6103440
BLAST score	87
E value	1.0e-41
Match length	95
% identity	98
NCBI Description	Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds

Seq. No.	400077
Seq. ID	LIB3431-030-P1-K2-B4
Method	BLASTN
NCBI GI	g5734616
BLAST score	227
E value	1.0e-125
Match length	235
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No.	400078
Seq. ID	LIB3431-030-P1-K2-B8
Method	BLASTX
NCBI GI	g132105
BLAST score	547
E value	4.0e-56
Match length	120
% identity	86
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400079
Seq. ID	LIB3431-030-P1-K2-C10
Method	BLASTX
NCBI GI	g4678303
BLAST score	184
E value	1.0e-13
Match length	52
% identity	63
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	400080
Seq. ID	LIB3431-030-P1-K2-C11
Method	BLASTN
NCBI GI	g19086
BLAST score	78
E value	1.0e-35
Match length	126
% identity	91
NCBI Description	Hordeum vulgare pot. psaE mRNA

Seq. No.	400081
Seq. ID	LIB3431-030-P1-K2-C2
Method	BLASTN
NCBI GI	g19094
BLAST score	54
E value	1.0e-21
Match length	66
% identity	95
NCBI Description	H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No.	400082
Seq. ID	LIB3431-030-P1-K2-C4
Method	BLASTX
NCBI GI	g4678303
BLAST score	205
E value	4.0e-16
Match length	57
% identity	65
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	400083
Seq. ID	LIB3431-030-P1-K2-C6
Method	BLASTX
NCBI GI	g2501189
BLAST score	618
E value	2.0e-64
Match length	129
% identity	92
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	400084
Seq. ID	LIB3431-030-P1-K2-C7
Method	BLASTX
NCBI GI	g4960154
BLAST score	316
E value	3.0e-29
Match length	97
% identity	65
NCBI Description	(AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]

Seq. No.	400085
Seq. ID	LIB3431-030-P1-K2-C8
Method	BLASTX
NCBI GI	g3776581
BLAST score	335
E value	3.0e-31
Match length	100
% identity	61
NCBI Description	(AC005388) Similar to Beta integral membrane protein homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	400086
Seq. ID	LIB3431-030-P1-K2-C9
Method	BLASTN
NCBI GI	g6016845
BLAST score	271
E value	1.0e-151
Match length	285
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	400087
Seq. ID	LIB3431-030-P1-K2-D10
Method	BLASTX
NCBI GI	g3126854
BLAST score	650
E value	3.0e-68
Match length	124
% identity	98
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	400088

Seq. ID	LIB3431-030-P1-K2-D11
Method	BLASTX
NCBI GI	g1488297
BLAST score	516
E value	2.0e-52
Match length	129
% identity	84
NCBI Description	(U63530) osRAD23 [Oryza sativa]

Seq. No.	400089
Seq. ID	LIB3431-030-P1-K2-D2
Method	BLASTX
NCBI GI	g3121731
BLAST score	642
E value	3.0e-67
Match length	143
% identity	83
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_2145473_emb_CAA65735_ (X97012) aconitate hydratase [Solanum tuberosum]

Seq. No.	400090
Seq. ID	LIB3431-030-P1-K2-D3
Method	BLASTX
NCBI GI	g132105
BLAST score	149
E value	4.0e-10
Match length	31
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400091
Seq. ID	LIB3431-030-P1-K2-D4
Method	BLASTX
NCBI GI	g671740
BLAST score	554
E value	6.0e-57
Match length	109
% identity	95
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	400092
Seq. ID	LIB3431-030-P1-K2-D6
Method	BLASTX
NCBI GI	g1654144
BLAST score	292
E value	4.0e-37
Match length	103

% identity	74
NCBI Description	(U38471) small GTP-binding protein rab [Brassica rapa]

Seq. No.	400093
Seq. ID	LIB3431-030-P1-K2-D7
Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	7.0e-11
Match length	35
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	400094
Seq. ID	LIB3431-030-P1-K2-E10
Method	BLASTX
NCBI GI	g3023816
BLAST score	584
E value	2.0e-60
Match length	132
% identity	86
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	400095
Seq. ID	LIB3431-030-P1-K2-E12
Method	BLASTX
NCBI GI	g1709620
BLAST score	505
E value	3.0e-51
Match length	116
% identity	82
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_508975 (U11496) protein disulfide isomerase [Triticum aestivum] >gi_1094851_prf__2106410A protein disulfide isomerase [Triticum aestivum]

Seq. No.	400096
Seq. ID	LIB3431-030-P1-K2-E2
Method	BLASTN
NCBI GI	g167086
BLAST score	69
E value	1.0e-30
Match length	167
% identity	85
NCBI Description	Hordeum vulgare photosystem I protein (PSI-L) mRNA, complete cds

Seq. No.	400097
Seq. ID	LIB3431-030-P1-K2-E4
Method	BLASTX
NCBI GI	g132105
BLAST score	628
E value	7.0e-72
Match length	135
% identity	99

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400098
Seq. ID	LIB3431-030-P1-K2-E6
Method	BLASTX
NCBI GI	g132105
BLAST score	737
E value	3.0e-78
Match length	163
% identity	86
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400099
Seq. ID	LIB3431-030-P1-K2-E7
Method	BLASTX
NCBI GI	g2583108
BLAST score	351
E value	4.0e-33
Match length	144
% identity	49
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	400100
Seq. ID	LIB3431-030-P1-K2-E8
Method	BLASTX
NCBI GI	g5802606
BLAST score	704
E value	2.0e-74
Match length	147
% identity	92
NCBI Description	(AF174486) methylenetetrahydrofolate reductase [Zea mays]

Seq. No.	400101
Seq. ID	LIB3431-030-P1-K2-E9
Method	BLASTX
NCBI GI	g3183079
BLAST score	157
E value	9.0e-11
Match length	86
% identity	47
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]

Seq. No.	400102
Seq. ID	LIB3431-030-P1-K2-F1
Method	BLASTX
NCBI GI	g133999
BLAST score	489
E value	2.0e-49
Match length	99
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_70904_pir__R3RZ7 ribosomal protein S7 - rice chloroplast >gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_226657_prf__1603356CH ribosomal protein S7 [Oryza sativa]

Seq. No.	400103
Seq. ID	LIB3431-030-P1-K2-F10
Method	BLASTX
NCBI GI	g132105
BLAST score	706
E value	1.0e-74
Match length	131
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400104
Seq. ID	LIB3431-030-P1-K2-F12
Method	BLASTX
NCBI GI	g1519251
BLAST score	443
E value	6.0e-44
Match length	111
% identity	83
NCBI Description	(U65957) GF14-c protein [Oryza sativa]

Seq. No.	400105
Seq. ID	LIB3431-030-P1-K2-F2
Method	BLASTN
NCBI GI	g3789951
BLAST score	71
E value	3.0e-32
Match length	91
% identity	95
NCBI Description	Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	400106
Seq. ID	LIB3431-030-P1-K2-F4
Method	BLASTX
NCBI GI	g2570523
BLAST score	567
E value	2.0e-58
Match length	128
% identity	80
NCBI Description	(AF022873) inorganic phosphate transporter [Lycopersicon esculentum]

Seq. No.	400107
Seq. ID	LIB3431-030-P1-K2-F5
Method	BLASTX
NCBI GI	g134944
BLAST score	718
E value	6.0e-82
Match length	179
% identity	84
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_100502_pir__A39173 acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) precursor - safflower >gi_167197 (M61109) stearoyl-acyl-carrier protein desaturase [Carthamus tinctorius]

Seq. No.	400108
Seq. ID	LIB3431-030-P1-K2-F6
Method	BLASTX
NCBI GI	g3777598
BLAST score	314
E value	6.0e-29
Match length	104
% identity	67
NCBI Description	(AF095707) 30S ribosomal protein S17 [Oryza sativa]

Seq. No.	400109
Seq. ID	LIB3431-030-P1-K2-F7
Method	BLASTX
NCBI GI	g3789952
BLAST score	279
E value	1.0e-45
Match length	102
% identity	96
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	400110
Seq. ID	LIB3431-030-P1-K2-F8
Method	BLASTX
NCBI GI	g3024697
BLAST score	274
E value	2.0e-24
Match length	91
% identity	65
NCBI Description	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)

(CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis thaliana]

Seq. No.	400111
Seq. ID	LIB3431-030-P1-K2-F9
Method	BLASTN
NCBI GI	g20177
BLAST score	40
E value	2.0e-13
Match length	94
% identity	88
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	400112
Seq. ID	LIB3431-030-P1-K2-G1
Method	BLASTX
NCBI GI	g1084455
BLAST score	517
E value	1.0e-52
Match length	116
% identity	85
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No.	400113
Seq. ID	LIB3431-030-P1-K2-G11
Method	BLASTX
NCBI GI	g4185499
BLAST score	167
E value	1.0e-11
Match length	65
% identity	49
NCBI Description	(AF096095) fertilization-independent seed 2 protein [Arabidopsis thaliana] >gi_4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No.	400114
Seq. ID	LIB3431-030-P1-K2-G5
Method	BLASTX
NCBI GI	g1353352
BLAST score	527
E value	1.0e-53
Match length	150
% identity	70
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	400115
Seq. ID	LIB3431-030-P1-K2-G6
Method	BLASTX
NCBI GI	g2316016
BLAST score	198
E value	1.0e-18
Match length	86
% identity	60

NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 400116
Seq. ID LIB3431-030-P1-K2-G9
Method BLASTX
NCBI GI g132105
BLAST score 179
E value 2.0e-13
Match length 49
% identity 69
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400117
Seq. ID LIB3431-030-P1-K2-H1
Method BLASTN
NCBI GI g1398998
BLAST score 190
E value 1.0e-102
Match length 275
% identity 100
NCBI Description Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II, complete cds

Seq. No. 400118
Seq. ID LIB3431-030-P1-K2-H12
Method BLASTX
NCBI GI g2407279
BLAST score 319
E value 9.0e-30
Match length 65
% identity 100
NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 400119
Seq. ID LIB3431-030-P1-K2-H2
Method BLASTX
NCBI GI g115787
BLAST score 535
E value 8.0e-55
Match length 121
% identity 86
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 400120
Seq. ID LIB3431-030-P1-K2-H3

Method	BLASTN
NCBI GI	g20262
BLAST score	306
E value	1.0e-172
Match length	341
% identity	98
NCBI Description	O.sativa light-induced mRNA

Seq. No.	400121
Seq. ID	LIB3431-030-P1-K2-H5
Method	BLASTX
NCBI GI	g2130127
BLAST score	322
E value	1.0e-29
Match length	70
% identity	86
NCBI Description	ferritin 1 precursor - maize >gi_1103628_emb_CAA58146_ (X83076) ferritin [Zea mays]

Seq. No.	400122
Seq. ID	LIB3431-030-P1-K2-H6
Method	BLASTX
NCBI GI	g4079798
BLAST score	214
E value	1.0e-17
Match length	43
% identity	98
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	400123
Seq. ID	LIB3431-030-P1-K2-H7
Method	BLASTX
NCBI GI	g2407281
BLAST score	399
E value	8.0e-39
Match length	112
% identity	71
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	400124
Seq. ID	LIB3431-030-P1-K2-H9
Method	BLASTX
NCBI GI	g1262847
BLAST score	166
E value	1.0e-11
Match length	42
% identity	71
NCBI Description	(U51632) type 2 light-harvesting chlorophyll a/b-binding polypeptide [Pinus palustris]

Seq. No.	400125
Seq. ID	LIB3431-030-P1-N1-A1
Method	BLASTN
NCBI GI	g169820
BLAST score	277

E value	1.0e-154
Match length	345
% identity	96
NCBI Description	Oryza sativa triosephosphate isomerase (Rictpi) mRNA, complete cds

Seq. No.	400126
Seq. ID	LIB3431-030-P1-N1-A2
Method	BLASTX
NCBI GI	g115787
BLAST score	403
E value	3.0e-39
Match length	76
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	400127
Seq. ID	LIB3431-030-P1-N1-A4
Method	BLASTX
NCBI GI	g3126854
BLAST score	339
E value	1.0e-31
Match length	64
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	400128
Seq. ID	LIB3431-030-P1-N1-A5
Method	BLASTN
NCBI GI	g5922603
BLAST score	57
E value	4.0e-23
Match length	80
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No.	400129
Seq. ID	LIB3431-030-P1-N1-A6
Method	BLASTX
NCBI GI	g729478
BLAST score	323
E value	6.0e-30
Match length	73
% identity	79
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	400130
Seq. ID	LIB3431-030-P1-N1-A7

Method	BLASTN
NCBI GI	g2305114
BLAST score	321
E value	1.0e-180
Match length	400
% identity	95
NCBI Description	Oryza sativa ferredoxin mRNA, complete cds

Seq. No.	400131
Seq. ID	LIB3431-030-P1-N1-A8
Method	BLASTX
NCBI GI	g132105
BLAST score	387
E value	2.0e-37
Match length	73
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400132
Seq. ID	LIB3431-030-P1-N1-A9
Method	BLASTX
NCBI GI	g671740
BLAST score	460
E value	8.0e-46
Match length	86
% identity	99
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	400133
Seq. ID	LIB3431-030-P1-N1-B10
Method	BLASTX
NCBI GI	g2344897
BLAST score	273
E value	6.0e-24
Match length	92
% identity	58
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	400134
Seq. ID	LIB3431-030-P1-N1-B3
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No.	400135
Seq. ID	LIB3431-030-P1-N1-B4
Method	BLASTN
NCBI GI	g5734616
BLAST score	409
E value	0.0e+00
Match length	499
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No.	400136
Seq. ID	LIB3431-030-P1-N1-B5
Method	BLASTX
NCBI GI	g3345477
BLAST score	331
E value	9.0e-31
Match length	62
% identity	100
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	400137
Seq. ID	LIB3431-030-P1-N1-B7
Method	BLASTX
NCBI GI	g3510256
BLAST score	229
E value	9.0e-19
Match length	79
% identity	56
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	400138
Seq. ID	LIB3431-030-P1-N1-B8
Method	BLASTX
NCBI GI	g132105
BLAST score	207
E value	8.0e-23
Match length	56
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400139
Seq. ID	LIB3431-030-P1-N1-B9
Method	BLASTX
NCBI GI	g4115536
BLAST score	293
E value	2.0e-26
Match length	114

% identity	47
NCBI Description	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No.	400140
Seq. ID	LIB3431-030-P1-N1-C1
Method	BLASTX
NCBI GI	g3789954
BLAST score	259
E value	2.0e-22
Match length	48
% identity	98
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	400141
Seq. ID	LIB3431-030-P1-N1-C12
Method	BLASTX
NCBI GI	g2191138
BLAST score	318
E value	3.0e-29
Match length	75
% identity	79
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No.	400142
Seq. ID	LIB3431-030-P1-N1-C2
Method	BLASTN
NCBI GI	g19094
BLAST score	58
E value	5.0e-24
Match length	66
% identity	97
NCBI Description	H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No.	400143
Seq. ID	LIB3431-030-P1-N1-C4
Method	BLASTX
NCBI GI	g3914466
BLAST score	455
E value	3.0e-45
Match length	84
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN subunit precursor [Zea mays]

Seq. No.	400144
Seq. ID	LIB3431-030-P1-N1-C6
Method	BLASTX
NCBI GI	g2501190
BLAST score	155
E value	3.0e-10
Match length	51
% identity	69
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR

>gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	400145
Seq. ID	LIB3431-030-P1-N1-C8
Method	BLASTX
NCBI GI	g3776581
BLAST score	350
E value	5.0e-33
Match length	118
% identity	58
NCBI Description	(AC005388) Similar to Beta integral membrane protein homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	400146
Seq. ID	LIB3431-030-P1-N1-C9
Method	BLASTX
NCBI GI	g1184112
BLAST score	410
E value	4.0e-40
Match length	111
% identity	75
NCBI Description	(U46138) Zn-induced protein [Oryza sativa]

Seq. No.	400147
Seq. ID	LIB3431-030-P1-N1-D1
Method	BLASTX
NCBI GI	g131176
BLAST score	352
E value	2.0e-33
Match length	70
% identity	96
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No.	400148
Seq. ID	LIB3431-030-P1-N1-D10
Method	BLASTX
NCBI GI	g3126854
BLAST score	635
E value	2.0e-66
Match length	123
% identity	98
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	400149
Seq. ID	LIB3431-030-P1-N1-D11
Method	BLASTX
NCBI GI	g1488297
BLAST score	257
E value	4.0e-22

Match length	60
% identity	83
NCBI Description	(U63530) osRAD23 [Oryza sativa]

Seq. No.	400150
Seq. ID	LIB3431-030-P1-N1-D12
Method	BLASTX
NCBI GI	g461595
BLAST score	183
E value	2.0e-13
Match length	95
% identity	44
NCBI Description	ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II) >gi_479533_pir__S34473 H+-transporting ATP synthase (EC 3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520_ (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]

Seq. No.	400151
Seq. ID	LIB3431-030-P1-N1-D2
Method	BLASTX
NCBI GI	g6093830
BLAST score	164
E value	2.0e-11
Match length	50
% identity	38
NCBI Description	PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

Seq. No.	400152
Seq. ID	LIB3431-030-P1-N1-D3
Method	BLASTX
NCBI GI	g132105
BLAST score	398
E value	1.0e-38
Match length	73
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400153
Seq. ID	LIB3431-030-P1-N1-D4
Method	BLASTX
NCBI GI	g132105
BLAST score	301
E value	2.0e-27
Match length	57
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400154
Seq. ID	LIB3431-030-P1-N1-D6
Method	BLASTX
NCBI GI	g1362066
BLAST score	546
E value	6.0e-56
Match length	126
% identity	86
NCBI Description	small GTP-binding protein - garden pea >gi_871510_emb_CAA90080_ (Z49900) small GTP-binding protein [Pisum sativum]

Seq. No.	400155
Seq. ID	LIB3431-030-P1-N1-D7
Method	BLASTX
NCBI GI	g167097
BLAST score	151
E value	1.0e-20
Match length	61
% identity	87
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	400156
Seq. ID	LIB3431-030-P1-N1-D8
Method	BLASTX
NCBI GI	g4586021
BLAST score	271
E value	8.0e-24
Match length	61
% identity	77
NCBI Description	(AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Seq. No.	400157
Seq. ID	LIB3431-030-P1-N1-E1
Method	BLASTX
NCBI GI	g2493650
BLAST score	438
E value	3.0e-43
Match length	89
% identity	97
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale cereale]

Seq. No. 400158

Seq. ID	LIB3431-030-P1-N1-E12
Method	BLASTX
NCBI GI	g1709620
BLAST score	178
E value	9.0e-13
Match length	55
% identity	71
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_508975 (U11496) protein disulfide isomerase [Triticum aestivum] >gi_1094851_prf__2106410A protein disulfide isomerase [Triticum aestivum]

Seq. No.	400159
Seq. ID	LIB3431-030-P1-N1-E2
Method	BLASTX
NCBI GI	g131225
BLAST score	337
E value	2.0e-31
Match length	94
% identity	70
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	400160
Seq. ID	LIB3431-030-P1-N1-E4
Method	BLASTX
NCBI GI	g347451
BLAST score	152
E value	7.0e-10
Match length	38
% identity	79
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No.	400161
Seq. ID	LIB3431-030-P1-N1-E6
Method	BLASTX
NCBI GI	g671740
BLAST score	512
E value	6.0e-52
Match length	94
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	400162
Seq. ID	LIB3431-030-P1-N1-E8
Method	BLASTX
NCBI GI	g5802606
BLAST score	498
E value	3.0e-50
Match length	104
% identity	86
NCBI Description	(AF174486) methylenetetrahydrofolate reductase [Zea mays]

Seq. No.	400163
Seq. ID	LIB3431-030-P1-N1-E9
Method	BLASTX
NCBI GI	g3183079
BLAST score	341
E value	6.0e-32
Match length	83
% identity	78
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]

Seq. No.	400164
Seq. ID	LIB3431-030-P1-N1-F1
Method	BLASTX
NCBI GI	g1173275
BLAST score	590
E value	4.0e-61
Match length	136
% identity	90
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_2119068_pir__S58630 ribosomal protein S7 - maize chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563) ribosomal protein S7 [Zea mays]

Seq. No.	400165
Seq. ID	LIB3431-030-P1-N1-F10
Method	BLASTX
NCBI GI	g132105
BLAST score	386
E value	1.0e-47
Match length	93
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400166
Seq. ID	LIB3431-030-P1-N1-F12
Method	BLASTX
NCBI GI	g1519251
BLAST score	244
E value	1.0e-20
Match length	47
% identity	100
NCBI Description	(U65957) GF14-c protein [Oryza sativa]

Seq. No.	400167
Seq. ID	LIB3431-030-P1-N1-F2
Method	BLASTX

NCBI GI	g1587206
BLAST score	186
E value	1.0e-13
Match length	39
% identity	97
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	400168
Seq. ID	LIB3431-030-P1-N1-F4
Method	BLASTX
NCBI GI	g5053118
BLAST score	495
E value	5.0e-58
Match length	165
% identity	72
NCBI Description	(AF156695) inorganic phosphate transporter [Solanum tuberosum]

Seq. No.	400169
Seq. ID	LIB3431-030-P1-N1-F5
Method	BLASTX
NCBI GI	g2281099
BLAST score	181
E value	3.0e-13
Match length	45
% identity	76
NCBI Description	(AC002333) stearoyl-ACP desaturase [Arabidopsis thaliana]

Seq. No.	400170
Seq. ID	LIB3431-030-P1-N1-F6
Method	BLASTX
NCBI GI	g3777598
BLAST score	327
E value	2.0e-30
Match length	78
% identity	85
NCBI Description	(AF095707) 30S ribosomal protein S17 [Oryza sativa]

Seq. No.	400171
Seq. ID	LIB3431-030-P1-N1-F7
Method	BLASTX
NCBI GI	g3789952
BLAST score	230
E value	6.0e-19
Match length	44
% identity	98
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	400172
Seq. ID	LIB3431-030-P1-N1-F9
Method	BLASTX
NCBI GI	g115787
BLAST score	505
E value	4.0e-51
Match length	96
% identity	100

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No.	400173
Seq. ID	LIB3431-030-P1-N1-G1
Method	BLASTX
NCBI GI	g1084455
BLAST score	379
E value	2.0e-36
Match length	72
% identity	100
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No.	400174
Seq. ID	LIB3431-030-P1-N1-G11
Method	BLASTX
NCBI GI	g4185499
BLAST score	226
E value	2.0e-18
Match length	68
% identity	51
NCBI Description	(AF096095) fertilization-independent seed 2 protein [Arabidopsis thaliana] >gi_4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No.	400175
Seq. ID	LIB3431-030-P1-N1-G4
Method	BLASTX
NCBI GI	g3643602
BLAST score	263
E value	7.0e-23
Match length	88
% identity	57
NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	400176
Seq. ID	LIB3431-030-P1-N1-G5
Method	BLASTX
NCBI GI	g1353352
BLAST score	184
E value	1.0e-13
Match length	51
% identity	71
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	400177
Seq. ID	LIB3431-030-P1-N1-G9
Method	BLASTX
NCBI GI	g671740
BLAST score	488

E value	4.0e-49
Match length	90
% identity	99
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	400178
Seq. ID	LIB3431-030-P1-N1-H1
Method	BLASTN
NCBI GI	g1398998
BLAST score	162
E value	8.0e-86
Match length	275
% identity	97
NCBI Description	Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II, complete cds

Seq. No.	400179
Seq. ID	LIB3431-030-P1-N1-H10
Method	BLASTN
NCBI GI	g2331130
BLAST score	259
E value	1.0e-144
Match length	271
% identity	99
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No.	400180
Seq. ID	LIB3431-030-P1-N1-H2
Method	BLASTX
NCBI GI	g3036951
BLAST score	451
E value	9.0e-45
Match length	86
% identity	99
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	400181
Seq. ID	LIB3431-030-P1-N1-H3
Method	BLASTX
NCBI GI	g417260
BLAST score	303
E value	2.0e-27
Match length	77
% identity	74
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	400182
Seq. ID	LIB3431-030-P1-N1-H6
Method	BLASTX
NCBI GI	g4079798
BLAST score	301
E value	2.0e-27

Match length	61
% identity	93
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	400183
Seq. ID	LIB3431-030-P1-N1-H8
Method	BLASTN
NCBI GI	g3377792
BLAST score	269
E value	1.0e-149
Match length	399
% identity	92
NCBI Description	Oryza sativa ribulose-1,5-bisphosphate carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No.	400184
Seq. ID	LIB3431-030-P1-N1-H9
Method	BLASTX
NCBI GI	g6093827
BLAST score	156
E value	2.0e-10
Match length	61
% identity	29
NCBI Description	PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_2956690_emb_CAA11248_ (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No.	400185
Seq. ID	LIB3431-031-P1-K1-A11
Method	BLASTX
NCBI GI	g2913893
BLAST score	262
E value	8.0e-23
Match length	56
% identity	82
NCBI Description	(AB011368) LIP5 [Oryza sativa]

Seq. No.	400186
Seq. ID	LIB3431-031-P1-K1-A12
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	400187
Seq. ID	LIB3431-031-P1-K1-A2
Method	BLASTX
NCBI GI	g134595
BLAST score	236

E value	1.0e-19
Match length	71
% identity	66
NCBI Description	SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir__S22508 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic copper/zinc-superoxide dismutase [Oryza sativa] >gi_1096504_prf__2111424A Cu/Zn superoxide dismutase [Oryza sativa]

Seq. No.	400188
Seq. ID	LIB3431-031-P1-K1-A3
Method	BLASTN
NCBI GI	g19094
BLAST score	53
E value	9.0e-21
Match length	65
% identity	95
NCBI Description	H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No.	400189
Seq. ID	LIB3431-031-P1-K1-A4
Method	BLASTN
NCBI GI	g20262
BLAST score	193
E value	1.0e-104
Match length	300
% identity	100
NCBI Description	O.sativa light-induced mRNA

Seq. No.	400190
Seq. ID	LIB3431-031-P1-K1-A5
Method	BLASTX
NCBI GI	g2407281
BLAST score	641
E value	3.0e-67
Match length	120
% identity	99
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	400191
Seq. ID	LIB3431-031-P1-K1-A6
Method	BLASTX
NCBI GI	g4914452
BLAST score	420
E value	3.0e-41
Match length	127
% identity	62
NCBI Description	(AL050398) putative protein [Arabidopsis thaliana]

Seq. No.	400192
Seq. ID	LIB3431-031-P1-K1-A7
Method	BLASTX
NCBI GI	g134595
BLAST score	615

E value	4.0e-64
Match length	116
% identity	100
NCBI Description	SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir__S22508 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic copper/zinc-superoxide dismutase [Oryza sativa] >gi_1096504_prf__2111424A Cu/Zn superoxide dismutase [Oryza sativa]

Seq. No.	400193
Seq. ID	LIB3431-031-P1-K1-A8
Method	BLASTX
NCBI GI	g5903036
BLAST score	316
E value	4.0e-29
Match length	132
% identity	52
NCBI Description	(AC008016) F6D8.5 [Arabidopsis thaliana]

Seq. No.	400194
Seq. ID	LIB3431-031-P1-K1-B1
Method	BLASTX
NCBI GI	g5702231
BLAST score	195
E value	7.0e-15
Match length	110
% identity	45
NCBI Description	(AF145386) hypersensitive reaction associated Ca2+-binding protein [Phaseolus vulgaris]

Seq. No.	400195
Seq. ID	LIB3431-031-P1-K1-B10
Method	BLASTX
NCBI GI	g320618
BLAST score	285
E value	5.0e-26
Match length	62
% identity	89
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	400196
Seq. ID	LIB3431-031-P1-K1-B2
Method	BLASTX
NCBI GI	g2754849
BLAST score	254
E value	7.0e-22
Match length	56
% identity	88
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	400197
Seq. ID	LIB3431-031-P1-K1-B9
Method	BLASTN
NCBI GI	g4138289
BLAST score	177
E value	8.0e-95
Match length	281
% identity	91
NCBI Description	Oryza sativa mRNA for thioredoxin M

Seq. No.	400198
Seq. ID	LIB3431-031-P1-K1-C1
Method	BLASTX
NCBI GI	g228403
BLAST score	655
E value	8.0e-69
Match length	145
% identity	89
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	400199
Seq. ID	LIB3431-031-P1-K1-C12
Method	BLASTX
NCBI GI	g132105
BLAST score	577
E value	1.0e-59
Match length	124
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400200
Seq. ID	LIB3431-031-P1-K1-C2
Method	BLASTX
NCBI GI	g320618
BLAST score	536
E value	7.0e-55
Match length	118
% identity	86
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	400201
Seq. ID	LIB3431-031-P1-K1-C3
Method	BLASTX
NCBI GI	g2072555
BLAST score	237

E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No.	400202
Seq. ID	LIB3431-031-P1-K1-C4
Method	BLASTX
NCBI GI	g132105
BLAST score	512
E value	5.0e-52
Match length	110
% identity	85
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	400203
Seq. ID	LIB3431-031-P1-K1-C7
Method	BLASTN
NCBI GI	g2780342
BLAST score	102
E value	1.0e-50
Match length	102
% identity	100
NCBI Description	Oryza sativa gene for PBZ1, complete cds >gi_3251321_dbj_E12488_E12488 Nucleotide sequence of Oryza sativa PBZ1 gene

Seq. No.	400204
Seq. ID	LIB3431-031-P1-K1-C8
Method	BLASTX
NCBI GI	g3660469
BLAST score	608
E value	3.0e-63
Match length	132
% identity	90
NCBI Description	(AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No.	400205
Seq. ID	LIB3431-031-P1-K1-D1
Method	BLASTN
NCBI GI	g3126853
BLAST score	47
E value	1.0e-17
Match length	63
% identity	94

NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	400206
Seq. ID	LIB3431-031-P1-K1-D10
Method	BLASTX
NCBI GI	g1658315
BLAST score	580
E value	5.0e-60
Match length	134
% identity	76
NCBI Description	(Y08988) osr40g3 [Oryza sativa]

Seq. No.	400207
Seq. ID	LIB3431-031-P1-K1-D8
Method	BLASTX
NCBI GI	g131225
BLAST score	607
E value	3.0e-63
Match length	128
% identity	92
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	400208
Seq. ID	LIB3431-031-P1-K1-E11
Method	BLASTX
NCBI GI	g1296955
BLAST score	596
E value	6.0e-62
Match length	134
% identity	38
NCBI Description	(X95402) duplicated domain structure protein [Oryza sativa]

Seq. No.	400209
Seq. ID	LIB3431-031-P1-K1-E12
Method	BLASTX
NCBI GI	g986969
BLAST score	318
E value	3.0e-29
Match length	127
% identity	51
NCBI Description	(L28005) TGACG-motif-binding protein [Glycine max]

Seq. No.	400210
Seq. ID	LIB3431-031-P1-K1-E4
Method	BLASTX
NCBI GI	g3126854
BLAST score	686
E value	2.0e-72
Match length	128
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]